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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: *Corynebacterium Glutamicum* Genes Encoding Metabolic Pathway Proteins

Enclosed are:

- ☒ 59 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 22 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 31 pages of Table 4;
- ☒ 199 pages of Appendix A;
- ☒ 63 pages of Appendix B;
- ☒ 1,536 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney;
- ☒ A pre-paid acknowledgment postcard.

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- ☒ Address all future communications (May only be completed by applicant, or attorney or agent of record) to **Elizabeth A. Hanley, Esq. at Customer Number: 000959** whose address is:

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC
PATHWAY PROTEINS**

Related Applications

- The present application claims priority to prior filed U.S. Provisional Patent
- 5 Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent
Application Serial No. 60/142101, filed July 2, 1999, U.S. Provisional Patent
Application Serial No. 60/148613, filed August 12, 1999, and also to U.S. Provisional
Patent Application Serial No. 60/187970, filed March 9, 2000. The present application
also claims priority to prior filed German Patent Application No. 19930476.9, filed July
- 10 1, 1999, German Patent Application No. 19931415.2, filed July 8, 1999, German Patent
Application No. 19931418.7, filed July 8, 1999, German Patent Application No.
19931419.5, filed July 8, 1999, German Patent Application No. 19931420.9, filed July
8, 1999, German Patent Application No. 19931424.1, filed July 8, 1999, German Patent
Application No. 19931428.4, filed July 8, 1999, German Patent Application No.
- 15 19931434.9, filed July 8, 1999, German Patent Application No. 19931435.7, filed July
8, 1999, German Patent Application No. 19931443.8, filed July 8, 1999, German Patent
Application No. 19931453.5, filed July 8, 1999, German Patent Application No.
19931457.8, filed July 8, 1999, German Patent Application No. 19931465.9, filed July
8, 1999, German Patent Application No. 19931478.0, filed July 8, 1999, German Patent
- 20 Application No. 19931510.8, filed July 8, 1999, German Patent Application No.
19931541.8, filed July 8, 1999, German Patent Application No. 19931573.6, filed July
8, 1999, German Patent Application No. 19931592.2, filed July 8, 1999, German Patent
Application No. 19931632.5, filed July 8, 1999, German Patent Application No.
19931634.1, filed July 8, 1999, German Patent Application No. 19931636.8, filed July
- 25 8, 1999, German Patent Application No. 19932125.6, filed July 9, 1999, German Patent
Application No. 19932126.4, filed July 9, 1999, German Patent Application No.
19932130.2, filed July 9, 1999, German Patent Application No. 19932186.8, filed July
9, 1999, German Patent Application No. 19932206.6, filed July 9, 1999, German Patent
Application No. 19932227.9, filed July 9, 1999, German Patent Application No.
- 30 19932228.7, filed July 9, 1999, German Patent Application No. 19932229.5, filed July
9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent
Application No. 19932922.2, filed July 14, 1999, German Patent Application No.
19932926.5, filed July 14, 1999, German Patent Application No. 19932928.1, filed July
14, 1999, German Patent Application No. 19933004.2, filed July 14, 1999, German
- 35 Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No.
19933006.9, filed July 14, 1999, German Patent Application No. 19940764.9, filed
August 27, 1999, German Patent Application No. 19940765.7, filed August 27, 1999,

German Patent Application No. 19940766.5, filed August 27, 1999, German Patent Application No. 19940832.7, filed August 27, 1999, German Patent Application No. 19941378.9, filed August 31, 1999, German Patent Application No. 19941379.7, filed August 31, 1999, German Patent Application No. 19941380.0, filed August 31, 1999, German Patent Application No. 19941394.0, filed August 31, 1999, German Patent Application No. 19941396.7, filed August 31, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942124.2, filed September 3, 1999, and German Patent Application No. 19942129.3, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for

transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The MP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules

of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine biosynthetic pathway protein or decreasing the activity of a lysine degradative pathway protein may result in an increase in the yield or efficiency of production of lysine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, a vitamin, or a nucleotide may increase the overall ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.

The nucleic acid and protein molecules of the invention may be utilized to directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and

necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MP), which are capable of, for example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules. In a preferred embodiment, the MP protein performs an enzymatic step related to the metabolism of one or more of the following: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to catalyze a reaction in a metabolic pathway for an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a

nucleic acid molecule of the invention encoding wild-type or mutated MP sequence as a transgene. In another embodiment, an endogenous MP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MP gene. In another embodiment, an endogenous or
5 introduced MP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is
10 modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

15 In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

20 Still another aspect of the invention pertains to an isolated MP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment,
25 the isolated MP protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

30 The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another
35 embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of

Appendix B. In other embodiments, the isolated MP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

agent which modulates MP protein activity or MP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression. Examples of agents which stimulate MP protein activity or MP nucleic acid expression include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules, and antisense MP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis protein has a direct impact on the production or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase of yield or efficiency of production of the desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include

5 organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty

10 acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids,

15 Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN:

20 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are

25 essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

30 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids

35 (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways

to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

5 Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly
10 used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-
15 methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others
20 described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

 The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev.*
25 *Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both
30 cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transfer of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step
35 biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction

catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is
5 formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation
10 and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own
15 production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

20 *B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses*

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active
25 substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry,
30 "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to
35 occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such

molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthanol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the

metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

- 5 The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.
- 10

- The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.
- 15

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

- Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).
- 20
- 25
- 30

- Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the
- 35

development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.

Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from
 5 which it can be collected using methods known in the art.

II. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MP nucleic acid and protein molecules, which play a
 10 role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways. In a preferred embodiment, the activity of the MP molecules of the present invention in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins,
 15 cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly
 20 modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, “MP protein” or “MP polypeptide” includes proteins which play a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways.
 25 Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and Appendix A. The terms “MP gene” or “MP nucleic acid sequence” include nucleic acid sequences encoding an MP protein, which consist of a coding region and also corresponding untranslated 5’ and 3’ sequence regions. Examples of MP genes include those set forth in Table 1. The terms “production” or “productivity” are art-recognized
 30 and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term “efficiency of production” includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term “yield” or
 35 “product/carbon yield” is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the

compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms “biosynthesis” or a “biosynthetic pathway” are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms “degradation” or a “degradation pathway” are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language “metabolism” is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins,

may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

- 5 The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MP DNAs and the predicted amino acid sequences of the *C. glutamicum* MP proteins are shown in Appendices A and B, respectively.
- 10 Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway proteins.

- The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially
- 15 homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at
- 20 least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

- The MP protein or a biologically active portion or fragment thereof of the invention can catalyze an enzymatic reaction in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have
- 25 one or more of the activities set forth in Table 1.

 Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

- 30 One aspect of the invention pertains to isolated nucleic acid molecules that encode MP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MP-encoding nucleic acid (*e.g.*, MP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic
- 35 DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides

of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated
5 from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP nucleic acid molecule can contain less than about
10 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other
15 chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MP DNA can be isolated from a *C. glutamicum* library
20 using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences
25 of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal
30 endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction
35 amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers

according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

5 In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* MP DNAs of the invention. This DNA comprises sequences encoding MP proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences
10 and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, RXS, or RXC
15 number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA00007, RXN00023, RXS00116, or RXC00128). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the sequences in Appendix
20 A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, RXS, or RXC designations as Appendix A, such that they can be readily
25 correlated. For example, the amino acid sequences in Appendix B designated RXA02229, RX00351, RXS02970, and RXC02390 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA02229, RX00351, RXS02970, and RXC02390, respectively, in Appendix A. Each of the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention has also been
30 assigned a SEQ ID NO, as indicated in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:5, designated, as indicated
on Table 1, as "F RXA01009", is an F-designated gene, as are SEQ ID NOs: 73, 75, and
35 77 (designated on Table 1 as "F RXA00007", "F RXA00364", and "F RXA00367", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include *C. glutamicum* those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MP homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The

oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in

5 Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone MP homologues. Probes based on the MP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred
10 embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MP protein, such as by measuring a level of an MP-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

15 In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used
20 herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to catalyze an
25 enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described
30 herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set forth in Table 1.

35 In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same MP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00115 (SEQ ID NO:185), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00131 (SEQ ID NO:991), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence

designated RXA00219 (SEQ ID NO:345). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest

5 GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%,

10 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MP nucleotide sequences shown in Appendix A, it will be appreciated by one of ordinary skill in the art that DNA sequence

15 polymorphisms that lead to changes in the amino acid sequences of MP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MP protein,

20 preferably a *C. glutamicum* MP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MP that are the result of natural variation and that do not alter the functional activity of MP proteins are intended to be within the scope of the invention.

25 Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

30 another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for

35 hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even

more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to one of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent

5 hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule

10 refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

In addition to naturally-occurring variants of the MP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be

15 introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MP protein, without altering the functional ability of the MP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be

20 altered from the wild-type sequence of one of the MP proteins (Appendix B) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MP

25 activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential for MP activity. Such MP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MP activities described herein. In

30 one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more activities set forth in

35 Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more

preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify

mutants that retain MP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

- 5 In addition to the nucleic acid molecules encoding MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA
- 10 sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MP protein. The term "coding region" refers to the region of the nucleotide sequence
- 15 comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXA02229) comprises nucleotides 1 to 825). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into
- 20 amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

- Given the coding strand sequences encoding MP disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MP mRNA, but
- 25 more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed
- 30 using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic
- 35 acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil,

hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes
5 (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO: 1 (RXA02229 in Appendix A). For example, a derivative of a *Tetrahymena* L-19 IVS
10 RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and
15 Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer*
20 *Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof). As
25 used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
30 autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
35 which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can

be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

5 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant
10 expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory
15 sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide
20 sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such
25 as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein
30 desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MP proteins, mutant forms of MP proteins, fusion proteins, etc.).

 The recombinant expression vectors of the invention can be designed for
35 expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992)

- “Foreign gene expression in yeast: a review”, *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) “Heterologous gene expression in filamentous fungi” in: *More Gene Manipulations in Fungi*, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) “Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of Fungi*, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants” *Plant Cell Rep.*: 583-586), or mammalian cells.
- 10 Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

- Expression of proteins in prokaryotes is most often carried out with vectors
- 15 containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the
- 20 solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their
- 25 cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant
- 30 protein. In one embodiment, the coding sequence of the MP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion
- 35 protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18,

pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

- 5 Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7
- 10 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into
- 15 *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

- One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in*
- 20 *Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid
 - 25 sequences of the invention can be carried out by standard DNA synthesis techniques.

- In another embodiment, the MP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), , 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987)
- 30 *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge
 - 35 University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the MP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (e.g., the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and

European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

- 5 The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MP mRNA. Regulatory sequences operatively
- 10 linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid
- 15 or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.
- 20 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due
- 25 to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or

30 mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via

35 conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*,

linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural
5 competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the
10 expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418,
15 hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

20 To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a
25 preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a “knock out” vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the
30 upstream regulatory region can be altered to thereby alter the expression of the endogenous MP protein). In the homologous recombination vector, the altered portion of the MP gene is flanked at its 5’ and 3’ ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional
35 flanking MP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5’ and 3’ ends) are included in the vector (see *e.g.*, Thomas, K.R., and

Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the endogenous MP gene are selected, using art-known techniques.

5 In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MP gene on a vector placing it under control of the lac operon permits expression of the MP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

10 In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still
15 another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MP gene and protein modifications may be readily
20 produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MP protein. Accordingly, the invention further provides methods for producing MP proteins using the host cells of the
25 invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or
30 the host cell.

C. Isolated MP Proteins

Another aspect of the invention pertains to isolated MP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion
35 thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MP

protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a

5 "contaminating protein"), more preferably less than about 20% of non-MP protein, still more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about

10 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one

15 embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein having less than about 30% (by dry weight) of chemical precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins

20 or biologically active portions thereof lack contaminating proteins from the same organism from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

An isolated MP protein or a portion thereof of the invention can catalyze an

25 enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to catalyze an enzymatic

30 reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MP protein has an amino acid sequence which is encoded by

35 a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at

least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%,
5 and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the
10 above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of
15 Appendix A, and which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of
20 the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or
25 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the MP activities described herein. Ranges and identity values intermediate to the
30 above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid
35 sequence of Appendix B.

Biologically active portions of an MP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MP protein, e.g., the an

amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an MP protein, which include fewer amino acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

The invention also provides MP chimeric or fusion proteins. As used herein, an MP "chimeric protein" or "fusion protein" comprises an MP polypeptide operatively linked to a non-MP polypeptide. An "MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to MP, whereas a "non-MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MP protein, *e.g.*, a protein which is different from the MP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MP polypeptide and the non-MP polypeptide are fused in-frame to each other. The non-MP polypeptide can be fused to the N-terminus or C-terminus of the MP polypeptide. For example, in one embodiment the fusion protein is a GST-MP fusion protein in which the MP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MP proteins. In another embodiment, the fusion protein is an MP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MP protein can be increased through use of a heterologous signal sequence.

Preferably, an MP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
5 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-
15 encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue" refers to a variant form of the MP protein which acts as an agonist or antagonist of the
20 activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum*
25 MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

In an alternative embodiment, homologues of the MP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP
30 protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MP
35 sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP

homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MP protein regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

- 10 The MP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the
- 15 extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*.
- 20 *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the
- 25 inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at
- 30 least 5,000 deaths since 1990.

- In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the
- 35 presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules

in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MP nucleic acid molecules of the invention may result in the production of MP proteins having functional differences from the wild-type MP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MP proteins of the invention is contacted with one or more test

compounds, and the effect of each test compound on the activity or level of expression of the MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned compounds, the modulation of activity of one of the proteins of the invention may still impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of

other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification**Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032**

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA
- 35 prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*,

- Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction

endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if

necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

- Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can
- 5 be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or
- 10 NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the microorganisms, the pH can also be controlled using gaseous ammonia.

- The incubation time is usually in a range from several hours to several days. This
- 15 time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably
- 20 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

- 25 If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract,
- 30 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

- 35 The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well

within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979)

- 5 Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.
- 10

- 15 The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as
- 20 beta-galactosidase, green fluorescent protein, and several others.

- 25 The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

25 **Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

- 30 The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical
- 35 chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in:

- Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)
- 10 In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons,
- 15 nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192
- 20 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art.
- 25 If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*
- 30 cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

- The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the
- 35 impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate

chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

20 **Example 11: Analysis of the Gene Sequences of the Invention**

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN
5 program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

- 10 The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the
15 GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

- A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a
20 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
25 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
30 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment

homology percentages set forth in Table 4 under the heading “% homology (GAP)” are listed in the European numerical format, wherein a ‘,’ represents a decimal point. For example, a value of “40,345” in this column represents “40.345%”.

5 **Example 12: Construction and Operation of DNA Microarrays**

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367;
 10 DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic
 15 acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
 20 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
 25 and design of the 5’ or 3’ oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
 30 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
 35 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or
5 fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as
10 described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations
15 based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

20

**Example 13: Analysis of the Dynamics of Cellular Protein Populations
(Proteomics)**

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein
25 populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing
35 polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the

consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway protein is selected from the group consisting of proteins involved in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
- 5 9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of claim 1.
- 10 11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
- 15 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
- 15 15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
- 20 16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
- 25 17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 30 18. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 35 19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 5 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 15 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 20 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 30 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 35 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.
- 5 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.
- 10 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC
PATHWAY PROTEINS**

Abstract of the Disclosure

5

Isolated nucleic acid molecules, designated MP nucleic acid molecules, which
encode novel MP proteins from *Corynebacterium glutamicum* are described. The
invention also provides antisense nucleic acid molecules, recombinant expression
vectors containing MP nucleic acid molecules, and host cells into which the expression
10 vectors have been introduced. The invention still further provides isolated MP proteins,
mutated MP proteins, fusion proteins, antigenic peptides and methods for the
improvement of production of a desired compound from *C. glutamicum* based on
genetic engineering of MP genes in this organism.

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**Attorney's
Docket
Number BGI-121CP**

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

Corynebacterium Glutamicum Genes Encoding Metabolic Pathway Proteins
the specification of which

(check one)

X is attached hereto.

was filed on _____ as _____

Application Serial No. _____

and was amended on _____
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☐ no such applications have been filed.

☒ such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19930476.9	07/01/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931415.2	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931418.7	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931419.5	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931420.9	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931424.1	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931428.4	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931434.9	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931435.7	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931443.8	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931453.5	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931457.8	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931465.9	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931478.0	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931510.8	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931541.8	07/08/00	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931573.6	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931592.2	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>

DE	19931632.5	07/08/99	<u>X</u> Yes	No _
DE	19931634.1	07/08/99	<u>X</u> Yes	No _
DE	19931636.8	07/08/99	<u>X</u> Yes	No _
DE	19932125.6	07/09/99	<u>X</u> Yes	No _
DE	19932126.4	07/09/99	<u>X</u> Yes	No _
DE	19932130.2	07/09/99	<u>X</u> Yes	No _
DE	19932186.8	07/09/99	<u>X</u> Yes	No _
DE	19932206.6	07/09/99	<u>X</u> Yes	No _
DE	19932227.9	07/09/99	<u>X</u> Yes	No _
DE	19932228.7	07/09/99	<u>X</u> Yes	No _
DE	19932229.5	07/09/99	<u>X</u> Yes	No _
DE	19932230.9	07/09/99	<u>X</u> Yes	No _
DE	19932922.2	07/14/99	<u>X</u> Yes	No _
DE	19932926.5	07/14/99	<u>X</u> Yes	No _
DE	19932928.1	07/14/99	<u>X</u> Yes	No _
DE	19933004.2	07/14/99	<u>X</u> Yes	No _
DE	19933005.0	07/14/99	<u>X</u> Yes	No _
DE	19933006.9	07/14/99	<u>X</u> Yes	No _
DE	19940764.9	08/27/99	<u>X</u> Yes	No _
DE	19940765.7	08/27/99	<u>X</u> Yes	No _
DE	19940766.5	08/27/99	<u>X</u> Yes	No _
DE	19940832.7	08/27/99	<u>X</u> Yes	No _
DE	19941378.9	08/31/99	<u>X</u> Yes	No _
DE	19941379.7	08/31/99	<u>X</u> Yes	No _
DE	19941380.0	08/31/99	<u>X</u> Yes	No _
DE	19941394.0	08/31/99	<u>X</u> Yes	No _
DE	19941396.7	08/31/99	<u>X</u> Yes	No _
DE	19942076.9	09/03/99	<u>X</u> Yes	No _
DE	19942077.7	09/03/99	<u>X</u> Yes	No _

DE	19942079.3	09/03/99	<u>X</u> Yes	No _
DE	19942086.6	09/03/99	<u>X</u> Yes	No _
DE	19942087.4	09/03/99	<u>X</u> Yes	No _
DE	19942088.2	09/03/99	<u>X</u> Yes	No _
DE	19942095.5	09/03/99	<u>X</u> Yes	No _
DE	19942124.2	09/03/99	<u>X</u> Yes	No _
DE	19942129.3	09/03/99	<u>X</u> Yes	No _

**ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

<u>60/141,031</u>	<u>June 25, 1999</u>
(Application Serial No.)	(Filing Date)

<u>60/142,101</u>	<u>July 2, 1999</u>
(Application Serial No.)	(Filing Date)

<u>60/148,613</u>	<u>August 12, 1999</u>
(Application Serial No.)	(Filing Date)

<u>60/187,970</u>	<u>March 9, 2000</u>
(Application Serial No.)	(Filing Date)

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

 (Application Serial No.)

 (Filing Date)

 (Status)
 (patented,pending,aband.)

 (Application Serial No.)

 (Filing Date)

 (Status)
 (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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TABLE 1: Included Genes

Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
1	2	RXA02229	GR00653	2793	3617	DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7)
3	4	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
5	6	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
7	8	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
9	10	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
11	12	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
13	14	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
15	16	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

Trehalose

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
17	18	RXN00351	VW0135	37078	38532	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
19	20	F RXA00351	GR00066	1486	2931	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
21	22	RXA00873	GR00241	3	758	trehalose synthase (EC 2.4.1.-)
23	24	RXA00891	GR00243	1005	4	trehalose synthase (EC 2.4.1.-)

Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
25	26	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
27	28	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
29	30	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
31	32	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18)
33	34	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
35	36	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
37	38	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
39	40	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
41	42	RXN00355	VW0135	31980	30961	MESO-DIAMINOPIMELATE D-DEHYDROGENASE
43	44	F RXA00352	GR00068	861	4	MESO-DIAMINOPIMELATE D-DEHYDROGENASE (EC 1.4.1.16)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
45	46	RXA00972	GR00274	3	1379	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA02653	GR00752	5237	7234	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
49	50	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
51	52	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
53	54	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
55	56	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
57	58	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
59	60	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
61	62	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
65	66	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
67	68	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
69	70	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

Glutamate and glutamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
71	72	RXN00367	VW0196	9744	14273	GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14)
73	74	F RXA00007	GR00001	7107	8912	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
75	76	F RXA00364	GR00074	1296	4	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
77	78	F RXA00367	GR00075	1806	964	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
79	80	RXN00076	VW0154	2752	4122	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
81	82	F RXA00075	GR00012	2757	3419	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
83	84	RXN00198	VW0181	7916	7368	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
85	86	F RXA00198	GR00031	2	283	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
87	88	RXN00365	VW0196	14607	15233	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
89	90	F RXA00365	GR00075	630	4	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
91	92	RXA00366	GR00075	961	605	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
93	94	RXA02072	GR00628	1259	2599	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4)
95	96	RXA00323	GR00057	3855	5192	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
97	98	RXA00335	GR00057	19180	17750	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
99	100	RXA00324	GR00057	5262	8396	GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (EC 2.7.7.42)
101	102	RXN03176	VW0332	2	862	GLUTAMINASE (EC 3.5.1.2)
103	104	F RXA02879	GR10017	2	862	GLUTAMINASE (EC 3.5.1.2)
105	106	RXA00278	GR00043	2612	1581	GLUTAMINE-BINDING PROTEIN PRECURSOR
107	108	RXA00727	GR00193	614	1525	GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Alanine and Aspartate and Asparagine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
109	110	RXA02139	GR00639	6739	4901	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
111	112	RXN00116	W0100	26974	25814	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
113	114	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
115	116	RXN00618	W0135	10288	9182	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
117	118	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
119	120	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
121	122	RXA02550	GR00729	1585	275	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
123	124	RXA02193	GR00645	1942	365	ASPARTATE AMONIA-LYASE (EC 4.3.1.1)
125	126	RXA02432	GR00708	2669	1695	L-ASPARAGINASE (EC 3.5.1.1)
127	128	RXN03003	W0138	680	6	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
129	130	RXN00508	W0086	4701	5783	ALANINE RACEMASE (EC 5.1.1.1)
131	132	RXN00636	W0135	20972	19944	ALANINE RACEMASE, BIOSYNTHETIC (EC 5.1.1.1)

beta-Alanine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
133	134	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
135	136	RXS00870				METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
137	138	RXS02299				ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)

Glycine and serine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
139	140	RXA01561	GR00435	1113	2042	L-SERINE DEHYDRATASE (EC 4.2.1.13)
141	142	RXA01850	GR00525	481	1827	L-SERINE DEHYDRATASE (EC 4.2.1.13)
143	144	RXA00580	GR00156	7343	6042	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
145	146	RXA01821	GR00515	10253	9876	SARCOSINE OXIDASE (EC 1.5.3.1)
147	148	RXN02263	W0202	11783	12160	SARCOSINE OXIDASE (EC 1.5.3.1)
149	150	F RXA02263	GR00654	33454	33813	SARCOSINE OXIDASE (EC 1.5.3.1)
151	152	RXA02176	GR00641	11454	12581	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
153	154	RXN02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
155	156	F RXA02479	GR00717	393	4	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
157	158	F RXA02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
159	160	F RXA02759	GR00766	5330	5220	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
161	162	RXA02501	GR00720	15041	13977	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
163	164	RXN03105	W0074	15857	15423	SARCOSINE OXIDASE (EC 1.5.3.1)
165	166	RXS01130				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
167	168	RXS03112				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)

Threonine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
169	170	RXN00969	VW0149	12053	13387	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
171	172	F RXA00974	GR00274	2623	3015	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
173	174	RXA00970	GR00273	161	1087	HOMOSERINE KINASE (EC 2.7.1.39)
175	176	RXA00330	GR00057	12968	14410	THREONINE SYNTHASE (EC 4.2.99.2)
177	178	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
179	180	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
181	182	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
183	184	RXC00152				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN THREONINE METABOLISM

Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
187	188	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
189	190	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
191	192	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
193	194	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
195	196	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
197	198	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
199	200	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
201	202	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
203	204	RXN00402	VW0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
205	206	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
207	208	RXA00405	GR00089	3289	3801	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
209	210	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
211	212	RXN02198	VW0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
213	214	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
215	216	RXN03074	VW0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
217	218	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
219	220	RXN00132	VW0124	3612	5045	ADENOSYLMHOMOCYSTEINASE (EC 3.3.1.1)
221	222	F RXA00132	GR00020	7728	7624	ADENOSYLMHOMOCYSTEINASE (EC 3.3.1.1)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
223	224	F RXA01371	GR00398	2339	3634	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
225	226	RXN02085				5-METHYLTRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
227	228	F RXA02085	GR00629	3496	5295	5-METHYLTRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
229	230	F RXA02086	GR00629	5252	5731	5-METHYLTRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
231	232	RXN02648				5-METHYLTRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
233	234	F RXA02648	GR00751	5254	4730	5-METHYLTRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
235	236	F RXA02658	GR00752	14764	15447	5-METHYLTRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
237	238	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES
						AND PANTOTHENATE
239	240	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDIMES AND
						ADENOSYLMETHIONINE

S-adenosyl methionine (SAM) Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
241	242	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

Cysteine metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243	244	RXA00780	GR00206	1689	2234	SERINE ACETYLTRANSFERASE (EC 2.3.1.30)
245	246	RXA00779	GR00206	550	1482	CYSTEINE SYNTHASE (EC 4.2.99.8)
247	248	RXN00402	VV0086	70787	70188	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
249	250	F RXA00402	GR00088	1	576	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
251	252	RXS00405				O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
253	254	RXC00164				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM
255	256	RXC01191				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM

Valine, leucine and isoleucine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
257	258	RXA02646	GR00751	3856	2588	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16)
259	260	RXA00766	GR00204	5091	4249	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
261	262	RXN01690	VV0246	1296	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
263	264	F RXA01690	GR00473	1248	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
265	266	RXN01026	VV0143	9171	7513	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
267	268	F RXA01026	GR00294	1	1602	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
269	270	RXN01127	VV0157	4491	3472	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
271	272	F RXA01132	GR00315	1349	1651	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
273	274	RXN00536	VV0219	6128	7498	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
275	276	F RXA00536	GR00137	6128	7360	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.1)
277	278	RXN02965	VV0143	7711	7121	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
279	280	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
281	282	F RXA01929	GR00555	2766	1960	/ DECARBOXYLASE (EC 4.1.1.44)
283	284	RXN01420	VV0122	15584	14643	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
285	286	RXS01145				4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.-.-.-)
287	288	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
						KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)

Arginine and proline metabolism

Enzymes of proline biosynthesis:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXA02375	GR00689	1449	223	GLUTAMATE 5-KINASE (EC 2.7.2.11)
291	292	RXN02382	VV0213	5162	3867	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
293	294	F RXA02378	GR00690	624	16	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
295	296	F RXA02382	GR00691	2493	1894	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
297	298	RXA02499	GR00720	11883	12692	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
299	300	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
301	302	RXS02262				ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
303	304	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
305	306	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Enzymes of proline degradation:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
307	308	RXN00023	VW0127	68158	64703	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
309	310	F RXA00023	GR00003	2	454	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
311	312	F RXA02284	GR00660	3028	5	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
313	314	RXC02498				PROTEIN INVOLVED IN PROLINE METABOLISM

Synthesis of 3-Hydroxy-proline:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXA01491	GR00423	5337	4687	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS

Enzymes of ornithine, arginine and spermidine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
317	318	RXA02155	GR00640	1913	3076	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) / AMINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1)
319	320	RXA02156	GR00640	3125	4075	ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
321	322	RXN02153	VW0122	14106	13327	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
323	324	F RXA02153	GR00640	757	1536	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
325	326	RXA02154	GR00640	1536	1826	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
327	328	RXA02157	GR00640	4079	5251	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
329	330	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
331	332	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.1.3.3)
333	334	RXA02158	GR00640	5268	6224	ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3)
335	336	RXA02160	GR00640	6914	8116	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)
337	338	RXN02162	VW0122	6683	5253	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
339	340	F RXA02161	GR00640	8180	8962	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
341	342	F RXA02162	GR00640	8949	9611	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
343	344	RXA02262	GR00654	32291	33436	ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
345	346	RXA00219	GR00032	19289	20230	SPERMIDINE SYNTHASE (EC 2.5.1.16)
347	348	RXA01508	GR00424	12652	14190	SPERMIDINE SYNTHASE (EC 2.5.1.16)
349	350	RXA01757	GR00498	2942	2142	PUTRESCINE OXIDASE (EC 1.4.3.10)
351	352	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
353	354	RXN02154	VW0122	13327	13037	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
355	356	RXS00147				CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
357	358	RXS00905				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
359	360	RXS00906				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
361	362	RXS00907				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
363	364	RXS02001				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
365	366	RXS02101				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
367	368	RXS02234				CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
369	370	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
371	372	RXS02565				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
373	374	RXS02937				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Histidine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
375	376	RXA02194	GR00645	2897	2055	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
377	378	RXA02195	GR00645	3186	2917	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (EC 3.6.1.31)
379	380	RXA01097	GR00306	4726	4373	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19)
381	382	RXA01100	GR00306	7072	6335	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE (EC 5.3.1.16)
383	384	RXA01101	GR00306	7726	7094	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
385	386	RXN01657	VV0010	39550	39351	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
387	388	F RXA01657	GR00460	2444	2944	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
389	390	RXA01098	GR00306	5499	4726	HISF PROTEIN
391	392	RXN01104	VV0059	7037	6432	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
393	394	F RXA01104	GR00306	10927	10322	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) / HISTIDINOL-PHOSPHATASE (EC 3.1.3.15)
395	396	RXN00446	VV0112	24181	23318	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
397	398	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
399	400	RXA01105	GR00306	12044	10947	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
401	402	RXA01106	GR00306	13378	12053	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
403	404	RXC00930				PROTEIN INVOLVED IN HISTIDINE METABOLISM
405	406	RXC01096				PROTEIN INVOLVED IN HISTIDINE METABOLISM
407	408	RXC01656				PROTEIN INVOLVED IN HISTIDINE METABOLISM
409	410	RXC01158				MEMBRANE SPANNING PROTEIN INVOLVED IN HISTIDINE METABOLISM

Metabolism of aromatic amino acids

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
411	412	RXA02458	GR00712	3056	4345	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
413	414	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
415	416	RXN00954	VV0247	3197	2577	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
417	418	F RXA00954	GR00263	3	590	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
419	420	RXN00957	VV0208	1211	2764	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
421	422	F RXA00957	GR00264	3	1130	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
423	424	RXA02687	GR00754	11306	12250	CHORISMATE MUTASE (EC 5.4.99.5) / PREPHENATE DEHYDRATASE (EC 4.2.1.51)
425	426	RXN01698	VW0134	11507	12736	CHORISMATE SYNTHASE (EC 4.6.1.4)
427	428	F RXA01698	GR00477	2	991	CHORISMATE SYNTHASE (EC 4.6.1.4)
429	430	RXA01095	GR00306	3603	2821	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
431	432	RXA00955	GR00263	586	2007	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) / N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
433	434	RXA02814	GR00795	598	128	ISOCHORISMATE MUTASE
435	436	RXA00229	GR00033	1715	936	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.125)
437	438	RXA02093	GR00629	12444	13247	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.125)
439	440	RXA02791	GR00777	6968	7795	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.125)
441	442	RXA01699	GR00477	984	1553	SHIKIMATE KINASE (EC 2.7.1.71)
443	444	RXA00952	GR00262	97	936	TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
445	446	RXN00956	VW0247	1140	4	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
447	448	F RXA00956	GR00263	2027	3157	TYROSINE AMINOTRANSFERASE (EC 2.6.1.5)
449	450	RXA00064	GR00010	2499	3776	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
451	452	RXN00448	VW0112	33959	32940	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
453	454	F RXA00448	GR00109	854	668	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
455	456	RXA00452	GR00110	854	1099	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
457	458	RXA00584	GR00156	11384	10260	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
459	460	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
461	462	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
463	464	RXN03007	VW0208	3410	3778	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
465	466	RXN02918	VW0086	25447	25887	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
467	468	RXN01116	VW0182	7497	6886	3-OXOADIPATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.6)
469	470	RXN01115	VW0182	10347	11099	3-OXOADIPATE ENOL-LACTONE HYDROLASE (EC 3.1.1.24) / 4-CARBOXYMUCONOLACTONE
471	472	RXS00116				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
473	474	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
475	476	RXS00391				O-SUCCINYL-BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
477	478	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.5.-)
479	480	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.5.-)
481	482	RXS00446				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
483	484	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
485	486	RXS00618				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
487	488	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
489	490	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
491	492	RXS01105				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
493	494	RXS02315				2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE / 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
495	496	RXS02550				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
497	498	RXS02319				NAPHTHOATE SYNTHASE (EC 4.1.3.36)
499	500	RXS02908				O-SUCCINYL-BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
501	502	RXS03003				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
503	504	RXS03026				3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
505	506	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
507	508	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN
509	510	RXC02080				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
511	512	RXC02789				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
513	514	RXC02295				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS

Aminobutyrate metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
515	516	RXN03063	VV0035	666	1697	4-aminobutyrate aminotransferase (EC 2.6.1.19)
517	518	RXN02970	VV0021	4714	6081	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
519	520	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Vitamins, vitamin-like substances (cofactors), nutraceuticals

Thiamine metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
521	522	RXA01551	GR00431	2945	4819	THIAMIN BIOSYNTHESIS PROTEIN THIC
523	524	RXA01019	GR00291	6	995	THIAMIN-MONOPHOSPHATE KINASE (EC 2.7.4.16)
525	526	RXA01352	GR00393	609	4	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
527	528	RXA01381	GR00403	3206	2286	THIF PROTEIN
529	530	RXA01360	GR00394	162	4	THIG PROTEIN
531	532	RXA01361	GR00394	983	378	THIG PROTEIN
533	534	RXA01208	GR00348	229	1032	HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
535	536	RXA00838	GR00227	1532	633	APBA PROTEIN
537	538	RXA02400	GR00699	1988	2557	THIAMIN BIOSYNTHESIS PROTEIN X
539	540	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
541	542	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
543	544	RXN01413	VV0050	27306	27905	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
545	546	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
547	548	F RXA01617	GR00451	2	616	PYRIDOXINE KINASE (EC 2.7.1.35)
549	550	RXS01807				CYTOSOLIC KINASE INVOLVED IN METABOLISM OF SUGARS AND THIAMIN
551	552	RXC01021				

Riboflavin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
553	554	RXN02246	VV0130	4388	5371	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
555	556	F RXA02246	GR00654	14299	15282	RIBG PROTEIN riboflavin-specific deaminase [EC:3.5.4.-]
557	558	RXA02247	GR00654	15286	15918	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
559	560	RXN02248	VV0130	6021	7286	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE
561	562	F RXA02248	GR00654	15932	17197	RIBA PROTEIN - GTP cyclohydrolase II [EC:3.5.4.25]
563	564	RXN02249	VV0130	7301	7777	6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
565	566	F RXA02249	GR00654	17212	17688	RIBH PROTEIN - 6,7-dimethyl-8-ribityllumazine synthase (dmr) synthase, lumazine synthase, riboflavin synthase beta chain) [EC:2.5.1.9]
567	568	RXA02250	GR00654	17778	18356	RIBX PROTEIN
569	570	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
571	572	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE
573	574	RXA01489	GR00423	3410	2388	PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
575	576	RXN01712	VV0191	8993	8298	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
577	578	F RXA01712	GR00484	2652	2152	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
579	580	RXN02384	VV0213	1386	679	ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE (EC 3.1.3.-)
581	582	RXN01560	VV0319	767	438	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
583	584	RXN00667	VV0109	1363	350	DRAP DEAMINASE
585	586	RXC01711				MEMBRANE SPANNING PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
587	588	RXC02380				PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
589	590	F RXA02380	GR00691	709	56	Predicted nucleotidyltransferases
591	592	RXC02921				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF RIBOFLAVIN AND LIPIDS
593	594	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN

Vitamin B6 metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
595	596	RXA01807	GR00509	7868	7077	PYRIDOXINE KINASE (EC 2.7.1.35), pyridoxal/pyridoxine/pyridoxamine kinase

Nicotinate (nicotinic acid), nicotinamide, NAD and NADP

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
597	598	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
599	600	F RXA02405	GR00701	774	4	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
601	602	F RXA02754	GR00766	3	488	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
603	604	RXA02112	GR00632	5600	6436	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLYATING) (EC 2.4.2.19)
605	606	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A

NAD Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
607	608	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)
609	610	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)

Pantothenate and Coenzyme A (CoA) biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
611	612	RXA02299	GR00662	10452	10859	ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)
613	614	RXA01928	GR00555	1957	1121	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
615	616	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
617	618	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
619	620	RXA01521	GR00424	25167	25964	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
621	622	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
623	624	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
625	626	RXA02239	GR00654	5784	7049	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
627	628	RXA00581	GR00156	7572	8540	PANTOTHENATE KINASE (EC 2.7.1.33)
629	630	RXS00838				2-DEHYDRO-PANTOATE 2-REDUCTASE (EC 1.1.1.169)
631	632	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE

Biotin metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
633	634	RXN03058	VV0028	8272	8754	BIOTIN SYNTHESIS PROTEIN BIOC

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
635	636	F RXA02903	GR10040	11532	12014	BIOTIN SYNTHESIS PROTEIN BIOC
637	638	RXA00166	GR00025	3650	4309	BIOTIN SYNTHESIS PROTEIN BIOC
639	640	RXA00633	GR00166	3556	2288	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (EC 2.6.1.62)
641	642	RXA00632	GR00166	2281	1610	DETHIOBIOTIN SYNTHETASE (EC 6.3.3.3)
643	644	RXA00295	GR00047	3407	4408	BIOTIN SYNTHASE (EC 2.8.1.6)
645	646	RXA00223	GR00032	23967	22879	NIFS PROTEIN
647	648	RXN00262	VW0123	16681	15608	NIFS PROTEIN
649	650	F RXA00262	GR00040	79	897	NIFS PROTEIN
651	652	RXN00435	VW0112	10037	11209	NIFS PROTEIN
653	654	F RXA00435	GR00100	3563	2949	NIFS PROTEIN
655	656	F RXA02801	GR00782	438	4	NIFS PROTEIN
657	658	RXA02516	GR00723	1724	2986	NIFS PROTEIN
659	660	RXA02517	GR00723	2989	3435	NIFU PROTEIN

Lipoic Acid

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
661	662	RXA01747	GR00495	2506	3549	LIPIC ACID SYNTHETASE
663	664	RXA01746	GR00495	1614	2366	LIPATE-PROTEIN LIGASE B (EC 6.---)
665	666	RXA02106	GR00632	472	1527	LIPATE-PROTEIN LIGASE A (EC 6.---)
667	668	RXS01183				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
669	670	RXS01260				LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
671	672	RXS01261				LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Folate biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXA02717	GR00758	18281	17400	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
675	676	RXN02027	VW0296	503	1003	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
677	678	F RXA02027	GR00616	500	6	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
679	680	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
681	682	RXN01321	VW0082	8868	9788	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
683	684	F RXA01321	GR00384	23	559	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
685	686	RXA00461	GR00116	428	1279	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9)
687	688	RXA01514	GR00424	20922	21509	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
689	690	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
691	692	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
693	694	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
695	696	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
697	698	RXA00989	GR00280	2903	1371	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
699	700	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
701	702	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
703	704	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
705	706	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
707	708	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
709	710	RXN02198	WV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
711	712	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
713	714	RXN02085	WV0126	8483	10717	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
715	716	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
717	718	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
719	720	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
721	722	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
723	724	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
725	726	RXS02197				5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
727	728	RXC00988				PROTEIN INVOLVED IN FOLATE METABOLISM
729	730	RXC01518				MEMBRANE SPANNING PROTEIN INVOLVED IN FOLATE METABOLISM
731	732	RXC01942				ATP-BINDING PROTEIN INVOLVED IN FOLATE METABOLISM

Molybdopterin Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
733	734	RXN02802	WV0112	17369	16299	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
735	736	F RXA02802	GR00783	7	474	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
737	738	F RXA00438	GR00103	362	796	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
739	740	RXN00437	WV0112	17824	17369	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
741	742	F RXA00437	GR00103	3	362	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
743	744	RXN00439	WV0112	18742	18275	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
745	746	F RXA00439	GR00104	2	196	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
747	748	F RXA00442	GR00105	830	1087	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
749	750	RXA00440	GR00104	196	654	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN CB
751	752	RXN00441	VV0112	19942	18779	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
753	754	F RXA00441	GR00105	2	793	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
755	756	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
757	758	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
759	760	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
761	762	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
763	764	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
765	766	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
767	768	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
769	770	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
771	772	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
773	774	RXA01719	GR00488	1264	704	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A
775	776	RXA01720	GR00488	2476	1268	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
777	778	RXS03223				MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
779	780	F RXA01970	GR00568	2	1207	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
781	782	RXA02629	GR00748	1274	690	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN
783	784	RXA02318	GR00665	9684	9962	(D90909) pterin-4a-carbinolamine dehydratase [Synechocystis sp.]
785	786	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE
						PHOSPHOKINASE (EC 2.7.6.3)
787	788	RXN01304	VV0148	4449	4934	MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN
789	790	RXS02556				FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
791	792	RXS02560				OXYGEN-SENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-) / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)

Vitamin B₁₂, porphyrins and heme metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
793	794	RXA00382	GR00082	2752	1451	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8)
795	796	RXA00156	GR00023	10509	9400	FERROCHELATASE (EC 4.99.1.1)
797	798	RXA00624	GR00163	7910	8596	FERROCHELATASE (EC 4.99.1.1)
799	800	RXA00306	GR00051	2206	1274	HEMK PROTEIN
801	802	RXA00884	GR00242	10137	11276	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)
803	804	RXN02503	VV0007	22456	22854	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
805	806	F RXA02503	GR00720	16906	17340	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
807	808	RXA00377	GR00081	1427	306	UROPORPHYRINOGEN DECARBOXYLASE (EC 4.1.1.37)
809	810	RXN02504	VV0007	22805	23362	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
811	812	F RXA02504	GR00720	17379	17816	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
813						
815	814	RXN01162	VV0088	1849	524	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
817	816	F RXA01162	GR00330	1248	4	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
819	818	RXA01692	GR00474	1498	749	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107)
	820	RXN00371	VV0226	4180	5973	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
821	822	F RXA00371	GR00078	929	6	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
823	824	F RXA00374	GR00079	1102	371	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
825	826	RXN00383	VV0223	4206	2863	UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
827	828	F RXA00376	GR00081	287	6	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
829	830	F RXA00383	GR00082	3876	2863	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
831	832	RXA01253	GR00365	2536	1787	PROTOPORPHYRIN-III SYNTHASE (EC 1.3.3.4)
833	834	RXA02134	GR00639	1721	801	COBYRIC ACID SYNTHASE
835	836	RXA02135	GR00639	2809	1736	COBALAMIN (5'-PHOSPHATE) SYNTHASE
837	838	RXA02136	GR00639	3362	2841	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
839	840	RXN03114	VV0088	1	552	COBINAMIDE KINASE / COBINAMIDE PHOSPHATE GUANYLYLTRANSFERASE
841	842	RXN01810	VV0082	1739	663	COBG PROTEIN (EC 1.-.-.-)
843	844	RXS03205				HEMIN-BINDING PERIPLASMIC PROTEIN HMUT PRECURSOR
845	846	F RXA00306				HEMK PROTEIN
847	848	RXC01715				HEMK PROTEIN CYTOSOLIC PROTEIN INVOLVED IN PORPHYRIN METABOLISM

Vitamin C precursors

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
849	850	RXN00420	VV0112	2511	1048	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
851	852	F RXA00420	GR00096	2	541	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
853	854	F RXA00426	GR00097	1737	2258	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
855	856	RXN00708	VV0005	4678	3872	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
857	858	F RXA00708	GR00185	2030	1359	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
859	860	RXA02373	GR00688	1540	626	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
861	862	RXS00389				ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
863	864	RXS00419				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
865	866	RXC00416				OXIDOREDUCTASE INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
867	868	RXC02206				

Vitamin K2

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
869	870	RXS03074				S-ADENOSYLMETHIONINE-2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
871	872	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.-.)
873	874	RXA02315	GR00665	8011	6383	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE /2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
875	876	RXA02319	GR00665	9977	10933	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
877	878	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.)
879	880	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.)
881	882	RXA00391	GR00086	2031	2750	O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
883	884	RXS02908				O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)

Ubiquinone biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
885	886	RXA00997	GR00283	2389	1808	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
887	888	RXA02189	GR00642	986	249	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
889	890	RXA02311	GR00665	3073	2384	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
891	892	RXN02912	VV0135	13299	12547	UBIQUINONE/MENAUQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE (EC 2.1.1.-)
893	894	RXS00998				COMA OPERON PROTEIN 2

Purines and Pyrimidines and other Nucleotides

Regulation of purine and pyrimidine biosynthesis pathways

Purine metabolism

Purine Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
895	896	RXA01215	GR00352	1187	213	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE, PRPP synthetase (EC 2.7.6.1)
897	898	RXN00558	VV0103	8235	9581	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
899	900	F RXA00558	GR00148	61	501	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
901	902	RXN00626	VV0135	11624	10362	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
903	904	F RXA00629	GR00165	1450	1713	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
905	906	F RXA00626	GR00164	1	780	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE, GARS (EC 6.3.4.13)
907	908	RXA02623	GR00746	4875	4285	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) / PHOSPHORIBOSYLFORMYLGLYCINAMINE CYCLO-LIGASE (EC 6.3.3.1) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2)
909	910	RXA01442	GR00418	10277	9054	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE 2 (EC 2.1.2.-)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
911	912	RXN00537	VV0103	3351	5636	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
913	914	F RXA02805	GR00786	54	638	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
915	916	F RXA00537	GR00138	23	697	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
917	918	F RXA00561	GR00150	2	280	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
919	920	RXA00541	GR00139	2269	2937	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
921	922	RXA00620	GR00163	3049	3939	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
923	924	RXN00770	VV0103	9614	10783	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
925	926	F RXA00557	GR00147	15	818	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
927	928	F RXA00770	GR00204	7809	7495	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
929	930	RXN02345	VV0078	4788	5984	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
931	932	F RXA02345	GR00676	1534	725	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
933	934	RXN02350	VV0078	8369	8863	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
935	936	F RXA02346	GR00677	127	5	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
937	938	F RXA02350	GR00678	1120	911	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
939	940	RXA01087	GR00304	498	1373	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21)
941	942	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
943	944	RXA02622	GR00746	4274	2715	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE FORMYLTRANSFERASE (EC 2.1.2.3) / IMP CYCLOHYDROLASE (EC 3.5.4.10)

GMP, GDP, AMP and ADP synthesis, from inosine-5'-monophosphate (IMP)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLYATE KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)

GMP/AMP degrading activities

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
967	968	RXA00489	GR00121	654	1775	GMP REDUCTASE (EC 1.6.6.8)
969	970	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
971	972	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)

Pyrimidine metabolism

Pyrimidine biosynthesis de novo:

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
973	974	RXA00147	GR00022	9722	10900	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
975	976	RXA00145	GR00022	7258	8193	ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN (EC 2.1.3.2)
977	978	RXA00146	GR00022	8249	9589	DIHYDROOROTASE (EC 3.5.2.3)
979	980	RXA02208	GR00647	2	1003	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
981	982	RXA01660	GR00462	591	1142	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
983	984	RXA02235	GR00654	3207	4040	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
985	986	RXN01892	VV0150	3020	3748	URIDYLATE KINASE (EC 2.7.4.-)
987	988	F RXA01892	GR00542	47	775	URIDYLATE KINASE (EC 2.7.4.-)
989	990	RXA00105	GR00014	16672	17346	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
991	992	RXA00131	GR00020	7621	7013	THYMIDYLATE KINASE (EC 2.7.4.9)
993	994	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
995	996	RXA00718	GR00188	4576	5283	CYTIDYLATE KINASE (EC 2.7.4.14)
997	998	RXA01599	GR00447	8780	10441	CTP SYNTHASE (EC 6.3.4.2)
999	1000	RXN02234	VV0134	24708	28046	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1001	1002	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1003	1004	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1005	1006	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1007	1008	RXN02272	VV0020	15566	16810	CYTOSINE DEAMINASE (EC 3.5.4.1)
1009	1010	F RXA02272	GR00655	6691	7935	CREATININE DEAMINASE (EC 3.5.4.21)
1011	1012	RXN03004	VV0237	1862	2341	DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
1013	1014	RXN03137	VV0129	9680	9579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
1015	1016	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1017	1018	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)

Purine and pyrimidine base, nucleoside and nucleotide salvage, interconversion, reduction and degradation:

Purines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1019	1020	RXA02771	GR00772	1329	1883	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
1021	1022	RXA01512	GR00424	17633	18232	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
1023	1024	RXA02031	GR00618	3820	3347	XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.22)
1025	1026	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1027	1028	RXN02772	VV0171	2045	1011	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1029	1030	F RXA02772	GR00772	1962	2741	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1031	1032	F RXA02773	GR00772	2741	2902	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1033	1034	RXA01835	GR00517	3147	3677	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1035	1036	RXA01483	GR00422	19511	18240	DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (EC 3.1.5.1)
1037	1038	RXN01027	VV0143	5761	6768	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1039	1040	F RXA01024	GR00293	661	5	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1041	1042	F RXA01027	GR00294	2580	2347	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1043	1044	RXA01528	GR00425	5653	5126	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1045	1046	RXA00072	GR00012	446	6	PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
1047	1048	RXA01878	GR00337	1239	2117	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-)
1049	1050	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1051	1052	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)
1053	1054	RXN01240	VV0090	30442	29420	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1055	1056	RXN02008	VV0171	1138	5	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)

Pyrimidine and purine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1057	1058	RXN01940	VV0120	10268	9333	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1059	1060	F RXA01940	GR00557	3	581	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1061	1062	RXA02559	GR00731	5418	6320	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1063	1064	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
1065	1066	RXN01079	VV0084	38084	35982	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1067	1068	F RXA01079	GR00301	693	4	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1069	1070	F RXA01084	GR00302	3402	2062	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1071	1072	RXN01920	VV0084	32843	31842	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (EC 1.17.4.1)
1073	1074	F RXA01920	GR00650	1321	908	RIBONUCLEOTIDE REDUCTASE SUBUNIT R2F
1075	1076	RXA01080	GR00301	1240	797	NRDI PROTEIN
1077	1078	RXA00867	GR00237	1	627	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1079	1080	RXA01416	GR00413	2	631	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1081	1082	RXA01486	GR00423	660	4	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1083	1084	RXA01678	GR00467	7162	7689	2'-3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1085	1086	RXA01679	GR00467	7729	8964	2'-3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1087	1088	RXN01488	VV0139	39842	40789	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1089	1090	RXC00540				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1091	1092	RXC00560				PROTEIN INVOLVED IN PURINE METABOLISM
1093	1094	RXC01088				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1095	1096	RXC02624				MEMBRANE SPANNING PROTEIN INVOLVED IN PURINE METABOLISM
1097	1098	RXC02665				PROTEIN INVOLVED IN PURINE METABOLISM
1099	1100	RXC02770				LIPOPROTEIN INVOLVED IN PURINE METABOLISM
1101	1102	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
1103	1104	RXC01946				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN PURINE METABOLISM

Pyrimidines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1105	1106	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1107	1108	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1109	1110	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1111	1112	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1113	1114	RXA00465	GR00117	337	828	CYTOSINE DEAMINASE (EC 3.5.4.1)
1115	1116	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
1117	1118	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41)
1119	1120	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
1121	1122	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1123	1124	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1125	1126	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1127	1128	F RXA01617	GR00451	2	616	CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1129	1130	RXC01600				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1131	1132	RXC01622				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDINES AND ADENOSYLMOCYSTEINE
1133	1134	RXC00128				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1135	1136	RXC01709				EXPORTED PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1137	1138	RXC02207				

Sugars

Trehalose

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
1139	1140	RXA00347	GR00065	246	1013	TREHALOSE-PHOSPHATASE (EC 3.1.3.12)
1141	1142	RXN01239	VV0090	32921	30489	maltooligosyltrehalose synthase
1143	1144	F RXA01239	GR00358	5147	7579	maltooligosyltrehalose synthase
1145	1146	RXA02645	GR00751	714	2543	maltooligosyltrehalose trehalohydrolase
1147	1148	RXN02355	VV0051	735	4	TREHALOSE/MALTOSE BINDING PROTEIN
1149	1150	RXN02909	VV0135	38532	39017	Hypothetical Trehalose-Binding Protein
1151	1152	RXS00349				TREHALOSE/MALTOSE BINDING PROTEIN
1153	1154	RXS03183				TRANSMEMBRANE PROTEIN INVOLVED IN TREHALOSE METABOLISM
1155	1156	RXC00874				

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argI; argB; argD; argF; argR; argG; argH	N-acetylglutamyolphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hlk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroeductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroeductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthraniolate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The Corynebacterium glutamicum accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5"-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> ,
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737 X69103	dapB csp2	Dihydrodipicolinate reductase Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855 X75083, X70584	GDHA mtrA	Glutamate dehydrogenase (NADP+) 5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyl/diaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R. M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X93649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-	Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate

GenBank™ Accession No.	Gene Name	alanine ligase; xylulokinase Gene Function	overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	Reference
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among coryne phages," <i>Virology</i> , 255(1):150-159 (1999)
Y18059		Attachment site Corynephage 304L	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z29563	thrC	Threonine synthase	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	
Z66534		Transposase	

¹ A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCIC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum								
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477			
Brevibacterium	flavum			B11478			
Brevibacterium	flavum	21127					
Brevibacterium	flavum			B11474			
Brevibacterium	healii	15527					
Brevibacterium	ketoglutamicum	21004					
Brevibacterium	ketoglutamicum	21089					
Brevibacterium	ketosoreductum	21914					
Brevibacterium	lactofermentum				70		
Brevibacterium	lactofermentum				74		
Brevibacterium	lactofermentum				77		
Brevibacterium	lactofermentum	21798					
Brevibacterium	lactofermentum	21799					
Brevibacterium	lactofermentum	21800					
Brevibacterium	lactofermentum	21801					
Brevibacterium	lactofermentum			B11470			
Brevibacterium	lactofermentum			B11471			
Brevibacterium	lactofermentum	21086					
Brevibacterium	lactofermentum	21420					
Brevibacterium	lactofermentum	21086					
Brevibacterium	lactofermentum	31269					
Brevibacterium	linens	9174					
Brevibacterium	linens	19391					
Brevibacterium	linens	8377					
Brevibacterium	paraffinolyticum				11160		
Brevibacterium	spec.					717.73	
Brevibacterium	spec.					717.73	
Brevibacterium	spec.	14604					
Brevibacterium	spec.	21860					
Brevibacterium	spec.	21864					
Brevibacterium	spec.	21865					

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum					B8183			
Corynebacterium	glutamicum					B8182			
Corynebacterium	glutamicum					B12416			
Corynebacterium	glutamicum					B12417			
Corynebacterium	glutamicum					B12418			
Corynebacterium	glutamicum					B11476			
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419						11594	
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090								
Corynebacterium	spec.	15954								20145
Corynebacterium	spec.	21857								
Corynebacterium	spec.	21862								
Corynebacterium	spec.	21863								

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saitama, Japan.

TABLE 4: ALIGNMENT RESULTS

<u>ID #</u>	<u>length</u> (NT)	<u>Genbank Hit</u>	<u>Length</u>	<u>Accession</u>	<u>Name of Genbank Hit</u>	<u>Source of Genbank Hit</u>	<u>% homology</u> (GAP)	<u>Date of</u> <u>Deposit</u>
rx000023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rx000044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT-1996
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC-1993
rx000064	1401	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	28-Jul-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx000072		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rx000105	798	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli K-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx000106	579	GB_EST15:AA494237	367	AA494237	ng83f04.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;, mRNA sequence.	Homo sapiens	42,896	20-Aug-97
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
rx000115	1170	GB_PR4:AC007110	148336	AC007110	Homo sapiens chromosome 17, clone hRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99

TABLE 4: ALIGNMENT RESULTS

rx000116	1284	GB_BA2:AF062345	16458	AF062345	Caulobacter crescentus SstI (sstI), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (psaA), putative acetyltransferase (psbB), putative perosamine synthetase (psC), putative mannitoltransferase (psdD), putative mannitoltransferase (psE), outer membrane protein (rsaF), and putative perosamine transferase (psE) genes, complete cds. Sequence 6 from patent US 5500353. nxbx0062D16r CUGI Rice BAC Library Oryza sativa genomic clone nxbx0062D16r, genomic survey sequence.	Caulobacter crescentus	36,235	19-OCT-1999
		GB_PAT:118647	3300	I18647	Unknown.		36,821	07-OCT-1996
		GB_GSS13:QA446197	751	AQ446197	Oryza sativa		38,124	8-Apr-99
rx000131	732	GB_BA1:MTY20811	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	43,571	17-Jun-98
		GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus mithramycin biosynthetic genes.	Streptomyces argillaceus	41,116	15-Jun-99
		GB_BA1:MTY20811	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	39,726	17-Jun-98
rx000132	1557	GB_BA1:MTY20811	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,788	17-Jun-98
		GB_IN2:TU040872	1882	U40872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	Trichomonas vaginalis	61,914	31-OCT-1996
		GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPCI-98 36.D.15 map 13C-13E strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 74 unordered pieces.	Drosophila melanogaster	51,325	22-Nov-99
rx000145	1059	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	63,365	18-Jun-98
		GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	Pseudomonas aeruginosa	56,080	26-Jul-93
		GB_BA1:LLPYRBDNA	1468	X84262	L. leichmannii pyrB gene.	Lactobacillus leichmannii	47,514	29-Apr-97
rx000146	1464	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	60,714	18-Jun-98
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	36,618	03-DEC-1996
rx000147	1302	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	61,527	18-Jun-98
		GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	59,538	15-Jun-96
		GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FtsJ homolog (ftsJ) gene, partial cds.	Pseudomonas aeruginosa	55,396	23-DEC-1996
rx000156	1233	GB_BA1:SC9B10	33320	AL009204	Streptomyces coelicolor cosmid 9B10.	Streptomyces coelicolor	52,666	10-Feb-99
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (act), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	54,191	26-MAR-1998
		GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	Propionibacterium freudenreichii	46,667	6-Feb-99
rx000166	783	GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172O13, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
		GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172O13, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
		GB_HTG4:AC010118	80605	AC010118	Drosophila melanogaster chromosome 3L/62B1 clone RPCI98-10D15, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	Drosophila melanogaster	38,627	16-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rx00198	672	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	92,113	13-MAR-1999
		GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	93,702	13-MAR-1999
		GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	34,221	31-Jan-99
rx00216	1113	GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,965	03-DEC-1999
		GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,965	03-DEC-1999
		GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	38,796	11-Nov-99
rx00219	1065	GB_HTG2:AC005079_0	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	38,227	22-Nov-98
rx00223	1212	GB_BA1:PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes.	48,826	2-Aug-96
		GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	40,135	22-MAR-1999
rx00229	803	GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L70C1 clone RPCI98-9B18, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces	39,527	16-OCT-1999
		GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	98,237	18-MAY-1999
		GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	36,616	18-Apr-98
		GB_HTG2:AC006907	188972	AC006907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	37,095	26-Feb-99
rx00241	1626	GB_BA1:CGLYSI	4232	X60312	C glutamicum lysI gene for L-lysine permease.	100,000	30-Jan-92
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	34,947	11-Aug-99
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces	34,947	11-Aug-99
rx00262	1197	GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	36,496	23-MAY-1997
		GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	37,544	23-MAY-1997
rx00266	531	GB_RO:AF016190	2939	AF016190	Mus musculus connexin-36 (Cx36) gene, complete cds.	41,856	9-Feb-99
		EM_PAT:E09719	3505	E09719	DNA encoding precursor protein of alkaline cellulase.	34,741	08-OCT-1997 (Rel. 52, Created)
rx00278	1155	GB_PAT:E02133	3494	E02133	gDNA encoding alkaline cellulase.	34,741	29-Sep-97
		GB_IN1:CELK05F6	36912	AF040653	Caenorhabditis elegans cosmid K05F6.	36,943	6-Jan-98

TABLE 4: ALIGNMENT RESULTS

							Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.						Corynebacterium glutamicum	36,658	9-Apr-97
							Rattus norvegicus clone N27 mRNA.						Rattus norvegicus	38,190	20-Aug-96
							Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.						Corynebacterium glutamicum	99,111	21-Nov-96
							Brevibacterium flavum gene for biotin synthetase, complete cds.						Corynebacterium glutamicum	98,489	3-Feb-99
							DNA sequence encoding Brevibacterium flavam biotin-synthase.						Corynebacterium glutamicum	98,207	29-Sep-97
							Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.						Mycobacterium tuberculosis	35,615	24-Jun-99
							Mycobacterium leprae cosmid B32 DNA sequence.						Mycobacterium leprae	60,917	15-Jun-96
							Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.						Mycobacterium tuberculosis	44,606	24-Jun-99
							Mycobacterium leprae cosmid B32 DNA sequence.						Mycobacterium leprae	52,516	15-Jun-96
							Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.						Mycobacterium tuberculosis	38,079	24-Jun-99
							Bovine elastin a mRNA, complete cds.						Bos taurus	39,351	27-Apr-93
							Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).						Corynebacterium glutamicum	99,808	17-Jun-97
							Sequence 4 from Patent WO 8809819.						Unknown.	99,617	02-DEC-1994
							Brevibacterium lactofermentum; ATCC 13869;; DNA (genomic);.						Corynebacterium glutamicum	99,170	20-Sep-95
							Corynebacterium glutamicum glnA gene.						Corynebacterium glutamicum	100,000	28-Aug-97
							Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.						Corynebacterium glutamicum	98,906	14-Jun-99
							Mycobacterium leprae cosmid B27 DNA sequence						Mycobacterium leprae	66,345	15-Jun-96
							LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime. mRNA sequence.						Drosophila melanogaster	34,510	09-MAR-1999
							Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site I for vector use.						Synechococcus PCC7942	37,084	29-OCT-1999
							oe75a02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN);, mRNA sequence.						Homo sapiens	37,500	21-Apr-98
							Mycobacterium leprae cosmid L296.						Mycobacterium leprae	52,972	09-MAR-1995
							Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.						Drosophila melanogaster	46,341	17-Jul-98
							Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.						Drosophila melanogaster	49,471	14-Jun-99
							Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.						Corynebacterium glutamicum	96,556	13-MAR-1999
							Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.						Mycobacterium tuberculosis	39,496	17-Jun-98
							Streptomyces coelicolor cosmid 3A3						Streptomyces coelicolor A3(2)	37,946	16-Aug-99
							Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.						Corynebacterium glutamicum	99,374	13-MAR-1999
							Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.						Mycobacterium tuberculosis	41,333	17-Jun-98
							Streptomyces coelicolor cosmid 3A3.						Streptomyces coelicolor A3(2)	37,554	16-Aug-99

TABLE 4: ALIGNMENT RESULTS

rx00367	4653	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	16-Aug-99
rx00371	1917	GB_V1:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2 and 3 DNA, complete cds.	Sugarcane bacilliform virus	35,843	12-Jun-93
		GB_EST37:AI967505	380	AI967505	Ljirnp03-215-c10 Ljirnp Lambda HybZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	42,593	24-Aug-99
rx00377	1245	GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98
		GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (hemE) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:ANSDGENE	1299	Y08866	A.nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
		GB_GSS4:AQ730303	483	AQ730303	HS_5505_B1_C04_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
rx00382	1425	GB_BA1:PAHEML	4444	X82072	P.aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx00383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_Q_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx00391	843	GB_EST38:AW017053	613	AW017053	EST272398 Schistosoma mansoni male, Phil LoVerde/Joel Merrick Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Sequence 20 from patent US 5849564.	Unknown.	38,586	29-Sep-99
		GB_VI:AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rx00393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
		GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
rx00402	623	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rx00403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI11288	750	AI11288	SWOvAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAV98MLW-OvAM) Onchocerca volvulus cDNA clone SWOvAMCAQ02A05 5', mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

TABLE 4: ALIGNMENT RESULTS

rx00405	613	GB_BA1:MTV016 GB_PR4:AC005145	53662 143678	AL021841 AC005145	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Mycobacterium tuberculosis Homo sapiens	57,259 34,179	23-Jun-99 08-DEC-1998
rx00420	1587	GB_BA1:MTV016 GB_BA1:MTY13D12 GB_BA1:MSGY126 GB_BA1:MSGB971CS GB_BA1:AFACBBTZ	53662 37085 37164 37566 2760	AL021841 Z80343 AD000012 L78821 M68904	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Mycobacterium tuberculosis H37Rv complete genome; segment 156/162 Mycobacterium tuberculosis sequence from clone y126. Mycobacterium leprae cosmid B971 DNA sequence. Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Ralstonia eutropha	40,169 62,031 61,902 39,651 38,677	23-Jun-99 17-Jun-98 10-DEC-1996 15-Jun-96 27-Jul-94
rx00437	579	GB_HTG4:AC009541 GB_HTG4:AC009541 GB_PR4:AC005951	169583 169583 155450	AC009541 AC009541 AC005951	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens Homo sapiens Homo sapiens	36,335 36,335 31,738	12-OCT-1999 12-OCT-1999 18-Nov-98
rx00439	591	GB_BA1:MTV016 GB_PL2:AF167358 GB_HTG3:AC009120	53662 1022 269445	AL021841 AF167358 AC009120	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Rumex acetosa expansin (EXP3) gene, partial cds. Homo sapiens chromosome 16 clone RPC1-11_484E3, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.	Mycobacterium tuberculosis Rumex acetosa Homo sapiens	37,088 46,538 43,276	23-Jun-99 17-Aug-99 3-Aug-99
rx00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
rx00441	1287	GB_BA1:SC2E1 GB_BA1:SC2E1 GB_PR2:HS173D1	38962 38962 117338	AL023797 AL023797 AL031984	Streptomyces coelicolor cosmid 2E1. Streptomyces coelicolor cosmid 2E1. Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33. Contains ESTs, STSs and GSSs, complete sequence.	Streptomyces coelicolor Streptomyces coelicolor Homo sapiens	42,931 36,702 38,027	4-Jun-98 4-Jun-98 23-Nov-99
rx00446	987	GB_HTG2:HSDJ719K3 GB_HTG2:HSDJ719K3 GB_BA1:SCD78 GB_HTG4:AC009367	267114 267114 36224 226055	AL109931 AL109931 AL034355 AC009367	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Streptomyces coelicolor cosmid D78. Drosophila melanogaster chromosome 3L76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Homo sapiens Homo sapiens Streptomyces coelicolor Drosophila melanogaster	34,521 34,521 56,410 34,959	03-DEC-1999 03-DEC-1999 26-Nov-98 16-OCT-1999
rx00448	1143	GB_HTG4:AC009367 GB_PR3:AC003670 GB_HTG2:AF029367 GB_HTG2:AF029367	226055 88945 148676 148676	AC009367 AC003670 AF029367 AF029367	Drosophila melanogaster chromosome 3L76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces. Homo sapiens 12q13.1 PAC RPC11-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence. Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces. Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens	34,959 35,682 31,373 31,373	16-OCT-1999 9-Jun-98 18-OCT-1997 18-OCT-1997

TABLE 4: ALIGNMENT RESULTS

rxa00450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:AI818057	412	AI818057	wk14a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rxa00461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC86E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
		GB_GSS15:AQ640325	467	AQ640325	927P1-2H3 TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rxa00465								
rxa00487	1692	GB_BA1:BAGUAA	3866	Y10499	B.ammoniaenes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
rxa00488	1641	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
rxa00489	1245	GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rxa00533	1155	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97
		GB_BA1:CGCYSCASD	1591	X82928	C.glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
rxa00534	1386	GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
		GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
		GB_BA1:CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavesens	98,701	11-Jun-93
		GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
rxa00536	1494	GB_BA1:CGLEUA	3492	X70959	C.glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-99
		GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	26-Feb-97

TABLE 4: ALIGNMENT RESULTS

rx00537	2409	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	63,187	21-Sep-99
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
		GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
rx00541	792	GB_PAT:192052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
rx00558	1470	GB_BA1:BAPURF	1885	X91252	B.ammoniaenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162	Mycobacterium tuberculosis	64,863	17-Jun-98
rx00579	1983	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
rx00580	1425	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created)
rx00581	1092	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	24-Jun-98
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created)
rx00584	1248	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
		GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
		GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
		GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
rx00618	1230	GB_EST19:AA802737	280	AA802737	GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
		GB_EST28:A1534381	581	A1534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858: Ani FBgn0011558 PID:g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,136	18-MAR-1999
rx00619	1551	GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
		GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rx00620	1014	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
		GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93

TABLE 4: ALIGNMENT RESULTS

rx00624	810	GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***; 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence	Caenorhabditis elegans	36,986	2-Sep-99
		GB_EST13:AA362167	372	AA362167	EST71561 Macrofrage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
rx00626	1386	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	57,971	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
		GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995
rx00632	795	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
		GB_PAT:E04041	675	E04041	DNA sequence coding for dethiobiotinsynthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase	Corynebacterium glutamicum	93,814	29-Sep-97
rx00633	1392	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
		GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-96
rx00688	666	GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
		GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
rx00708	930	GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
rx00717	1083	GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rx00718	831	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12:AQ420755	671	AQ420755	RPCI-11-188G18:TJ RPCI-11 Homo sapiens genomic clone RPCI-11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rx00727	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; on bw sp. *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; on bw sp. *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; on bw sp. *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99

TABLE 4: ALIGNMENT RESULTS

rx00766	966	GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
rx00770	1293	GB_BA1:D90810	20476	D90810	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	36,526	29-MAY-1997
		GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	66,193	24-Jun-99
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	61,443	09-MAR-1995
		GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	59,938	21-Sep-99
rx00779	1056	GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	64,896	14-OCT-1998
		GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	64,896	14-OCT-1998
		GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Groys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	57,970	3-Nov-99
rx00780	669	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	54,410	17-Jun-98
		GB_BA1:AVINIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifP, nifV, nifZ and nifM genes, complete cds.	51,729	26-Apr-93
		GB_BA2:AF001780	6701	AF001780	Cyanothece PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	36,309	08-MAR-1999
rx00838	1023	GB_EST1:Z30506	329	Z30506	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TA1306 3', mRNA sequence.	44,308	11-MAR-1994
		GB_PL2:AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	35,571	28-DEC-1998
		GB_EST37:A1998439	455	A1998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	36,044	8-Sep-99
rx00863	867	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,539	16-Aug-93
		GB_PAT:E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	99,539	28-Jul-99
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	99,539	28-Jul-99
rx00864	873	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	99,885	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	100,000	1-Apr-93
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	100,000	28-Jul-99
rx00865	1026	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	99,805	28-Jul-99
		GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	99,805	29-Sep-99
rx00867	650	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsI) gene, complete cds.	69,706	25-OCT-1996
rx00873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism cluster.	61,617	29-MAR-1999

TABLE 4: ALIGNMENT RESULTS

rx000884	1263	GB_BA1:D78198 GB_BA1:MTCY253 GB_BA1:MSGY222 GB_GSS15:AQ654600	2304 41230 41156 468	D78198 Z81368 AD000010 AQ654600	Pimelobacter sp. DNA for trehalose synthase, complete cds. Mycobacterium tuberculosis H37Rv complete genome; segment 106/162 Mycobacterium tuberculosis sequence from clone Y222. Sheared DNA-1O14. TF Sheared DNA Trypanosoma brucei genomic clone	60,594 37,785 38,006 33,974	Pimelobacter sp. Mycobacterium tuberculosis Mycobacterium tuberculosis Trypanosoma brucei	5-Feb-99 17-Jun-98 03-DEC-1996 22-Jun-99
rx000891	1102	GB_BA1:MTCI418B GB_BA1:SCO01206 GB_BA1:SCO001205 EM_PAT:E10963	11700 9184 9589 3118	Z96071 AJ001206 AJ001205 E10963	Sheared DNA-1O14, genomic survey sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 7/162. Streptomyces coelicolor A3(2). glycogen metabolism cluster II. Streptomyces coelicolor A3(2) glycogen metabolism clusterI. gDNA encoding tryptophan synthase.	63,297 61,965 61,727 99,688	Mycobacterium tuberculosis Streptomyces coelicolor Streptomyces coelicolor Corynebacterium glutamicum	18-Jun-98 29-MAR-1999 29-MAR-1999 08-OCT-1997 (Rel. 52, Created)
rx000954	644	GB_BA1:BLTRP GB_PAT:E01688 GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01688 EM_PAT:E10963	7725 7725 7726 7725 7725 7726 7725 7725 7725 3118	X04960 E01688 E01375 E01688 X04960 E01375 X04960 E01688 E10963	Brevibacterium lactofermentum tryptophan operon. Genomic DNA of trp operon of prepibacterium latophelmentamn. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepibacterium latophelmentamn. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Brevibacterium lactofermentum tryptophan operon. Genomic DNA of trp operon of prepibacterium latophelmentamn. gDNA encoding tryptophan synthase.	98,847 98,428 98,758 98,758 98,758 98,372 98,372 98,242 98,949	Corynebacterium glutamicum unidentified Corynebacterium glutamicum unidentified Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum unidentified Corynebacterium glutamicum	10-Feb-99 29-Sep-97 29-Sep-97 29-Sep-97 10-Feb-99 29-Sep-97 10-Feb-99 29-Sep-97 08-OCT-1997 (Rel. 52, Created)
rx000957	1677	GB_BA1:BLTRP GB_PAT:E01375 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:CGHOMTHR	7725 7726 7725 7726 7725 7725 7726 7725 3685	X04960 E01375 X04960 E01375 E01688 X04960 E01375 E01688 Y00546	Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepibacterium latophelmentamn Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepibacterium latophelmentamn. Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase.	99,107 98,945 99,165 98,927 98,867 98,792 98,792 98,658 99,905	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum unidentified Corynebacterium glutamicum Corynebacterium glutamicum unidentified Corynebacterium glutamicum	10-Feb-99 29-Sep-97 10-Feb-99 29-Sep-97 29-Sep-97 10-Feb-99 29-Sep-97 29-Sep-97 12-Sep-93
rx000972	1458	GB_PAT:I09077 GB_PAT:E01358 GB_PAT:E16755	3685 2615 3579	I09077 E01358 E16755	Sequence 1 from Patent WO 8809819. DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK). gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-tRNA synthase.	99,810 97,524	Unknown. Corynebacterium glutamicum	02-DEC-1994 29-Sep-97
rx000981	753	GB_PAT:AR038110 GB_PAT:E14508 GB_OV:GGA245664 GB_PL2:AC007887	3579 3579 512 159434	AR038110 E14508 AJ245664 AC007887	Sequence 15 from patent US 5804414. DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase. Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene). Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence.	99,931 99,931 37,538 37,600	Unknown. Corynebacterium glutamicum Gallus gallus Arabidopsis thaliana	29-Sep-99 28-Jul-99 28-Sep-99 04-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_GSS1:CNS00RNV 542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	41,264	28-Jun-99
rx00989	1644	GB_BA1:MTV008 63033 GB_BA1:SCVALSFP 3619 GB_BA1:MTV008 63033 GB_BA2:CGU31225 1817	AL021246 Y13070 AL021246 U31225	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162. S.coelicolor valS, fpgs, ndk genes. Mycobacterium tuberculosis H37Rv complete genome; segment 108/162. Corynebacterium glutamicum L-proline:NADP+ 5-oxidoreductase (proC) gene, complete cds.	40,773 58,119 38,167 40,841	17-Jun-98 03-MAR-1998 17-Jun-98 2-Aug-96
	705	GB_HTG1:CEY39C12 282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	36,416	26-OCT-1999
	1110	GB_IN1:CEB0001 39416 GB_HTG2:AC005052 144734	Z69634 AC005052	Caenorhabditis elegans cosmid B0001, complete sequence. Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	36,416 39,172	2-Sep-99 12-Jun-98
		GB_HTG2:AC005052 144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	39,172	12-Jun-98
		GB_GSS9:AQ171808 512	AQ171808	HS_3179_A1_G03_T7 C1T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.	34,661	17-OCT-1998
rx01026	1782	GB_BA1:SC1C2 42210 GB_BA1:ATLEUCD 2982	AL031124 X84647	Streptomyces coelicolor cosmid 1C2. A.teichomyceticus leuC and leuD genes.	68,275 65,935	15-Jan-99 04-OCT-1995
rx01027	1131	GB_BA1:MTV012 70287 GB_BA1:MLCB037 44882 GB_BA1:MTCY349 43523 GB_BA1:SPUNGJUTX 1172	AL021287 Z99263 Z83018 Z21702	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162. Mycobacterium leprae cosmid B637. Mycobacterium tuberculosis H37Rv complete genome; segment 131/162. S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	40,454 38,636 51,989 38,088	23-Jun-99 17-Sep-97 17-Jun-98 15-Jun-94
rx01073	954	GB_BA1:BACOUTB 1004 GB_PR4:AC007938 167237 GB_PL2:ATAC006282 92577	M15811 AC007938 AC006282	Bacillus subtilis outB gene encoding a sporulation protein, complete cds. Homo sapiens clone UWGC:djs201 from 7q31, complete sequence. Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	53,723 34,322 36,181	26-Apr-93 1-Jul-99 13-MAR-1999
rx01079	2226	GB_BA2:AF112535 4363 GB_BA1:CANRDFGEN 6054	AF112535 Y09572	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds. Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	99,820 75,966	5-Aug-99 18-Apr-98
rx01080	567	GB_BA1:MTV012 70287 GB_BA2:AF112535 4363	AL021287 AF112535	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162. Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	38,296 100,000	23-Jun-99 5-Aug-99
		GB_BA1:CANRDFGEN 6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	65,511	18-Apr-98
rx01087	999	GB_BA1:STNRD 4894 GB_IN2:AF063412 1093 GB_PR3:HS24M15 134539	X73226 AF063412 Z94055	S.lyphimurium nrdEF operon. Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds. Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restriclin), EST.	52,477 43,750 37,475	03-MAR-1997 29-MAR-1999 23-Nov-99
		GB_IN2:ARU85702 1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	37,319	16-Jul-97

TABLE 4: ALIGNMENT RESULTS

rx01095	857	GB_BA1:MTCY01B2 GB_HTG5:AC011632	35938 175917	Z95554 AC011632	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162. Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Mycobacterium tuberculosis Homo sapiens	43,243 36,471	17-Jun-98 19-Nov-99
rx01097	477	GB_BA2:AF030405 GB_BA2:AF030405	774 774	AF030405 AF030405	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces. Corynebacterium glutamicum cyclase (hisF) gene, complete cds. Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Homo sapiens Corynebacterium glutamicum Corynebacterium glutamicum	36,836 100,000 41,206	19-Nov-99 13-Nov-97 13-Nov-97
rx01098	897	GB_BA2:AF030405 GB_BA1:MSGY223 GB_BA1:MLCB1610 GB_BA2:AF051846	774 42061 40055 738	AF030405 AD000019 AL049913 AF051846	Corynebacterium glutamicum cyclase (hisF) gene, complete cds. Mycobacterium tuberculosis sequence from clone y223 Mycobacterium leprae cosmid B1610. Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum Mycobacterium tuberculosis Mycobacterium leprae Corynebacterium glutamicum	97,933 40,972 61,366 97,154	13-Nov-97 10-DEC-1996 27-Aug-99 12-MAR-1998
rx01100	861	GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
rx01101	756	GB_HTG1:HSDJ140A9 GB_BA2:AF060558 GB_BA1:SC4G6	221755 636 36917	AL109917 AF060558 AL096884	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds. Streptomyces coelicolor cosmid 4G6.	Homo sapiens Corynebacterium glutamicum Streptomyces coelicolor A3(2)	30,523 94,462 38,378	23-Nov-99 29-Apr-98 23-Jul-99
rx01104	729	GB_BA1:STMHISOPA GB_BA1:STMHISOPA GB_BA1:SC4G6	3981 3981 36917	M31628 M31628 AL096884	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds. Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor Streptomyces coelicolor Streptomyces coelicolor A3(2)	60,053 58,333 39,045	26-Apr-93 26-Apr-93 23-Jul-99
rx01105	1221	GB_BA1:MTCY336 GB_BA1:MTCY336 GB_BA1:MSGY223 GB_BA1:MLCB1610 GB_BA1:MSGY223 GB_BA1:MSHISCD	32437 32437 42061 40055 42061 2298	Z95586 Z95586 AD000019 AL049913 AD000019 X65542	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162. Mycobacterium tuberculosis H37Rv complete genome; segment 70/162. Mycobacterium tuberculosis sequence from clone y223. Mycobacterium leprae cosmid B1610. Mycobacterium tuberculosis sequence from clone y223. M.smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol-phosphate aminotransferase, respectively.	Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium tuberculosis Mycobacterium smegmatis	60,364 60,931 36,851 60,902 37,233 60,111	24-Jun-99 24-Jun-99 10-DEC-1996 27-Aug-99 10-DEC-1996 30-Jun-93
rx01145	1137	GB_BA1:MTCY336 GB_BA1:CORAIA GB_BA1:BRLILVCA	32437 4705 1364	Z95586 L09232 D14551	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162. Corynebacterium glutamicum acetoaldehyde acid synthase (ilvB) and (ilvN) genes, and acetoaldehyde acid isomerase (ilvC) gene, complete cds. Brevibacterium flavum ilvC gene for acetaldehyde acid isomerase, complete cds.	Mycobacterium tuberculosis Corynebacterium glutamicum Corynebacterium glutamicum	58,420 100,000 99,560	24-Jun-99 23-Feb-95 3-Feb-99
rx01162	1449	GB_PAT:E08232 GB_PAT:A60299 GB_PR3:HS24E5	1017 2869 35506	E08232 A60299 Z82185	DNA encoding acetoaldehyde-acid isomerase. Sequence 18 from Patent WO9706261. Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	Corynebacterium glutamicum Aspergillus niger Homo sapiens	99,803 38,675 36,204	29-Sep-97 06-MAR-1998 23-Nov-99

TABLE 4: ALIGNMENT RESULTS

rxa01208	846	GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	Homo sapiens	38,363	6-Jul-98
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
					unordered pieces.			
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
					unordered pieces.			
		GB_PL2:TAU55859	2397	U55859	Triticum aestivum heat shock protein 80 mRNA, complete cds.	Triticum aestivum	37,269	1-Feb-99
rxa01209	1528	GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
					31 unordered pieces.			
		GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
					31 unordered pieces.			
		GB_PL1:AB010077	77380	AB010077	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.	Arabidopsis thaliana	36,803	20-Nov-99
rxa01215	1098	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	37,047	17-Jun-98
		GB_IN1:LEIPRPP	1887	M76553	Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds.	Leishmania donovani	50,738	7-Jun-93
		GB_HTG2:HSJ799D16	130149	AL050344	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,135	29-Nov-99
					in unordered pieces.			
rxa01239	2556	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	38,139	17-Jun-98
		GB_PR2:AB029032	6377	AB029032	Homo sapiens mRNA for KIAA1109 protein, partial cds.	Homo sapiens	39,394	4-Aug-99
		GB_GSS9:AQ107201	355	AQ107201	HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence.	Homo sapiens	41,408	28-Aug-98
rxa01253	873	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	Arabidopsis thaliana	36,118	23-DEC-1998
		GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	Arabidopsis thaliana	35,574	23-DEC-1998
rxa01321	1044	GB_IN1:CELC06G1	31205	U41014	Caenorhabditis elegans cosmid C06G1.	Caenorhabditis elegans	38,560	30-Nov-95
		GB_GSS14:AQ518843	441	AQ518843	HS_5105_A1_D10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
		GB_HTG2:AC007473	194859	AC007473	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	40,634	2-Aug-99
					60 unordered pieces.			
		GB_HTG4:AC011696	115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	38,290	26-OCT-1999
					108 unordered pieces.			
rxa01352	706	GB_PL2:ATAC005167	83260	AC005167	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825	97380	AC005825	Arabidopsis thaliana chromosome II BAC T24121 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
rxa01360	259	GB_HTG3:AC011150	127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
		GB_EST32:AI725583	728	AI725583	BNLGHi12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
		GB_PR2:HS227P17	82951	Z81007	Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.	Homo sapiens	39,738	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

rx01361	629	GB_EST34:AV171099	173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 320002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
		GB_RO:AB008915S1	530	AB008915	Mus musculus mGpi1 gene, exon 1.	Mus musculus	45,574	28-Sep-99
		GB_EST22:AI050532	293	AI050532	uc83d10.y1 Sugano mouse kidney nkia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P.; mRNA sequence.	Mus musculus	44,097	9-Jul-98
rx01381	944	GB_RO:AB008895	3062	AB008895	Mus musculus mRNA for mGpi1p, complete cds.	Mus musculus	41,316	23-Nov-97
		GB_PL1:AB005237	87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
		GB_GSS5:AQ766840	491	AQ766840	HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
rx01393	993	GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
		GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
		GB_PR3:AC004054	112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
rx01394	822	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_GSS5:AQ769223	500	AQ769223	HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99
rx01416	630	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	33,665	24-Feb-97
		GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	62,726	10-Aug-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,159	22-Aug-97
rx01442	1347	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,340	17-Jun-98
		GB_BA1:D90827	18886	D90827	E.coli genomic DNA, Kohara clone #336(41.2-41.6 min.).	Escherichia coli	58,517	21-MAR-1997
		GB_BA1:D90828	14590	D90828	E.coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.).	Escherichia coli	56,151	21-MAR-1997
rx01446	1413	GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.	Escherichia coli	56,021	12-Nov-98
		GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	39,037	04-MAY-1999
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	40,130	17-Jun-98
		GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	37,752	27-Aug-99
rx01483	1395	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	39,057	17-Jun-98
		GB_BA1:MSGB1229CS	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.	Mycobacterium leprae	54,382	15-Jun-96
		GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; rRNA-Asn gene, complete sequence.	Mycobacterium smegmatis	52,941	16-Jan-98
rx01486	757	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	40,941	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,451	22-Aug-97
		GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	61,194	10-Aug-98
rx01489	1146	GB_BA1:CORFADS	1547	D37967	Corynebacterium ammoniagenes gene for FAD synthetase, complete cds.	Corynebacterium ammoniagenes	58,021	8-Feb-99
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,414	22-Aug-97
		GB_BA1:SC10A7	39739	AL078618	Streptomyces coelicolor cosmid 10A7.	Streptomyces coelicolor	36,930	9-Jun-99
rx01491	774	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,062	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

rxa01508	1662	GB_EST13:AA356956	255	AA356956	EST65614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	37,647	21-Apr-97
		GB_OV:OMDAPRO1	7327	X92380	O.mossambicus prolactin l gene.	Tilapia mossambica	38,289	19-OCT-1995
		GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	37,984	23-Nov-98
		GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	38,469	23-Nov-98
rxa01512	723	GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	39,021	19-MAY-1999
		GB_BA1:MAU88875	840	U88875	Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene, complete cds.	Mycobacterium avium	57,521	05-MAR-1997
rxa01514	711	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
		GB_BA1:MTCY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
		GB_PL1:EGGTPCHI	242	Z49757	E.gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
rxa01515	975	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-96
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-96
		GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
rxa01516	513	GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-Drosophila melanogaster 1).	Drosophila melanogaster	36,346	13-Aug-99
		GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BAGR01106 (D1054) RPCI-98 01.1.6 map 55D-55D strain y; on bw sp. *** SEQUENCING IN PROGRESS ***, 86 unordered pieces.	Drosophila melanogaster	37,897	20-Aug-99
rxa01517	600	GB_IN2:AF132179	4842	AF132179	Drosophila melanogaster clone LD21677 unknown mRNA.	Drosophila melanogaster	36,149	3-Jun-99
		GB_PL2:F6H8	82596	AF178045	Arabidopsis thaliana BAC F6H8.	Arabidopsis thaliana	35,846	19-Aug-99
		GB_PL2:AF038831	647	AF038831	Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saponariae	40,566	13-Apr-99
		GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
rxa01521	921	GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from Tq31, complete sequence.	Homo sapiens	36,623	20-Aug-97
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from Tq31, complete sequence.	Homo sapiens	34,719	20-Aug-97
rxa01528	651	GB_RO:MM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
rxa01551	1998	GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,064	17-DEC-1993
		GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,775	8-Jul-99
rxa01561	1053	GB_IN1:CEY62H9A	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
		GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1999
		GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
rxa01599	1785	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
		GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	29-Sep-94
		GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97

TABLE 4: ALIGNMENT RESULTS

rx01617	795	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
		GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
		GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
rx01657	723	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 1171162.	Mycobacterium tuberculosis	40,656	17-Jun-98
		GB_EST6:D79278	392	D79278	HUM213D06B Human aorta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-96
		GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
rx01660	675	GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome, segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
		GB_RO:MMFV1	6480	X97719	M.musculus retrovirus restriction gene Fv1.	Mus musculus	35,364	29-Aug-96
		GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
rx01678	651	GB_VI:TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene, partial cds.	Tula virus	41,894	28-OCT-1997
		GB_VI:TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene, partial cds.	Tula virus	41,712	28-OCT-1997
		GB_VI:TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene, partial cds.	Tula virus	39,576	28-OCT-1997
rx01679	1359	GB_EST5:H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_ma1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence	Homo sapiens	39,157	29-Nov-95
		GB_STS:G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
		GB_PL2:AF139451	1202	AF139451	Gossypium robinsonii CelA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
rx01690	1224	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
		GB_EST22:A064232	493	A064232	GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
		GB_IN2:AF117896	1020	AF117896	Drosophila melanogaster neurotrophin F (ntr) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
rx01692	873	GB_BA2:AF067123	1034	AF067123	Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
		GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
		GB_RO:RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp.	37,093	14-Jul-95
rx01698	1353	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98
		GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	62,780	15-Jun-96
rx01699	693	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidI) gene, partial cds; polyketide synthase modules 1 through 7 (nidA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	40,260	07-DEC-1997
		GB_EST9:C19712	399	C19712	C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence.	Oryza sativa	45,425	24-OCT-1996
rx01712	805	GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	40,876	29-OCT-1998

TABLE 4: ALIGNMENT RESULTS

GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	41,367	29-OCT-1998
GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	35,651	23-Nov-99
GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	35,651	23-Nov-99
GB_EST27:AI447108	431	AI447108	mq91e08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.	39,671	09-MAR-1999
GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	35,817	18-MAR-1999
GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.	35,698	12-Jul-97
GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	37,243	18-MAR-1999
GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	42,812	22-MAY-1995
GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	42,655	22-MAY-1995
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	59,294	17-Jun-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	57,584	22-Aug-97
GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	61,810	22-Jul-99
GB_EST21:AA918454	416	AA918454	om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP-F28F8.3 CE09757 SMALL NUCLEAR RIBONUCLEOPROTEIN E.; mRNA sequence.	39,655	23-Jun-98
GB_EST4:H34042	345	H34042	EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp cDNA clone RPNB181 5' end, mRNA sequence.	35,942	2-Apr-98
GB_EST20:AA899038	450	AA899038	NCP6G877 Perithecial Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.	40,000	12-Apr-98
GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	40,067	22-Jun-99
GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	100,000	7-Jan-99
GB_RO:RATALGL	7601	M24108	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	38,692	15-DEC-1994
GB_OV:APIGY2	1381	X78272	Anas platyrhynchos (Super M) IgY upslion heavy chain gene, exon 2.	36,962	15-Feb-99
GB_EST30:AI629479	353	AI629479	486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	38,109	26-Apr-99
GB_STS:G48245	515	G48245	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	37,021	26-MAR-1999
GB_GSS3:B49052	515	B49052	RPC111-4112.TV RPC1-11 Homo sapiens genomic clone RPC1-11-4112, genomic survey sequence	37,021	8-Apr-99

TABLE 4: ALIGNMENT RESULTS

rx01850	1470	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,196	U18997
		GB_BA2:AE000392	10345	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome.	Escherichia coli	38,021	12-Nov-98
		GB_BA2:U32715	13136	U32715	Haemophilus influenzae Rd section 30 of 163 of the complete genome.	Haemophilus influenzae Rd	39,860	29-MAY-1998
rx01878	1002	GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,576	14-OCT-1998
rx01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162.	Mycobacterium tuberculosis	35,910	19-Jun-98
		GB_BA1:MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	64,260	27-Aug-99
		GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	64,260	15-Jun-96
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELLF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E:19 map 36E-37C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01920	1125	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds	Corynebacterium glutamicum	99,733	5-Aug-99
		GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdL, nrdE, nrdF genes.	Corynebacterium ammoniagenes	70,321	18-Apr-98
		GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
rx01928	960	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	15-Sep-99
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	15-Sep-99
rx01929	936	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_BA1:XCU33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	19-Sep-96
rx01940	1059	GB_BA1:XANHRPB6A	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
		GB_IN2:CFU43371	1060	U43371	Critidia fasciculata inosine-uridine preferring nucleoside hydrolase (LUNH) gene, complete cds.	Critidia fasciculata	61,417	18-Jun-96
		GB_BA2:AE001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,560	20-Jan-99
		GB_RO:AF175967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.	Mus musculus	40,275	26-Sep-99
rx02022	1230	GB_BA1:CGDAPE	1966	X81379	C.glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
		GB_BA1:CGDNAAROP	2612	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
		GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds.	Anabaena PCC7120	36,647	17-Feb-96
rx02024	859	GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98

GB BA1:MSGB1912CS 38503 L01536 M. leprae genomic dna sequence, cosmid b1912.

GB_BA1:MSGB1912CS	38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
GB_BA1:CGGDHA	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,367	30-Jul-99
GB_BA1:PAE18494	1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	6-Feb-99
GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
GB_BA1:ECOUW85	91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737 5', Homo sapiens mRNA sequence.	Homo sapiens	34,163	4-Jun-97
GB_EST17:AA641937	444	AA641937	ns18b10.r1 NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963 5', Homo sapiens mRNA sequence.	Homo sapiens	35,586	27-OCT-1997
GB_PR3:AC003074	143029	AC003074	Human PAC clone DJ0596O09 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
GB_BA1:SC1A6	37620	AL023496	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
GB_PR4:AC005553	179651	AC005553	Homo sapiens chromosome 17, clone hRPK 112_J_9, complete sequence.	Homo sapiens	34,274	31-DEC-1998
GB_EST3:R49746	397	R49746	y971g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN	Homo sapiens	41,162	18-MAY-1995
GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
GB_BA1:U00010	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	37,909	24-Sep-99
GB_GSS3:B09839	1191	B09839	121 unordered pieces.	Arabidopsis thaliana	37,843	14-MAY-1997
GB_HTG3:AC010579	157658	AC010579	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Drosophila melanogaster	37,909	24-Sep-99
GB_BA1:SCSECYDNA	6154	X83011	09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***	Streptomyces coelicolor	36,533	02-MAR-1998
GB_EST32:AI731596	568	AI731596	121 unordered pieces.	Gossypium hirsutum	33,451	11-Jun-99
GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998
GB_EST32:AI731596	568	AI731596	BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	33,451	11-Jun-99
GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998

TABLE 4: ALIGNMENT RESULTS

rx02135	1197	GB_PR3:HS525L6	168111	AL023807	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG island, complete sequence	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	34,325	9-Jun-99
rx02136	645	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98
		GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
rx02139	1962	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rx02153	903	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGC:JBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGC:JBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02155	1287	GB_BA1:CGARGC:JBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSGB1133CS	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96

TABLE 4: ALIGNMENT RESULTS

rx02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA1:CGARGC:JBD	4355	X86157		Corynebacterium glutamicum	100,000	25-Jul-96
rx02157	1296	GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	1-Jul-98
		GB_BA1:CGARGC:JBD	4355	X86157		Corynebacterium glutamicum	99,612	25-Jul-96
rx02158	1080	GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds. C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA2:AF031518	2045	AF031518		Corynebacterium glutamicum	99,898	5-Jan-99
		GB_BA1:CGARGC:JBD	4355	X86157		Corynebacterium glutamicum	100,000	25-Jul-96
rx02159	636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
		GB_BA2:AF031518	2045	AF031518		Corynebacterium glutamicum	88,679	5-Jan-99
rx02160	1326	GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds. S. clavuligerus argG gene and argH gene (partial)	Corynebacterium glutamicum	99,774	1-Jul-98
		GB_BA2:AF030520	1206	AF030520		Corynebacterium glutamicum	99,834	19-Nov-97
		GB_BA1:SCARGGH	1909	Z49111		Streptomyces clavuligerus	65,913	22-Apr-96

TABLE 4: ALIGNMENT RESULTS

rx02162	1554	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98
		GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
rx02176	1251	GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
		GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
		GB_PL2:PGU65399	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
rx02189	861	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
		GB_BA1:MSGB1970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
rx02193	1701	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
		GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-96
rx02194	966	GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
		GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
rx02195	393	GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds.	Corynebacterium glutamicum	100,000	8-Feb-99
		GB_BA1:EAY17145	6019	Y17145	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
rx02197	551	GB_STS:G01195	332	G01195	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
rx02198	2599	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-99
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
rx02208	1025	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
		GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	39,442	22-Jun-99
		GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hC1T.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
rx02229	948	GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
rx02234	3462	GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome, segment 61/162.	Mycobacterium leprae	71,723	18-Jun-98
		GB_BA2:U01072	4393	U01072	Mycobacterium bovis BCG orotidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993

TABLE 4: ALIGNMENT RESULTS

rx02235	727	GB_BA1:MSU91572	960	U91572	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and orotidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
rx02237	693	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST22:AU017763	586	AU017763	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0744A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
rx02239	1389	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
rx02240	1344	EM_PAT:E09855	1239	E09855	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
		GB_PAT:A37831	5392	A37831	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
rx02246	1107	GB_BA2:AF117274	2303	AF117274	Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds; and S-adenosylmethionine synthetase (metK) gene, complete cds	Streptomyces spectabilis	65,000	31-MAR-1999
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	52,909	29-Sep-97
rx02247	756	GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	52,909	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel. 52, Created)
rx02248	1389	GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	29-Sep-97
rx02249	600	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,346	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	64,346	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	64,346	6-Feb-97

TABLE 4: ALIGNMENT RESULTS

rxs02250	643	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:132742	5589	I32742	Sequence 1 from patent US 5589335.	Unknown	56,318	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1997 (Rel. 52, Created)
rxs02262	1269	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C. glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
rxs02263	488	GB_VI:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	human herpesvirus 5	38,651	10-Feb-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
rxs02272	1368	EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1997 (Rel. 52, Created)
rxs02281	1545	GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	7-Aug-98
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	36,264	20-Feb-99
		GB_GSS12:AQ411010	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence.	Homo sapiens	36,197	17-MAR-1999
		GB_EST23:A1128623	363	A1128623	qa62c01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
rxs02299	531	GB_PL2:ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
		GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
		GB_GSS9:AQ164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.	Homo sapiens	37,278	16-OCT-1998
rxs02311	813	GB_VI:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98	Drosophila melanogaster	36,454	27-OCT-1999
					48.G.5 map 91F1-91F13 strain y, cn bw sp, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.			
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98	Drosophila melanogaster	36,454	27-OCT-1999
					48.G.5 map 91F1-91F13 strain y, cn bw sp, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.			

TABLE 4: ALIGNMENT RESULTS

rxa02315	1752	GB_BA1:MSGY224	40051	AD000004	Myco bacterium tuberculosis sequence from clone y224.	Myco bacterium tuberculosis	49,418	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Myco bacterium tuberculosis H37Rv complete genome; segment 28/162.	Myco bacterium tuberculosis	49,360	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Myco bacterium tuberculosis sequence from clone y224.	Myco bacterium tuberculosis	38,150	03-DEC-1996
rxa02318	402	GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3:AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999
rxa02319	1080	GB_BA1:MSGY224	40051	AD000004	Myco bacterium tuberculosis sequence from clone y224.	Myco bacterium tuberculosis	37,792	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Myco bacterium tuberculosis H37Rv complete genome; segment 28/162.	Myco bacterium tuberculosis	37,792	17-Jun-98
		GB_EST23:AI117213	476	AI117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5' mRNA sequence.	Mus musculus	35,084	2-Sep-98
rxa02345	1320	GB_BA1:BAPURKE	2582	X91189	B.ammonia genes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97
rxa02350	618	GB_BA1:MTCY71	42729	Z92771	Myco bacterium tuberculosis H37Rv complete genome; segment 141/162.	Myco bacterium tuberculosis	39,624	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Myco bacterium tuberculosis H37Rv complete genome; segment 141/162.	Myco bacterium tuberculosis	39,847	10-Feb-99
		GB_BA1:BAPURKE	2582	X91189	B.ammonia genes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97
rxa02373	1038	GB_PL1:SC130KBXV	129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97
		GB_PAT:I06030	1853	I06030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1994
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	21-MAY-1993
rxa02375	1350	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Opg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	99,332	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	36,115	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
rxa02380	777	GB_BA1:MTCY253	41230	Z81368	Myco bacterium tuberculosis H37Rv complete genome; segment 106/162.	Myco bacterium tuberculosis	38,088	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rx02382	1419	GB_BA1:CGPROAGEN	1783	X82929	C.glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Olg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
rx02400	693	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:186191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:113693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
rx02432	1098	GB_GSS15:AQ06842	574	AQ06842	HS_5404_B2_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99
		GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDG63 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006699	77363	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
rx02458	1413	GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds.	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-0033 Winter flourider ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
		GB_GSS15:AQ650027	728	AQ650027	Sheared DNA-5L2, TF Sheared DNA Trypanosoma brucei genomic clone	Trypanosoma brucei	39,281	22-Jun-99
rx02469	1554	GB_BA1:MTCY359	36021	Z83859	Sheared DNA-5L2, genomic survey sequence.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium tuberculosis H37Rv complete genome, segment 84/162.	Mycobacterium leprae	59,343	27-Aug-99
		GB_BA1:SCAJ10601	4692	AJ010601	Mycobacterium leprae cosmid B1788.	Streptomyces coelicolor	48,899	17-Sep-98
rx02497	1050	GB_BA2:CGU31224	422	U31224	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Corynebacterium glutamicum (ppx) gene, partial cds.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	16911	AL049819	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Streptomyces coelicolor	39,510	10-MAY-1999
rx02499	933	GB_BA2:CGU31225	1817	U31225	Streptomyces coelicolor cosmid E7.	Corynebacterium glutamicum	97,749	2-Aug-96
		GB_BA1:NG17PILA	1920	X13965	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoeductase (proC) gene, complete cds.	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_HTG2:AC007984	129715	AC007984	Neisseria gonorrhoeae pilA gene.	Drosophila melanogaster	33,406	2-Aug-99
rx02501	1188	GB_BA1:MTCY20G9	37218	Z77162	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCI-98 05.C.10 map 97D-97E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***. 87 unordered pieces.	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium leprae	51,768	01-MAR-1994
		GB_VI:HE1CG	152261	X14112	Mycobacterium leprae cosmid B2168.	human herpesvirus 1	39,378	17-Apr-97
rx02503	522	GB_PR3:AC005328	35414	AC005328	Herpes simplex virus (HSV) type 1 complete genome.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	3-Sep-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	34,911	28-Jul-98
rx02504	681	GB_BA1:MTCY20G9	37218	Z77162	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005328	35414	AC005328	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Homo sapiens	41,265	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	41,265	3-Sep-98
rx02516	1386	GB_BA1:MLCL536	36224	Z99125	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Mycobacterium leprae	37,723	04-DEC-1998

TABLE 4: ALIGNMENT RESULTS

rx02517	570	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,723	01-MAR-1994
		GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	61,335	17-Jun-98
		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,018	04-DEC-1998
rx02532	1170	GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,018	01-MAR-1994
		GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	37,071	12-Jul-99
		GB_OV:AF137219	831	AF137219	Amia calva mixed lineage leukemia-like protein (Mll) gene, partial cds.	Amia calva	36,853	7-Sep-99
		GB_EST30:AI645057	301	AI645057	vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	41,860	29-Apr-99
		GB_EST20:AA822595	429	AA822595	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	42,353	17-Feb-98
rx02536	879	GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_PL1:ATT12J5	84499	AL035522	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAll project).	Arabidopsis thaliana	35,063	24-Feb-99
rx02550	1434	GB_BA1:MTCY279	9150	Z97991	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
		GB_BA1:MSGB1970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	39,024	15-Jun-96
rx02559	1026	GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	37,906	19-OCT-1999
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	47,358	18-Jun-98
		GB_PAT:128684	5100	I28684	Sequence 1 from patent US 5573915.	Unknown.	39,138	6-Feb-97
		GB_BA1:MTU27357	5100	U27357	Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis	39,138	26-Sep-95
		GB_BA2:AE001780	11997	AE001780	Thermotoga maritima section 92 of 136 of the complete genome.	Thermotoga maritima	44,914	2-Jun-99
rx02622	1683	GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	39,732	17-Aug-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	36,703	17-Aug-99
		GB_GSS5:AQ818728	444	AQ818728	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence.	Homo sapiens	38,801	26-Aug-99
rx02629	708	GB_HTG5:AC011083	198586	AC011083	Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces.	Homo sapiens	35,714	19-Nov-99
		GB_GSS6:AQ826948	544	AQ826948	HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	Homo sapiens	39,146	27-Aug-99
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	37,013	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	37,013	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	37,013	28-Apr-93

TABLE 4: ALIGNMENT RESULTS

rx02645	1953	GB_PAT:A45577 GB_PAT:A45581 GB_BA1:CORILVA	1925 1925 1925	A45577 A45581 L01508	Sequence 1 from Patent WO9519442. Sequence 5 from Patent WO9519442. Corynebacterium glutamicum threonine dehydratase (livA) gene, complete cds.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum	39,130 39,130 39,130	07-MAR-1997 07-MAR-1997 26-Apr-93
rx02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (livA) gene, complete cds.	Corynebacterium glutamicum	99,138	26-Apr-93
rx02648	1326	GB_PAT:A45585 GB_PAT:A45583 GB_OV:ICTCNC GB_EST11:AA265464	1925 1925 2049 345	A45585 A45583 M83111 AA265464	Sequence 9 from Patent WO9519442. Sequence 7 from Patent WO9519442. Ictalur punctatus cyclic nucleotide-gated channel RNA sequence. mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5' mRNA sequence.	Corynebacterium glutamicum Corynebacterium glutamicum Ictalur punctatus Mus musculus	99,066 99,066 38,402 38,655	07-MAR-1997 07-MAR-1997 24-MAY-1993 20-MAR-1997
rx02653		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14. TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	36,074	27-Jun-98
rx02687	1068	GB_BA1:CORPHEA GB_PAT:E04483 GB_PAT:E06110 GB_PL1:HVC4H GB_PR2:HS310H5	1088 948 948 59748 29718	M13774 E04483 E06110 Y14573 Z69705	C.glutamicum pheA gene encoding prephenate dehydratase, complete cds. DNA encoding prephenate dehydratase. DNA encoding prephenate dehydratase. Hordeum vulgare DNA for chromosome 4H. Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Hordeum vulgare Homo sapiens	99,715 98,523 98,523 36,593 36,089	26-Apr-93 29-Sep-97 29-Sep-97 25-MAR-1999 22-Nov-99
rx02754	1461	GB_PR3:AC004754 GB_HTG2:AC008223	39188 130212	AC004754 AC008223	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence. Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.L18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Homo sapiens Drosophila melanogaster	36,089 32,757	28-MAY-1998 2-Aug-99
rx02758	1422	GB_HTG2:AC008223 GB_BA1:MTCY71 GB_HTG5:AC011678 GB_HTG5:AC011678 GB_BA2:AF064070	130212 42729 171967 171967 23183	AC008223 Z92771 AC011678 AC011678 AF064070	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.L18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces. Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS***, 20 unordered pieces. Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS***, 20 unordered pieces. Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds, and putative galactosyl transferase gene, partial cds.	Drosophila melanogaster Mycobacterium tuberculosis Homo sapiens Homo sapiens Burkholderia pseudomallei	32,757 37,838 35,331 33,807 36,929	2-Aug-99 10-Feb-99 5-Nov-99 5-Nov-99 20-Jan-99

TABLE 4: ALIGNMENT RESULTS

rxs02771	678	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcbAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
		GB_IN1:CELT19B4	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
		GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
rxs02772	1158	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcbAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,914	14-Sep-98
		GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
		GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
rxs02790	1266	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
rxs02791	951	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
		GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
		GB_BA1:MSASDASK	5037	Z17372	M.smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
rxs02802	1194	GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ; mRNA sequence	Homo sapiens	40,828	27-OCT-1998
		GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ; mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
rxs02814	494	GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	58,418	17-Jun-98
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	40,496	17-Jun-98
		GB_PR1:HSAJ2962	778	AJ002962	Homo sapiens mRNA for hb-FABP.	Homo sapiens	39,826	8-Jan-98
rxs02843	608	GB_BA1:CGAJ4934	1160	AJ004934	Corynebacterium glutamicum dapD gene, complete CDS.	Corynebacterium glutamicum	100,000	17-Jun-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	37,710	17-Jun-98
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	39,626	09-MAR-1995
rxs03205	963	GB_BA1:BLSIGBGN	2906	Z49824	Blactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	98,854	25-Apr-96
		GB_EST21:AA980237	377	AA980237	ua32a12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1348414 5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN. ; mRNA sequence.	Mus musculus	41,489	27-MAY-1998
		GB_EST23:AI158316	371	AI158316	ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112 5', mRNA sequence.	Mus musculus	38,005	30-Sep-98
rxs03223	1237	GB_IN1:LMFL2743	38368	AL031910	Leishmania major Friedlin chromosome 4 cosmid L2743.	Leishmania major	39,869	15-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RPI-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,930	17-DEC-1999

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TABLE 4: ALIGNMENT RESULTS

GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,634	17-DEC-1999
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APPENDIX A: DNA SEQUENCES

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>RXA00145-downstream
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>RXA00146-upstream
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>RXA00146
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>RXA00147
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>RXA00147-downstream
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>RXA00156-upstream
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>RXA00156
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>RXA00156-downstream
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>RXA00166-upstream
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>RXA00166
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>RXA00198
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>RXA00198-downstream
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>RXA00216-upstream
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>RXA00216
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>RXA00216-downstream
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>RXA00219-upstream

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>RXA00219

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>RXA00219-downstream

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>RXA00223-upstream

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>RXA00223

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>RXA00223-downstream

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>RXA00229

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>RXA00229-downstream
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>RXA00241-upstream
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>RXA00241
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>RXA00241-downstream
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>RXA00254
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>RXA00254-downstream
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>RXA00262-upstream
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>RXA00262
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>RXA00262-downstream
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>RXA00266-upstream
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>RXA00266
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>RXA00266-downstream
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>RXA00278-upstream
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>RXA00278
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>RXA00278-downstream
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>RXA00295-upstream
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>RXA00295
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>RXA00374
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>RXA00376
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>RXA00377

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>RXA00382

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>RXA00383

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>RXA00391
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>RXA00402

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>RXA00426-upstream
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>RXA00426
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>RXA00440

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>RXA00442

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>RXA00448

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>RXA00450-upstream

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>RXA00450

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>RXA00488

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>RXA00489-upstream

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>RXA00489

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>RXA00492-upstream

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>RXA00533

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>RXA00579

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>RXA00580-upstream

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>RXA00770
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>RXA00779
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>RXA00780

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>RXA00838

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>RXA00863

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>RXA00891

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>RXA00956--upstream

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>RXA00956

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>RXA00957

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>RXA01087-upstream
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>RXA01087
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>RXA01098-upstream
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>RXA01100
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>RXA01105-downstream

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>RXA01106-upstream

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>RXA01106

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>RXA01132

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>RXA01145

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>RXA01208
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>RXA01209-upstream
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>RXA01215

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>RXA01239-upstream

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>RXA01239

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>RXA01381

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>RXA01491

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>RXA01512-upstream

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>RXA01512

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>RXA01690-downstream

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>RXA01692-upstream

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>RXA01692

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>RXA01698
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>RXA01699
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>RXA01720
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>RXA01894-upstream

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>RXA01928-upstream

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>RXA01928

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>RXA01928-downstream

TAGTACCAACCCTGCGTTGCAGC

>RXA01929-upstream

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>RXA01929

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>RXA01929-downstream

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>RXA01940

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>RXA01940-downstream

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>RXA01970

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>RXA01970-downstream
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>RXA02022-upstream
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>RXA02022
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>RXA02022-downstream
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>RXA02024-upstream
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>RXA02024
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>RXA02027-upstream

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>RXA02027

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>RXA02031-upstream

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>RXA02031

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>RXA02031-downstream

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>RXA02072-upstream

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>RXA02072

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>RXA02072-downstream
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>RXA02085-upstream
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>RXA02085
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>RXA02085-downstream
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>RXA02086-upstream
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>RXA02086
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>RXA02093-upstream
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>RXA02093
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>RXA02093-downstream
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>RXA02106-upstream
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>RXA02106
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>RXA02106-downstream
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>RXA02111-upstream

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>RXA02111

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>RXA02111-downstream

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>RXA02112-upstream

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>RXA02112

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>RXA02112-downstream

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>RXA02134-upstream

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>RXA02134

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>RXA02246-upstream
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>RXA02311-upstream

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>RXA02311

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>RXA02319-upstream
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>RXA02319
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>RXA02319-downstream
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>RXA02345
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>RXA02346
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>RXA02350-upstream
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>RXA02350
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>RXA02350-downstream
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>RXA02373-upstream
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>RXA02373
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>RXA02375
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>RXA02378
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>RXA02378-upstream
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>RXA02378
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>RXA02380
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>RXA02382
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>RXA02400-upstream
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>RXA02400
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>RXA02405
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>RXA02432-upstream

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>RXA02432

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>RXA02432-downstream

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>RXA02458-upstream

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>RXA02458

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>RXA02458-downstream

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>RXA02469-upstream

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>RXA02469

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>RXA02499-upstream
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>RXA02499
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>RXA02717

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>RXA02758-upstream

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>RXA02758

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>RXA02843-upstream

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>RXA02857-upstream

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>RXA02857

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>RXA02903

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>RXA02903-downstream

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>RXA02906-upstream

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>RXA02906

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>RXA02906-downstream

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>RXN00023-upstream

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>RXN00023

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>RXN00116-downstream
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>RXN00262-downstream
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>RXN00351

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>RXN00355-upstream
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>RXN00365-upstream
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>RXN00365

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>RXN00367-upstream

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>RXN00367

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>RXN01712-upstream

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>RXN01810-upstream

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>RXN03137-upstream

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>RXN03137

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GGCTACGATCCACACCCATTGATCCGCGGCAAGGTCGCCGTA

>RXN03137-downstream

TGATCGGTGCGATTGCGGCACAA

>RXN03171-upstream

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>RXN03171

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>RXN03176

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>RXS00116 - upstream

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>RXS00116

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>RXS00116 - downstream
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>RXS00147 - upstream
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>RXS00147

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>RXS00147 - downstream
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>RXS00349 - upstream
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>RXS00349

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>RXS00349 - downstream
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>RXS00389 - upstream
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>RXS00389
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>RXS00389 - downstream
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>RXS00391 - upstream
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>RXS00391

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>RXS00391 -downstream
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>RXS00393 - upstream
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>RXS00393
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>RXS00393 - downstream
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>RXS00405 - upstream
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>RXS00405
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>RXS00419 - upstream
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>RXS00419
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>RXS00419 - downstream
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>RXS00446 - upstream
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>RXS00446
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>RXS00446 - downstream
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>RXS00618 - upstream
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>RXS00618
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>RXS00618 - downstream

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>RXS00838 - upstream

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>RXS00838

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CTT

>RXS00838 - downstream

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>RXS00870 - upstream

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>RXS00870

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>RXS00870 - downstream

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>RXS00905 - upstream

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>RXS00905

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>RXS00905 - downstream
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>RXS00906 - upstream

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>RXS00906

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>RXS00906 - downstream
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>RXS00907 - upstream

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>RXS00907

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>RXS00907 - downstream
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>RXS00998 - upstream

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>RXS00998

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>RXS00998 - downstream
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>RXS01105 - upstream
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>RXS01105 downstream
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>RXS01130 - upstream
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>RXS01130
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>RXS01130 - downstream
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>RXS01145 - upstream
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>RXS01145
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>RXS01183 - upstream
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>RXS01260
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>RXS01261 - upstream
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>RXS01261
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>RXS01261 - downstream
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>RXS01807 - upstream
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>RXS01807
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>RXS01807 - downstream
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>RXS02001 - upstream
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>RXS02001
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>RXS02001 - downstream
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>RXS02021 - upstream
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>RXS02021
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>RXS02021 - downstream
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>RXS02101 - upstream
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>RXS02101
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>RXS02101 - downstream
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>RXS02157 - upstream
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>RXS02157
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>RXS02157 - downstream
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>RXS02197
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>RXS02197 - downstream
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>RXS02234 - upstream
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>RXS02234
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>RXS03158 - downstream
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>RXS03159 - upstream
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>RXS03159
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>RXS03159 - downstream
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>RXS03183
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>RXS03205
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>RXS03223

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>RXC00152 - upstream

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>RXC00164

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>RXC00164 - downstream
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>RXC00416
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>RXC00540
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>RXC00540 - downstream
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>RXC00552
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>RXC00560 - upstream
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>RXC00560
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>RXC00560 - downstream
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>RXC00657
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>RXC00657 - downstream
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>RXC00733
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>RXC00866
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>RXC01709
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>RXC01711 - downstream
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>RXC01715
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>RXC01946
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>RXC02207
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>RXC02238 - upstream
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>RXC02238
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>RXC02238 - downstream

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>RXC02295 - upstream

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>RXC02380 - upstream

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>RXC02380

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>RXC02390 - upstream

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>RXC02665 - upstream
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 TTGACTGAGCAGCTCACCTTGGCCAGTGCCGGTGTGTTTTACGCTGCGGAGGCCCCGCGAGGCGTTTGGC
 GCCTGCGTTGACCAGGAAGCGGTGGCTGCGGCGTCTCAAGCATCTCTGGAATCGATGTGCCTGCCGTA
 GGTGTGCACTCGGTGCGTCACCAAAATCCGGTCTGTCACCAAAATCGGTGATCTGCCAGCACAGCACATG
 GCGGTGGATATTAATGCCGCATCAGCGTTGGCGGGTCAATCCATCCGCATTGGCTACGACGGACCCGAT
 GAGCGCAAGGCTGCAATGGTGGAGGCGATTGCCAAAGTTGTGAGCCTGCCGGTATCACCGTTATCGAT
 GCGTGCAGGAGGCTGTTAGTCTTAATGATCTCAGTCGAACCGAAGTCAGTGAATGGGGCTATGAGCAG
 TACTTCGAAGGGACACTTGACGCTGTTCTGCGTACAGTGGATCCACATCGGGAGTATGAAAATGCCAAT
 ACCATTGGAAGTATGCGGAGTCGACGAGGCGCACTGAAGAACAATTTGGGCTGAAGTCCCATCAATT
 CCCTAGCAGCGCAACCCCGAGTGTGTTGATAGATCGCACAGTCGGTAACGTTGTTGTTAATACAGAC
 CTAGCCGGTATCGGATGGAACATGGACCGTTGGTCCAGAAGTGAGGAA

>RXC02770 - downstream
 TAAGTAGTGAGCGAACAAGCTCT

>RXC02789 - upstream
 TTCTTCCGTACGGCTATGCTTAAAAGCTAAATTTGTCTTTGTGCTTGCAACACATTAATTTCTTAACA
 CTAAACAATGGAAAGGTAAGCGGGTTTTTCT

>RXC02789
 ATGAAGGTTTCCGCCGATACACCCGGTCACGATGATCCAGGCCAGGCCGGCGCCTTGGCTTAGATGTC
 GGCACCGTGCGCATCGGAGTGGCAGCCTCTGACCGCGATGCCAAGCTTGCCATGCCTGTGGAACCGTT
 CCGCGGGAAACTGGATTCAAAGGGCCAGACCTGGCCGATATTGATCGGTTGGTCCGCATCGTTGAGGAA
 TACAACGCCGTGGAAGTCATTGTTGGTCTACCCACAGATCTGCAGGGAATGGCTCCGCCAGTGTGAAG
 CATGCAAAGGAAATGCTTTCCGCGTCCGTCGGCGCCTCACCAATGCTGGAAAGAACATTCCGGTACGG
 CTTGGCGACGAACCGCTCACCCGTCGTTGGCCACCCAAGCCTTGCAGGCGCTCAGGAGTCAGCGAAAAA
 GCGGGACGTAAAGTTATTGATCAAGCTGCCGCGAGTAGAAATCCTTCAAACCTGGTTGGATGCTCGCACC
 CGAGCCCTTGAACCACAATCCACAGACACCCAAGATTTGCACGAGAAGGGAAATTTCCAGGA

>RXC02789 - downstream
 TGAACCAATCCGAAACCGCCGG

>RXC02921 - upstream
 TGGAAACTGGGAAGGGTTGACGTTGCGGAATCTCTCCGCAGCGTCGGTTCGGACCCTAAAAAGGGTG
 AGGAACCACATGAGCTGTTTAAAGGAATTTT

>RXC02921
 GTGTCTGCACTTGAAGAGTCGATCCGCATCGCGACCATCGCGGCGAAAGCAGCGGATGAAAAGAAGGCC
 GATGACATCGCTGTCATCGATGTCTCTGACATGATCGCAATCACCGATTGCTTTGTTGTTGCATCTGCT
 GACAATGAGCGCCAGGTGGGCGCCATTGTTGAGGAGATCGAAGATGAGATGACCAAGGCTGGTTTCGAG
 CCTAAGCGCCGTGAAGGCAACCGCGAAAACCGTTGGGTTCTCCTTGACTACGGATTGGTTGTTATCCAC
 GTTCAGCGACAGGCAGAGCGCGAGTTCTACGGACTGGATCGTCTGTACCGCGACTGCCCACTCATTGAA
 ATTGAAGGACTTGAAACCTTCAAGCGTGAATCCTCCTGGTCTGATGAGGCGGATATCCGCAACATCGAC
 AGCATTGATGAACTCCCACCTTTGCCAGCTGAATACGAGCCTGGCTACGAGGACGAT

>RXC02921 - downstream
 TAAGAGGTAGTCCTGTGACTCGT

>RXC03185 - upstream
 AGCGCCCAACCGTTCAGACCAGCGGTTTCTCTGAGGATGCAAAGTCCATGATGGGTNAGGTCACTGAGC
 TGTCCGAAACCACC

>RXC03185
 ATGAATGATCTTGCAGCTGAAGGTGAAAACGATCCTTACCGCATGGTTTCAGCAGCTGCGCCGCAAGCTC
 TCTCGCTTCGTCGAGCAGAAGTGGAAGCGCCAGCCGGTCATCATGCCAACCCTCATTCGGATGACTGCG
 GAAACCACGCACATCGGTGACGATGAGGTTTCGCGCTTCACGCGAGTCCCTG

>RXC03185 - downstream
 TAAAAGCATTTTCGCTTTTCGACG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00007 (1-1806, translated) 602 residues

MKPQGLYNPA HEHDACGVAF IADIHGRPSR SIVDRALEAL RNIDHRGAAG AEKNTGDGAG
ILMQIPDGFY REVSGIELPE AGEYATGIAF LPRGRMAMMD AQKEIERIAK QEGADVLGWR
MVPFDSRDLG SMAEEAMPSF AQIFLTVPKG SGEDLDRVMF FIRKRCEREL GTTNGRDTVY
FPSLSSRTII YKGLMTTLQL EGFFEDLGDA RLESAIAIVH SRFSTNTFPS WPLAHPYRFV
AHNGEINTVR GNENWMRARE ALIKNDKLG N LSSVLPICTP EGSDTARFDE ALELLHLGGY
SLPHAVAMMI PQAWEHNKTL SPELRDFEY HSCLMFPWDG PAALAFDGR FVGAVLDRNG
LRPGRITITD SGLVVMASES GVLDLREESV VKRTRVQPGR MFLVDTAAGR IVEDEEIKQK
LSEAQPYGEW IRDNFVHLDR LPQTRYNYMA HSRVLRQRV FGITEEDVDL LLLPMARQGA
EAIGSMGSDT PIAALSQRPR MLYDFFAQRF AQVTNPPLDS IREKPVTSMF TLLGAQSDVL
NPGPDAAARI RLESPIDNH ELATLINANA HGEWDSFGAA VISGLYPVAH HGAGMKAAIA
RV

> RXA00023 (1-453, translated) 151 residues

HFPLRPAEVV LRLDDSATPR ETARALLAAR RAGVTPRVLQ TPGVSEQVRE VLSAAGVSAE
TVDDSVFISN VLRGEYDENS SVRVRYLGKV SDTVRERLSV RPEVVLLDDA VTASGRVELR
YWLKEQAISM TLHRFGNPVA AFHELAEEK R

> RXA00044 (1-936, translated) 312 residues

MASATFTGVI PPVMTPLHAD GSVDVESLRK LVDHLINGGV DGLFALGSSG EAAFLTRAQR
KLALTTIIIEH TAGRVPTAG VIETTTARVI ELVEDALEAG AEGLVATAPF YTRTHDVEIE
EHFRKIHAHA PELPLFAYNI PVSVHNLNP VMLLTAKDG VLAGTKDSSG NDGAIRSLIE
ARDDAGLTEQ FKILTGSETT VDFAYLAGAD GVVPG LGNVD PAAYAALAKL CLDGKWAEAA
ALQKRINHLF HIVFVGDTSH MSGSSAGLGG FKTALAH LGI IESNAMAVPH QSLSDEETAR
IHAIVDEFLY TA

> RXA00064 (1-1278, translated) 426 residues

MSSVSLQDFD AERIGLFHED IKRKFDLKS KNLKLDLTRG KPSSEQLDFA DELLALPGKG
DFKAADGTDV RNYGGLDGIV DIRQIWADLL GVPVEQVLG DASSLNIMFD VISWSYIFGN
NDSVQPSKE ETVKWICPVP GYDRHFSITE RFGFEMISVP MNEDGPDMDA VEELVKNPQV
KGMWVVPVFS NPTGFTVTED VAKRLSAMET AAPDFRVVWD NAYAVHTLTD EFPEVIDIVG
LGEAAGNPNR FWAFTSTSKI TLAGAGVSFF LTS AENRKWY TGHAGIRGIG PNKVNQLAHA
RYFGDAEGVR AVMRKHAASL APKFNKVLEI LDSRLAEYGV AQWTV PAGGY FISLDVVP GT
ASRVAELAKE AGIALTGAGS SYPLRQDPEN KNLRLAPSLP PVEELEVAMD GVATCVLLAA
AEHYAN

> RXA00072 (1-441, translated) 147 residues

MSFQLVNALK NTGSVKDPEI SPEGPRTTTP LSPEVAKHNE ELVEKHAAAL YDASAEILE
WTAEHAPGAI AVTLSMENTV LAELAARHLP EADFLFLDTG YHFKETLEVA RQVDERSQK
LVTALPILKR TEQDSIYGLN LYRSNPA

> RXA00075 (1-663, translated) 221 residues

MTTPLRVAVI GAGPAGIYAS DLLIRNEERE VFVDLFEQMP APFGLIRYGV APDHPRIKGI
VKSLHNVL DKL PRLRL LGNIE IGKDITVEEL RDYYDAVVFS TGAVADRDLN IPGIEAEGSF
GAGEFVG FYD GNPRFERSWD LSAQSVAVIG VGNVGLDVAR ILAKTGDELK VTEISDNVYD
SLKENKXXEV HVFGRRWPST QQVHPTGTXR TXPLPHQRG C

> RXA00105 (1-675, translated) 225 residues

MTVPTPYEDL LRKIAEEGSH KDDRTGTGTT SLFGQQIRFD LNEGFP LLTT KKVHFH SVVG
ELLWFLQGDS NVKWLQDN NI RIWNEWADED GELGPVYGVQ WRSWPTPDGR HIDQISGALE
TLRNNPDSRR NIVSAWNVSE LENMALPPCH LLFQLYVADG KLSCQLYQRS ADMFLGV PFN
IASYALLTHM FAQQAGLEV G EFIWTGGDCH IYDNHKEQVA EQLSR

> RXA00106 (1-456, translated) 152 residues

MIGAIWAQGR DGIIGDGTDM PWHIPEDLKH FKKTMTGQPV IMGRRTWESL PFKPLPGREN
FILSSREPGD WSAGGTVVTE IPKSGWIMGG GEVYKATVGS ADVLEITLID ATFDVSTPVY
APEIPANFNL DDESEWFTSG EYRYKFQRYI KV

> RXA00115 (1-1047, translated) 349 residues

MLDNSFYTAE VQGPYETASI GRLELEEGGV IEDCWLAYAT AGTLNEDKSN AILIPTWYSG
 THQTWFQQYI GTDHALDPSK YFIISINQIG NGLSVSPANT ADDSISMSKF PNVIRIGDDVV
 AQDRLLRQEF GITELEFAVVG GSMGAQQTYE WIVRFPDQVH RAAPIAGTAK NTPHDFIFTQ
 TLNETVEADP GFNGGEYSSH EEVADGLRRQ SHLWAAMGFS TEFWKQEAWR RLGLESKESV
 LADFLDPLFM SMDPNTLLNN AWKWOHGDVS RHTGGDLAAA LGRVKAKTFV MPISEDMPFP
 VRDCAAEQAL IPGSELRVIE DIAGHLGLFN VSENYIPQID KNLKELFES

> RXA00116 (1-507, translated) 169 residues
 MTQRAVEAGA INLGQGFPE DGPRRMLEIA SEQILGGNNQ YSAGRGDASL RAAVARDHLE
 RFDLEYNPDS EVLITVGATE AITATVLGLV EPGDEVIVLE PYYDAYAAAI ALAGATRVAV
 PLQEVENSWD VDVKLHAAV TKKTRMIIVN SPHNPTGSVF SKKALKQLA

> RXA00131 (1-609, translated) 203 residues
 MIVSIEGIDG AGKNTLVSA TQVIDAKVLA FPRYETSIIH QLAAEALHGR MGDLTDSAYA
 MATLFALDRH FAIDDLNAPG VVLLDRYVAS NAAITAARLL DDDAPRWVAD LEFGRLGLPR
 PTLQVLLDTP AEVAQDRARR REALDSARAR DRYESDSALQ QRTAEHYRRL AADNWESPMI
 VVAPDEDPGH VAQRIVEFLG TIN

> RXA00132 (1-105, translated) 35 residues
 HVEALGGQLT ELTKQAEYI GVDVAGPFKP EHYRY

> RXA00145 (1-936, translated) 312 residues
 MKHLLSISDL SKDEIVGLLD EADRFKEVLE GREVKKLPTL RGRITFTLFY ENSTRTRSSF
 ETAGKWSAD VINISASSSS VKKGESLKDT GLTSLAIGAD AIIMRHPASG AAQQLAQFVA
 PGGNGPSVIN AGDGSHQHPT QALLDALTIR QRTGRIEGLK VVIVGDCCLS RVVRSNVDLL
 STLGAEVVLV APPTLLPIGV ENWPVRFSDY MDAEIADADV VMMLRVQQR MQGGFFPSHR
 EYATLYGMSK EREARLKDSA IIMHPGPMRL GMEINFQVAD APRTAVLQQV SNGVHMRMAI
 LFALVAGSDA TI

> RXA00146 (1-1341, translated) 447 residues
 VVDSNTQYPE TGALAPAPAD SLLISNVLVY GEGEPTNVFV KDGVI A AIGG THEADRTIDG
 NGGVLLPGFV DMHVHLREPG REDTETIATG SAAAAGGGFT AVFTMANTTP VMDQPVIAES
 VWFKGQNI GL CDVHPVGSIT KGLEGKELTE FGMMARSEAK VRMFSDDGKC VDDPQVMRRA
 LEYAKGMDVL IAQHAEDHRL TEGASAHEGE NAARLGLRGW PRVAEESIV RDAIMARDYG
 NRVHICHAST EGTVELLRWA KSQGIPITAE VTPHHLTLTD ERLETYDAVN KVNPPRESR
 DAEALKKALL DGTIDVVATD HAPHGSEDKC CEFENAKPGM LGLETSLSII VDTFVATGLA
 DWRFVARVMS ERPAEITRLP GQGRPIAEGE PANLAIVDPG KWTASGADF ASKAENTPFE
 GQEFSAKVTH TVLRGKVTC A DGVAQNA

> RXA00147 (1-1179, translated) 393 residues
 VSKDTTTYQG VTEIGSVPAY LVLADGRFTT GFGFGAIGTT LGEAVFTTAM TGYQETMTDP
 SYHRQIVVAT APQIGNTGWN DEDNESRDGK IWVAGLVIRD LAARVSNWRA TTSLQQEMAG
 QGIVGIGGID TRALVRHLRN EGSIAAGIFS GADAQRPVEE LVEIVKNQPA MTGANLSVEV
 SADETYVIEA EGEERHTVVA YDLGIKQNTF RRFSARGVRT VIVPAETPFE DIKQYNPSGV
 FISNGPGDPA AADVMVDIVR EVLEADIPFF GICFGNQILG RAFGMETYKL KFGHRGINVP
 VKNHITGKID ITAQNHGFAL KGEAGQEFET DFGTAIVTHT CLNDGVVEGI ALKSGRAYSV
 QYHPEAAAGP NDASPLFDQF VELMDADAQK KGA

> RXA00156 (1-1110, translated) 370 residues
 MNERTSDAFD ALLVLSFGGP EGHEEVRPFL ENVTHGRGIP PERLDEVAVH YHHFGGISPI
 NALNREIIAN VEKELASRDH KLPVYFGNRN WKPFNDNEAAE QMADDGVKNA LVLATSAGG
 YSGCRQYQED IQGMIKHLES QGQSITFTKL RQFYDHPRFV STMAQLVQDS YAKLPDELRLD
 EARLVFTAHS IPLTADNAAG TPEDGSLYST QVKEASALIA EAVGVSDFDV VWQSRSGSPH
 TPWLEPDIVD HAVELNEKGQ KALVVCVGF ISDHMEVIWD LDSELMEEA E KRNMMVERVA
 TVGPTDEFAA LVVDLIEEAE LKRVIERLGLK LPARGSSVNG APCGDGCCGT AKHK TARVNP
 NARSAAPAAAN

> RXA00166 (1-660, translated) 220 residues
 VELARGFGRV LDVGAGTGKL TSELTADQVL ALDPSMDMLR VFRSALPAVP CWQATAEHTG
 IRDNAVDLIT CAQTWHWVDV TAASAEFDRV IAPGAVLLV WNNLDTSIAW VHRLSRIMHA
 GDVLKPGFTP ETAAPWIIDR EIRTTWNQHL TPETIIQLAH TRSYWLNASE KIKERVDQNL

QWYLYEHLGF SPDNPVELPY RCDAFLLSRS GTLAGRSSNL

> RXA00198 (1-282, translated) 94 residues
LVLVALGFTG AEQGGLAHEL GVGFDGRRI LRDSEYRSPT NSRVYIAGDN GRGQSLIVWA
IAEGRACAAA IDADLMGETA LPVAVAPQDV PLAV

> RXA00216 (1-990, translated) 330 residues
LGAYGLGELP GKSAEEAADI IQGETGDLH IPQLPARGLG ADLIGRTVGL LDMINVDRGA
RSWVMSTRPS RLTHLTGDFL DMDLDACEET WGTGVDKLKI QVAGPWTGLA RIELANGHRV
LSDRGAMRDL TQALIAGIDA HARKVAGRFR AEVQVQIDEP ELKSLIDGSL PGTSTFDIIP
AVNVADASER LQQVFSSIEG PTYLNLTGQI PTWDVARGAG ADTVQISMDQ VRGNEHLDGF
GETITSGIRL GLGITTKDV VDELLERPRQ KAVEVARFFD RLGVRNYLV DAVDIHPGED
LVQGTITEAA QAYRMARVMS EMLSKDSCDL

> RXA00219 (1-942, translated) 314 residues
VARKKNTSDQ SRSQAANTPI AGTYEGEYSV IELEADSYTT DGWLISINGV PSSHIVLGQP
QALEFEYMRW IATGARAFID AHQDASKLRI THLGGGACTM ARYFADVYPQ SRNTVVVELDA
ELARLSREWF DIPRAPRVKI RVDDARMVAE SFTPASRDVI IRDVFAGAIT PQNFTTVEFF
EHCHRGLAPG GLYVANCGDH SDRGAKSEL AGMMEVFEHV AVIADPPMLK GRRYGNILM
GSDTEFFSSN STEASAITRE LLGGGVPAQY KDESWVRKFA SGAQARHDGV STLQMPSDTP
QHPAETPEHS NTQP

> RXA00223 (1-1089, translated) 363 residues
MREVAANAAM ENAQALNPAS QYSGSRKARS VADSAREEIA SLLGCEPIEV VFTASGTEAD
NLAVQGLFHA SPLNRIISTP IEHPGILETV KALELGGAEA ELMPIGPDGR VSSFEALDKP
AAVATMMWAN NETGAIQPVV EFIAAAQASG TPTHIDAVQV VGHLPPNFDE LGATTLAASA
HKFGGPRGVG LLLVRRSPAP SAVLHGGGQE RGIRPGTLDV AGAAATAAAL REAVAELDGE
ATRLRGLKKM LLDAILHTIP NVLVHTTEPS LPHGLHLSFP GAEGDSLIML LDSLRIEAST
GSACSNVNR ASHVLLAMGI SETDARGAIR FTLGRITTEE SIKAVIAVIE DVVTRARTAG
MAF

> RXA00229 (1-780, translated) 260 residues
EAKGLAQGRA TVYRRIDTLG SRASQDLNT LLDAALYLGF SGLNITHPYK QAVLPLLGEV
SEQATQLGAV NTVVMDATGH TTGHNTDVSG FGRGMEEGLP NAKLDSVVQV GAGGVENAVA
YALVTHGVQK LQVADLDTSR AQALADVINN AVGREAVGV DARGIEDVIA AADGVVNATP
MGMPAHPGTA FVDSCLTKDH WVGDVVYMPI ETELLKAARA LGCETLDGTR MAIHQAVDAF
RLFTGLEPDV SRMRETFLSL

> RXA00241 (1-1503, translated) 501 residues
VNTQSDSAGS QGAAATSRTV SIRTIALII GSTVGAGIFS IPQNIQSVAG PGAMLIGWLI
AGVGMLSVAF VFHVLARRKP HLDGSGVYAYA RVGLGDYVGF SSAWGYWLGS VIAQVGYATL
FFSTLGHYVP LFSQDHPFVS ALAVSALTWL VFGVVSARGIS QAAFLTTVTT VAKILPLLCF
IILVAFGLFS WEKFTVDLWA RDGGVGSIFD QVRGIMVYTV WVFIEGAS VYSRQARSRS
DVSRAVIGF VAVLLLLVSI SLSFGVLTQ QELAALPDNS MASVLEAVVG PWGAALISLG
LCLSVLGAYV SWQMLCAEPL ALMAMDGLIP SKIGAINSRG AAWMAQLIST IVIQIFIIIF
FLNETTYVSM VQLATNLVLYV PYLFSAFYLV MLATRGKGIT HPHAGTRFDD SGPEISRREN
RKHLIVGLVA TVYSVWLFYA AEPQFVLFGA MAMLPGLIPY VWTRIYRGEQ VFNRFIEGVV
VVLVVAASAG VIGLVNGSL L

> RXA00254 (1-594, translated) 198 residues
QPLKLGAHAV LHSTTKYIGG HSDVVGGLVV TNDQEMDEEL LFMQGGIGPI PSVFDAYLTA
RGLKTLAVRM DRHCDNAEKI AEFLLSRPEV STVLYPGLKN HPGHEVAAKQ MKRFGGMISV
RFAGGEEAAK KFCTSTKLIC LAESLGGVES LLEHPATMTH QSAAGSQLEV PRDLVRISIG
IEDIEDLLAD VEQALNNL

> RXA00262 (1-819, translated) 273 residues
VAGHLITPI EHDSVLETA YLERFHDFFI TYLSPDHTGL ISPEGLRKAV RPDITLISIG
YANNEVGTIQ PIAELAAVSS TPFHTDAVQA AHLTFDLGVD ALSLSGHKFG APKGIGVLWS
KLPLEPVIHG GGQEKGRSG TENVAGIAF ATAELARAE SYPDLGEFIE EVLTIPGAHL
TGHPRMRIDG HASFLFDSIG SETVLLELER QGIVCSPGSA CGSGEVSHVL LALGLEEDQA
RTAVRCTFST THSREDALVA ASALKSAVAL IRG

> RXA00266 (1-408, translated) 136 residues
 MTERTLILIK PDGVTNGHVG EIIARIERKG LKLAALDLRV ADRETAEKHY EEHADKPFPG
 ELVEFITSAP LIAGIVEGER AIDAWRQLAG GTDPVAKATP GTIRGDFALT VGENVVHGSD
 SPESAEREIS IWFPNL

> RXA00278 (1-1032, translated) 344 residues
 MHAFRRPPPL TTRVGAALLA ATLLASCTPT PVEPAETLTA LDPDAGPPLP PDSSIEAPGE
 KEPIVEVIEN WPGSLRPDDL TPEERVPGIV NRGRIIVGVD QSQNLLSFRD PVTGELRGFE
 VELAREISRD IFGDPNKVDF RFVGSSDRLR SLDQGDVDIV IRSVTITDER AKLVEFSTPY
 LRTQTRMLTM ESSGITSIAD LPGHTICVTD GSTSLQART IAPEASILKT RNWSDCLMAL
 QQHQAQVILG DDVILSGIAA QDPYTEILDT SLDSHSYGVA AASTTAETDS SGLIRQVNYT
 IERIRTRDMW WTMFDDWFGP YLWSYGPPQL QYMPEEEGTE NDEG

> RXA00295 (1-1002, translated) 334 residues
 MTIPGTILDT ARTQVLEQGI GLNQQQLMEV LTLPEEQIPD LMELAHQVRL KWCGEIEVE
 GIISLKTGGC PEDCHFCSQS GLFESPVRV WLDIPNLVEA AKQTAKTGAT EFCIVAAVKG
 PDERLMTQLE EAVLAIHSEV EIEVAASIGT LNKEQVDRLA AAGVHRYNHN LETARSYFPE
 VVTHTTWEER RETLRLVAEA GMEVCSGIL GMGETLEQRA EFAVQLAELD PHEVPMNFLD
 PRPGTPFADR ELMDSRDALR SIGAFRLAMP HTMLRFAGGR ELTLGDKGSE QALLGGINAM
 IVGNYLTTLG RPMEDDLDM DRLQLPIKVL NKVI

> RXA00306 (1-933, translated) 311 residues
 DSGIPTQLVE GSWFEPVRGR TFDRIIANPP FVVGPPPEIGH VYRDSGMDLD GATALVVKEA
 CAHLNPGGTA HLLGAWVHSA DQSWQQRVAE WLPDNGYVAW VIERDAVSPA QYVGTWLSDE
 SLDLRSPEAA ARTTAWLNHF EKAKVQGVGF GFIAIQRLEE DEADEKSDIL AESMTQYFED
 PLGPEIEEYF TRTAWLREQT RDSILSSRFK VRPGVAREQI SLADAEEMGM FSPVTLRLTR
 TDGPRWSDHV DEHVASIVAG LNPHGLPFEE ILEMYAMAQG IEGESLHNGA IAALVDLIRH
 GLVLPADLLD S

> RXA00323 (1-1338, translated) 446 residues
 MNSEQEFVLS AIEERDIKFV RLWFTDILGH LKSVVVAPAE LESALEEGIG FDGSAIEGYA
 RISEADTIAR PDPSTFQVLP LEAGISKLQA ARLFCDVTMP DGQPSFSDPR QVLRQVQLA
 ADEGLTCMIS PEIEFYLVQS LRTNGLPPVP TDNGGYFDQA TFNEAPNFRR NAMVALEELG
 IPVEFSHHET APGQQEIDLR HADALTMADN IMTFRYIMKQ VARDQGVGAS FMPKPFQEHA
 GSAMHTHMSL FEGDTNAFHD PDDSYMLSKT AKQFIAGILH HAPEFTAVTN QWVNSYKRIV
 YGNEAPTAAT WGVSNRSALV RVPTYRLNKE ESRRVEVRLP DTACNPYLAF SVMLGAGLKG
 IKEYELDEP AEDDISNLSF RERRAMGYND LPSSLDQALR QMEKSELVAD ILGEHVFEFF
 LRNKWREWRD YQEQITPWEL RNNLDY

> RXA00324 (1-3135, translated) 1045 residues
 MSGPLRSERK VVGfVRDPLP KVGSLSLKSE HAQADLEHLG WRNVESLDLL WGLSGAGDPD
 VALNLLIRLY QALEAIGEDA RNELDQEIRO DEKLRLVRLFA LLGGSSAVGD HLVANPLQWK
 LLKLDAPSRE EMFQALLESV KAQPAVLEVE DFSDAHNIAR DDLSTPGFYT ASVTGPEAER
 VLKWTYRTLL TRIAHDLAG TYPTDMRRKG GDPVPFSTVT MQLSDLADAA LTAALAVAIA
 NVYGEKPVD ALSVIAMGKC GAQELNYISD VDVFVVAEPA NSKSTRTAAE LIRIGSNSFF
 EVDAALRPEG KSGALVRSLD SHMAYYKRW ETEWFQALLK ARPMTGDINL GQSYVDALSP
 LIWTASQRES FVTDVQAMRR RVLDNVPEDL RDRELKLRG GLRDVEFAVQ LLQMVHGRID
 ETLRVRSTVN ALHVLVDQGY VGREDGHNLI ESYEFLRLLE HRLQLERIKR THLLPKPDDR
 MNMRWLARAS GFTGSMEQSS AKAMERHLRK VRLQIQSLHS QLFYRPLLNS VVNLSDAIR
 LSPDAAKLQL AALGYLHPSR AYEHLTALAS GASRKAKIQA MLLPTLMEWL SQTAEPDAGL
 LNYRKLSDAS YDRSWFLRML RDEGVVGQRL MRILGNSPYI SELIISTPDF MKQLGDAASG
 PKLLATAPTQ VVKAIKATVS RHESPDAIQ AARSLLRQEL ARIASADLLN MLTVQEVCSQS
 LSLVWDAVLD AALDAEIRAA LNDPQKPDQP LANISVIGMG RLGGAEELGY SDADVNFVCE
 PVAGVEEHEA VTWSIAICDS MRSRLAQPSG DPPLEVDLGL RPEGRSGAIV RTVDSYVKYY
 EKWGETWEIQ ALLRAAWVAG DRELGIKLE SIDRFYRPVD GATQAQLREV RRIKARVDNE
 RLPRGADRNT HTKLGRGALT DIEWTVQLLT MMHAHEIPEL HNTSTLEVLE VLEKHQIINP
 VQVQTLREAW LTATAARNAL VLVRGKRLDQ LPTPGPHLAQ VAGASGWDPN EYQYELNYL
 KVTRKSRQVV DEFWGVDSM EQREF

> RXA00330 (1-1443, translated) 481 residues

VDYISTRDAS RTPARFSDIL LGGLAPDGGI YLPATYPQLD DAQLSKWREV LANEGYAALA
 AEVISLFVDD IPVEDIKAIT ARAYTYPKFN SEDIVPVTEL EDNIYLGHLG EGPTAAFKDM
 AMQLLGELFE YELRRRNETI NILGATSGDT GSSAEYAMRG REGIRVFMLT PAGRMTPFQQ
 AQMFGLDDPN IFNIALDGVF DDCQDVVKAV SADAEFKKDN RIGAVNSINW ARLMAQVYY
 VSSWIRTTTS NDQKVSFSVP TGNFGDICAG HIARQMGLPI DRLIVATNEN DVLDEFFRTG
 DYRVRSSADT HETSSPSMDI SRASNFERFI FDLLGRDATR VNDLFGTQVR QGGFSLADDA
 NFEKAAAEYG FASGRSTHAD RVATIADVHS RLDVLIDPHT ADGVHVARQW RDEVNTPIIV
 LETALPVKFA DTIVEAIGEA PQTPERFAAI MDAPFKVSDL PNDTDAVKQY IVDAIANTSV
 K

> RXA00335 (1-1431, translated) 477 residues
 VAFETPEEIV KFIKDENVF VDVRFDTLPG TEQHFSIPAA SFDADTIEEG LAFDGSSIRG
 FTTIDESDMN LLPDLGTATL DPFKAKTLN VKFFVHDPFT REAFSRDPRN VARKAEQYLA
 STGIADTCNF GAEAEFYLFV SVRYSTEMNS GFYEVDTEEG WWRNGKETNL DGTPNLGAKN
 RVKGGYFPVA PYDQTVDVVD DMVRNLAASG FALERFHHEV GGGQQEINYR FNTMLHAADD
 IQTFKYIKN TARLHGKAAT FMPKPLAGDN GSGMHAHQSL WKDGKPLFHD ESGYAGLSDI
 ARYYIGGILH HAGAVLAFTN ATLNSYHRLV PGFEAPINLV YSQNRNSAAV RIPITGSNPK
 AKRIEFRAPD PSGNPYLGFA AMMAGLDGI KNRIEPHAPV DKDLYELPPE EAASIPQAPT
 SLEASLKALQ EDTDFLTESD VFTEDLIEAY IQYKYDNEIS PVRLRPTPQE FELYFDC

> RXA00347 (1-768, translated) 256 residues
 MTLTIEEIAK TKKLLVVSDF DGTIAGFSKD AYNVPINQKS LKAVKDLSQQ ADTDVVLISG
 RHLEGLKTVL DLGQYDITMV GSHGSEDSSR PRTLTPPEVA RLAKIEADLE KIVDGIEGAF
 VEIKPFHRVL HFIRVSDKDK VQGILAQAAH VDSSGLKVTN GKSIEYSIS STTKGTWLKE
 YVDRTEPTGV IFLGDDTTDE HGFKALEND D RALTVKVGEG DTAAKTRVDD VDNVGIFLEK
 LAYHRMQYAE SVRLGI

> RXA00351 (1-1446, translated) 482 residues
 MDDSNSFVVV ANRLPVDMTV HPDGSYSISP SPGGLVTGLS PVLEQHRGCW VGWPGTVDVA
 PEPFRDGTGV LLHPVVLTA DYEGFYEGFS NATLWPLFHD LIVTPVYNTD WWHAFREVN
 KFAEAVSQVA AHGATVWVD YQLLLVPGIL RQMRPDLKIG FFLHIPFPSP DLFRQLPWRE
 EIVRGMLGAD LVGFHLVQNA ENFLALTQQV AGTAGSHVGQ PDTLQVSGEA LVREIGAHVE
 TADGRRVSVG AFPSIDVEM FGEASKSAVL DLLKTLDEPE TVFLGVDRLD YTKGILQRL
 AFEELLESQA LEADKAVLLQ VATPSRERID HYRVSRSQVE EAVGRINGRF GRMGRPVVHY
 LHRSLSKNDL QVLYTAADVM LVTPFKDGMN LVAKEFVANH RDGTGALVLS EFAGAATELT
 GAYLCNPFV ESIKRQMVAA VHDLKHNPE AATRMKTNSE QVYTHDVNVW ANSFLDCLAQ
 SG

> RXA00352 (1-858, translated) 286 residues
 MHLGKLDQDS ATTILEDYKN MTNIRVAIVG YGNLGRSVEK LIAKQPDMDL VGIFSRRLATL
 DTKTPVFDVA DVDKHADDVD VLFLCMGSAT DIPEQAPKFA QFACTVDTYD NHRDIPRHRQ
 VMNEAATAAG NVALVSTGWD PGMFSINRVY AAVALAEHQH HTFWGPGLSQ GHSDALRRIP
 GVQKAVQYTL PSEDALEKAR RGEAGDLTGK QTHKRQCFVV ADAADHERIE NDIRTMPDYF
 VGYEVEVNF DEATFDSEHT GMPHGGHVIT TGD TGGFNHT VEYILK

> RXA00364 (1-1293, translated) 431 residues
 LPRPEEHAHR ELDLGGEYKW RREGEYHLFN PETIFKLQHA TRSGSYEIFK DYTRKVDQDS
 TRLGITIRGLF EFSTDRKPIS VSEVEPVSEI VKRFSTGAMS YGSISAEAEH VLAIAMNRLG
 GMSNSGEGGE DARRFDVEPN GDWKRSAIKQ VASGRFGVTS HYLNNCTDIQ IKMAQGAQPG
 EGGQLPPNKV YPWVAEVRIT TPGVGLISPP PHHDIYSIED LAQLIHD LKN ANPRARIHV
 LVAEQGVGTV AAGVSKAHAD VVLISGHDGG TGASPLTSLK HAGGPWELGL AETQQTLLN
 GLRDRIRVQC DGQLKTGRDV VIAALLGAE FGFATAPLVV EGCIMMRVCH LDTCPVGIAT
 QNPDLRSKFT GKAEHVNF TFIQAEVREY LAQLGFRSID EAVGQAQVLR KRS GIPADSR
 AAHLDSLPIF I

> RXA00365 (1-627, translated) 209 residues
 MILSPSKTFE LEIVEKAFRE GWVQPVIPSM STGLSVAVVG SGPAGLAAAQ QLTRAGHSVT
 VFERDDRLGG LMRYGVPEYK MENRWIDRRI EQMEAEGTTF QVGTSPRAAE LALFDAILLA
 TGTPVARELS VPGHDLNGIH AAMDYLTAQN RINEGDGEVS PINAKGKKVV IIGGGDTGTD
 CFGTALRQGA ESVTQFDIRP RAFFQRAQS

> RXA00366 (1-357, translated) 119 residues
MADPQGFIKY SRREPAHRPV PLRLMDHSEV YEKAPAGQIE EQAARCMDCG VPFCHEGCPL
GNIIEPWNDL VRQGRWKEAY DRLHATNNFP EFTGRLCPAP CEGACVLGIN DDSVTIKNV

> RXA00367 (1-843, translated) 281 residues
HSLEKALDNA FIDKASDTIT RAAAGVETSI VIDSSISNVN RSVGTMLGSA VSRVAGAQGL
PDGTITLNLQ GCAGNSFGAF IPRGITINLT GDANDFVGKG LSGGKIVIKP SAQAPKQLKN
NPNIIAGNVL GYGATSGELF IRGQVGERFC VRNSGATAVV EGIGNHGCEY MTGGRVLVLG
PVGENFGAGM SGGIAYLANS PDLNQKINGE LVDVVPLSAD DLTWADELIA RHRELTGSET
KLRAQDLVKI MPRDFQKVLN IITAHAEQG DPAIKIMEAV S

> RXA00371 (1-924, translated) 308 residues
MTIAHKPEMA ETTGIETNQV SETIGVESLT HGNLRPVSSF EGQHEGQTEE LLPGKVIFVG
AGPGNPDLT VRAREVLGNA VRAITDEQVL SGVRAFVATE IPVPEDKLQA AEDEYERICI
EAKENGARRK PPRPAPPTAA EITEVSEATP AQIVELVQDA LSYGGDVIRL VTGNPLSSDA
TLAEISAVSE AGLEFQVVP GMSLPATVPAF AGIALGSTYT ETDVNGQNLD WDQLASAPQP
LVLQARVDDL SRIAQELKAR NMSLETVPVS TANGTTRLQR TYDTTLGLLH KLDAELSGPL
VVTLGKGV

> RXA00374 (1-732, translated) 244 residues
TISVEPPRNP AQMERAIKGI VEGRYQWVVL TSVNAVKA VV KKITEFGLDS RSFAGVRIAA
VGEKTA AEIR ALGITPELLP ARTRQNAQGL VDVFPPEYFEE LDPVGRVLLP RADIATDVLV
DGLTHLGWEV EDVVAYRTVR AAPPSADIRD MIKTGGF DAV AFTSSSTVKN LVGIAGKPHF
RTIVACIGPM TAATAEELGL RVDVMPEIAE VPELIDALAE HVADLRAKGE LPPPRKKRRR
RKAS

> RXA00376 (1-282, translated) 94 residues
MRFAIIGAGL AGLTAAEIH KADPTAQIDV LEAGERIGGK LFTVPFASGP TDIGAEAF LA
ARSDAVEFFT ELGLADSLVS PSAAKSQYFA GGAL

> RXA00377 (1-1122, translated) 374 residues
VWLLFLNWDK WGKIERMSAL TIPAARRTLN NAPIIDAANG KTPTRTPVWF MRQAGRSLPE
YKKVREGISM LDSCFMPELL AEITLQPVRR HDVDAAILFS DIVVPLRAAG VGVEIVAGRG
PVLDAVRSR GDVLNLPILE GNVPEVEQGI GIILDELSDS QALIGFAGAP FTLASYLVEG
GPSKNHEKTK AMMHGDPETW HALMARLVPT IVNSLSQID AGIDAVQLFD SWAGFLTERD
YTEFVLPYST EILEEVGKYQ LPRIHFGVGT GELLGAMSKA GSEVMGVDWR VPLDKAAERI
AAVSGPKVLQ GNLDPALIFA GRAPLTKEIE RIKAEAQTA V DAGHATGHIF NLGHGVLPNT
VAEDITEAVS IIHS

> RXA00382 (1-1302, translated) 434 residues
MTSSNTARSA EWFEKAQKLT PGGVNSPVRA FGSVGGQARF IEKAHGSTLI DVDGNEYVDL
VCSWGPMMLG HAHPAVVEAV QKAVVDGLSF GAPTIGLEVEL AQDIVKRTSV EEVRLVNSGT
EATMSAVRLA RGYTQRSKIL KFEGCYHGHV DALLASAGSG VATFALPDSP GITGAQTS DT
IVVPYNDIEA VRNAFAEYPG EIACIIAEAA GGNMGTVAPK DNFNDKLLAI AHADGALLIL
DEVMTGFRTS YRGWFGVDKV AADLVTFGKV VSGGLPAAAF GGKAEIMNML APQGPVYQAG
TLSGNPVAVA AGRASLKLAD ESLYTTINAN ADRLHGLISD ALTHEGVAHH IQRASNMLSI
RFAEGEGHNF SDMKAADIFR FAPFFHTLLD NGVYAPPSVF ETWVSSALT DDDFSKIEQA
LKPAARAAAE AKAS

> RXA00383 (1-1014, translated) 338 residues
AGAQDTAFDW TPGQDISVGA LVRROYGDEI VDTVVSLLG GVSSTADDL GVRASVPALA
AALDQLAEAG EPVTLSAAVK AVEAQREAAK TTSETRPVFQ TFKGGYAELY EALAEQCGAD
IHLDSFVSAI TKDGEGFAIK GGEGGYDKV ILAVPAPTAA VLLRDLAPAA APHLRAIKLA
SSAVVGMFRD SSEGLPDNSG VLVAVNEPGI TAKAFTFSSK KWPHLEARGG ALVRASFGR L
GDEASARMDE DLLVDAALDD LLTITGFDGR AAGLGEIFVQ RWFGGLPAYG VDHIATVSAA
RAEIAAVPGV EAIGAWAGGV GVPAVIADAQ AAVHRLLG

> RXA00391 (1-720, translated) 240 residues
LLRDSQRVGL AIDPSIALVM ATSGSTGTPK GAQLTPLNLV SSADATHQFL GGEGQWLLAM
PAHHIAGMQV LLRSIAGVE PLAIDLSTGF HIDAFAGAAA ELKNTGDRVY TSLTPMQLLK

AMDSLOGIEA LKLFVDVILVG GAALSKQARI SAEQLDINIV TTYGSSETSG GCVYDGKPIP
GAKVRISDER IELGGPMIAQ GYRNAPEHPD FANEGWFTTS DSGELHDGIL TVTGRVDTRH

> RXA00393 (1-882, translated) 294 residues
MSHTEPQPNs VTLSDWIQGA RPRTWANAFa PVIAGSGVAA FHDGFVWWKA LLALVVAWAL
IIGVNYANDY SDGIRGTDED RTGPLRLTGS GLAEPKKVKA AAFISFGIAG VAGTALSLLS
AWWLILIGIL CVLGAWFYTG GKNPYGYRGL GEIAVFIFFG LVAVMGTQFT QTGSVSWAGL
AAAVGVGSMS AGVNLANNIR DIPTDSKTGK ITLAVRLGDA GARKLFLALI STPFIMSICL
AFVAWPALIA IIVFPLALKA AGPIRNNATG KDLIPSSAQQ GAPWRCGPCS RAWH

> RXA00402 (1-576, translated) 192 residues
VLPYFVTPDA AYHGLKYADL GAPAFGLKVR VGLLRDTGST LSAFNAAWAAV QGIDTLsLRL
ERHNENAIKV AEFLNNHEKV EKVNFAGLKD SPWYATKEKL GLKYTGsvLT FEIKGGKDEA
WAFIDALKLH SNLANIGDVR SLVVHPATTT HSQSDEAGLA RAGVTQSTVR LSVGIETIDD
IIADLEGGFA AI

> RXA00403 (1-1110, translated) 370 residues
MPTLAPSGQL EIQAIGDVST EAGAIITNAE IAYHRWGEYR VDKEGRSNVv LIEHALTGDS
NAADWWADLL GPGKaintDI YCVICTNVIG GCNGSTGPGS MHPDGNFWGN RFPATSIRDQ
VNAEKQFLDA LGITTVAaVL GGSMGGARTL EWAAMYpETV GAAAVLAVSA RASAWQIGIQ
SAIKAIEND HHWHegNYyE SGCNPATGLG AARRIAHLTY RGELEIDERF GTKAQKNENP
LGPYRKPDQR FAVESYLDYQ ADKLvQRfDA GSYVLLTDAL NRHDIGRDRG GLNKALesIK
VPVLVAGVDt DILYPYHQQE HLSRNlGNLL AMAKIVSPVG HDAFLTESRQ MDRIVRNFFS
LISPDEDNPS

> RXA00405 (1-513, translated) 171 residues
MPKYDnsNAD QWGFETRSIH AGQSVDAQTS ARNLPIYQST AFVFDsAEHA KQRFALeDLG
PVYSRLTNPT VEALenRIAS LEGGVHAvAF SSGQAATTNA ILNLAGAGDH IVTSPrLYGG
TETLFLITLH RLGIDVSFVE NPDDPESWQA AVQPNTKAFF GETFANPQAD V

> RXA00420 (1-540, translated) 180 residues
WTLNKLTLsA VGVAyyAMGA PAKNQVKNLt QFYQPLDLIG EWNRGYGSKG FLQYQFVVPT
EAVEPFKDII RDMQKSGHYS ALNVFKLFGP GNRAPLSYPM PGWNVcVDFP IRPGLGAFLD
DLDKRVMEFG GRlyLAkesR TSAENFHAMY PGMEGWlKTR NEIDPTGVFA SDMSRRLELS

> RXA00426 (1-522, translated) 174 residues
MNSSHGtSSS GASAGAHGAL PLEAQKLNGW GRTAPTtAEV LTTPDLdIIV DAVRQVAEQN
DSKPDYLKRG VIARGMGRSY GDPAQNAGGL VIDMQPLNKi HSiDPDSaIV DvdGGVTLdQ
LMKAALPYGL WVPVLPGTRQ VTIGGAIGPD IHGKNHHSAG SFGDHVVSME LLVA

> RXA00435 (1-615, translated) 205 residues
VDATTYAAYR PLRLDEWEAD IVMLDLGELG GPQISALIFR DTSMFPRlDR TVPLELPASS
LPHGLLGgVP NLVRHLGNLD ENAPSVVEAM GEMAKFHKGL FEHLVESLEG LHAVHIVGIS
GDAAGQDAPF LDRVPRLTFT MEGVPADMVY RRLVDNRLIT TVSPADPLLE AMGVTEAGGS
ITIGLSPFST YyEVDQlTRV LASLA

> RXA00437 (1-360, translated) 120 residues
KNGVCTEAMG ALVTfEGIVR DHDGGARVTS LTYTAHPTAP QVLSAVADSI VEKHPRTRLW
TAHRTGALKI GDAAFLVVAA SAHRADAFaa CSDLADAVKA QVPIWKEQTR LDGSTDWVGL

> RXA00438 (1-435, translated) 145 residues
VKNLDIARYR RQIMLGEIGQ QKQQSLFDaK VSVIGAGGLG SPALLYLAGA GVGHIHIIDD
DLVDLSNLHR QVIHTTAGVG TPkaEsAREA MLALNPSVKV TVSVRRLDWS NALSELADSD
VILDGSDNFD TRHLASWAAA KLGIP

> RXA00439 (1-195, translated) 65 residues
TDGVRIEASV KTRGVtGVEM EALTAVSTAA LTVYDMIKAV DKMAVIDGIR VLSKTGGKSG
DWSVQ

> RXA00440 (1-459, translated) 153 residues
VTALVIVAST RAAAGVYEDR SGPILVSWLR AKGFDTPAPV IVADANLPaF LDELEFPQVv

LISGGTGLTP DDITVDTLIP RLDKEIPGIA HAFWNYSMDA VPTAVLSRTV AGTIGGSFIM
ALPGSTGAAR DATAVLDP LI DHITGTLQGH HEH

> RXA00441 (1-792, translated) 264 residues
IPATPQQQFI RLQGS DITAG DEIIPAGTEL NSVHIGVLAS QSIKSIEVAA KPRVLIITGG
SEISEQH GPA TIPDANGPLL RSLCARNNIE VIAGLHTNDD PERLRFELN AIDQYQPDVI
ITSGGISHGK FEVFRQILEG TPNSWFGHVD QPQGGPQGIS TFAETPVISL PGNPISTLVS
FTLLVAPALN RQPLRHLDAR ITAPVQGLQD NREQFLRGTI SYRNGPRPRH ASPGHQFPPA
GSSCHRR LSD QDPGADYGGG KRHR

> RXA00442 (1-258, translated) 86 residues
MSELTHVRAD GSAHMDVDTG KNETSRTAVA EGFVKMRGDV VKQLFSAGLP KGDALPVARI
AGIMGAKKTP DIIPLCHPLP LGKITV

> RXA00446 (1-522, translated) 174 residues
MEKVPNDVVV GLDEAYFEFN RADDTPVATE EIHRHDNVIG LRTFSKAYGL AGLRVGYAFG
NAEIIAAMNK VAIPFAVNSA AQAAALASLN SADELMERVE ETVEKRDAVV SALGAAPTQA
NFWVLPGE GA AELAAKLA EH GIVIRAFPEG ARISVTNAEE TDKLLRAW EA INAG

> RXA00448 (1-666, translated) 222 residues
YVGSHPMAGT ANSGWSASMD GLFKRAVWV V TFDQLFDGTD INSTWISIWK DVVQMALAVG
AEVVP SRVGP HDAAAARVSH LTHILAETLA IVGDNGGALS LSLAAGSYRD STRVAGTDPG
LVRAMCESNA GPLVKALDEA LAILHEAREG LTAEQPNIEQ LADNGYRSRI RYEARSQQR
AKESVSPTIT SSRPVLR LHP GTPNWEKQLI HAETLGARIE VF

> RXA00450 (1-318, translated) 106 residues
VGVLVPQARI KDDERRMRHA LDIARQTPEG DVPVGAVIYA PTGEILATAT NRREADRDPT
AHAETIALRR AARRFSDGWR LSDCTAVVTL EPCSMCAGAL VGARIG

> RXA00452 (1-246, translated) 82 residues
VTTKDISRPV CILGLGLIGG SLLRDLHAAN HSVFGYNRSR SGAKSAVDEG FDVSADLEAT
LQRAAAEDAL IVLAVPMTAI DS

> RXA00461 (1-852, translated) 284 residues
VTAIKLDGNL YRGEIFADLE QRVAALKEKG IVPGLATVLV GDDPASHSYV KMKHRDCEQI
GVNSIRKDL P ADVTQEELFA VIDELNND DS CTGYIVQLPL PKHLDENAVL ERIDPAKDAD
GLHPVNLGKL VLNEPAPLPC TPNGSISLLR RFGVELDGAK VVIGRGVTV GRPIGLMLTR
RSENSTVTLC HTGTKDLAAE TRAADVIIAA AGQPHMLTAD MVKPGA AVL D VGSVRKDGKL
LGDVHPDVWE VAGAVSPNPG VVGPLTRAFL VHNVVERAEK LAGL

> RXA00465 (1-492, translated) 164 residues
MTEDDL DLLH RTVELATQAL KQGN SPYGS L LVDPFGAVVF EDHNRDADGD LTKHPEFAIA
KYAIENYSAS ERAACTVYTS TEHCAMCAGA HAWAGLGKIY CATTGGQTAA WYAKWGAESG
PLNPISADKI SPNISIEGPA SRFEVLYEL HRWFYLGQSP NKAL

> RXA00487 (1-1386, translated) 462 residues
VSLQTNHRPV LVVDFGAQYA QLIARRVREA GIYSEVIPHT ATADDVRAKN AAALVLSGGP
SSVYAEGAPS L DAEILD LGL PVFGICYGFQ AMTHALGGTV ANTGKREYGR TDINVAGGVL
HEGLEACHKV WMSHGDAVSE APEGFVVTAS SEGAPVAAFE NKERKMAGVQ YHPEVLHSPH
GQAVLTRFLT EIAGLEQNW T AANIAEELIE KVREQIGEDG RAICGLSGGV DSAVAGALVQ
RAIGDRLTCV FVDHGLLRAG EREQVEKDFV AATGAKLVTV DERQAFLSKL AGVTEPEAKR
KAIGAEFIRS FERAVAGVLE EAPEGSTVDF LVQGTLYPDV VESGGGSGTA NIKSHHNVGG
LPDDVEFKLV EPLRDLFKDE VRAVGRELGL PEEIVGRQPF PGPGLGIRII GEVTEDRLET
LRHADLIART ELTEAGLDGV IWQCPVLLA DVRSVG VQGD GR

> RXA00488 (1-534, translated) 178 residues
QITAIMEAAV PAHKAGVPII ADGGMQFSGD IAKALAAGAN SVMLGSM LAG TAEAPGETIT
INGKQYKRYR GMGSMGAMQG RGLSGEKRSY SKDRYFQSDV KSEDKLVP EG IEGRV PFRGP
IGDIIHQQVG GLRAAMGYTG SSTIEELHNA RFVQITSAGL KESHPHHIQQ TVEAPNYH

> RXA00489 (1-1122, translated) 374 residues

MRDHVEIGIG REARRTYSLD DISVVSSRRT RSSKDVDTTW HIDAYKFDLP FMNHPSDALA
 SPEFVIEMGK QGGLGVINAE GLWGRHADLD EAIKAVIAAY EEGDQAAATR TLQELHAAPL
 DTELLSERIA QVRDSGEIVA VRVSPQNVRE IAPIVIKAGA DLLVIQGTLI SAEHVNTGGE
 ALNLKEFIGS LDVPVIAGGV NDYTTALHMM RTGAVGIIVG GGENTNSLAL GMEVSMATAI
 ADVAAARRDY LDETGGRYVH IIADGSIENS GDVVKAIACG ADAVVLGSPL ARAEEAAGKG
 YFWPAVAHP RFPRGVVTES VDLDEAAPSL EQILHGPSTM PWGVENFEGG LKRALAKCGY
 TDLKSFQKVS LHVN

> RXA00492 (1-474, translated) 158 residues
 MTTQSRVSTG GDNPNKVALV GLTFDDVLLL PDASDVVPSE VDTSTQLTRN IRLNTPILSA
 AMDTVTEAM AIGMARHGGI GVLHRNLSIQ EQAENVELVK RSESGMVTDP VTCTPDMSIQ
 EVDDLCAFR ISGLPVVDEA GKLVGICTNR DMRFESDM

> RXA00533 (1-1032, translated) 344 residues
 MTTIAVVGAT GQVQVMRTL LEERNFPADT VRFFASPRSA GRKIEFRGTE IEVEDITQAT
 EESLKDIDVA LFSAGGTASK QYAPLFAAAG ATVVNDSSAW RKDDEVPLIV SEVNPSDKDS
 LVKGIIANPN CTTMAAMPVL KPLHDAAGLV KLHVSSYQAV SGSGLAGVET LAKQVAAVGD
 HNVEFVHDGQ AADAGDVGPY VSPIAYNVLP FAGNLVDDGT FETDEEQKLR NESRKILGLP
 DLKVSGETCVR VPVFTGHTLT IHAEFDKAIT VDQAEILGA ASGVKLVDVP TPLAAAGIDE
 SLVGRIQDS TVDDNRGLVL VVSGDNLRKG AALNTIQIAE LLVK

> RXA00534 (1-1263, translated) 421 residues
 VALVVQKYGG SSLESAERIR NVAERIVATK KAGNDVVVVC SAMGDTTDEL LELAAAVNPV
 PPAREMDMLL TAGERISNAL VAMAIESLGA EAQSFTGSQA GVLTERHGN ARIVDVTGPR
 VREALDEGKI CIVAGFQGVN KETRDVTTLG RGGSDTTAVA LAAALNADVC EIYSDVDGVY
 TADPRIVPNA QKLEKLSFEE MLELAAGVSK ILVLSRVEYA RAFNVPLVR SSYSNDPGTL
 IAGSMEDIPV EEAVLTGVAT DKSEAKVTVL GISDKPGEAA KVFRALADAE INIDMVLQNV
 SSVEDGTTDI TFTCPRSDDR RAMEILKKLQ VQGNWNTNLY DDQVGKVS LV GAGMKSHPGV
 TAEFMEALRD VNVNIELIST SEIRISVLIR EDDLDAARA LHEQFQLGGE DEAVVYAGTG
 R

> RXA00536 (1-1233, translated) 411 residues
 MSPNDAFISA PAKIETPVGP RNEGQPAWNK QRGSSMPVNR YMPFEVEVED ISLPDRTWPD
 KKITVAPQWC AVDLRDGNQA LIDPMSPERK RRMFELLVQM GFKEIEVGFP SASQTDFFDV
 REIIEKGMIP DDVTIQVLVQ AREHLIRRTF EACEGAKNVI VHFYNSTSL QRNVVFRMDK
 VQVKLATDA AELIKTIAQD YPDNWRWQY SPESFTGTEV EYAKEVVDV VEVMDPTPEN
 PMIINLPSTV EMITPNVYAD SIEWMHRNLN RDSIILSLH PHNDRGTGVG AAELGYMAGA
 DRIEGCLFGN GERTGNVCLV TLALNMLTQG VDPQLDFTDI RQIRSTVEYC NQLRVPERHP
 YGGDLVFTAF SGSHQDAVNK GLDAMAAKVQ PGASSTEVSUW EQLRDEWEV P

> RXA00537 (1-675, translated) 225 residues
 VYHRAVLNAT SAATPFKQKN ANAGVLRIDE ETXRGVAISA DASGRYTKLE PNTGAQLALA
 EAYRNVVSTG ARPVAVTNCL NFGSPENAGV MWQFKEAVHG LADGSKLLGI PVSGGNVSFY
 NQTGDEPILP TPVVGVLGVL DNVEQSIGNV LPSEDNDLYL LGETFDEFEG SIWQQVSGAG
 LNLPLPVVDL LNEQRLADLF VGSDLFAASH DLSEGGGQT LAELA

> RXA00541 (1-669, translated) 223 residues
 VSAKIGVITF PGTLDVDAA RAARIAGAEV ISLWHAEDL KGVDVVVPG GFSYGDYLRT
 GAISALAPVM QSVIEQAGKG MPVLGICNGF QILTEARLLP GALTRNKGLH FHCVDALVV
 ENNTTAWTNT LEKGQQILIP AKHGEGRFQA DAETIAQLEG EGRVVFRTD NFNGSVNDIA
 GITNETGRIV GLMPHPEHAV EKLTGPSIDG LELFLSAVGT IAA

> RXA00557 (1-804, translated) 268 residues
 LLSPYAWGLS RALLDSYVPN KFQTPAGEAK YTMSDHQDTT AEGVSYAAAG VDIEAGDRAV
 ELFAPMAKRA TRPEVLGNLG GFAGLFELGK YKKPILAAGS DGVGTLKLVIA QMMDKHDITIG
 IDLVAMCVDD LVVTGAEPFL QDYIAIGKV VPEHVAEIVS GIAEGCVQAG CALLGGETAE
 HPGVMEPDHY DVSATAVGVV EADELLGPDR VRAGDVLIGM ASSGLHSNGY SLARHVLEK
 AGLALDGHIE ELGRTPGEEL LEPTRMYA

> RXA00558 (1-441, translated) 147 residues
 VVKKPAGIAV GDGEQILVFK DLGLVSQVFD QPILES LRGN IAIGHTRYTT AGGNTWENAG

PMFRMAPDGT DIALGHNGNL INYIELLDKA TELGLVDPK KPSDTPDLTG LLASGVHDGN
NLFDSAPELL PSVKGAYCLT FTDGHTL

> RXA00561 (1-279, translated) 93 residues
LFPDPPPIVH LTCLLSPASR IVVATNRGEE LEKRAAELGV PVFKLGCTND SAVIAVKGAD
VEFTVSVEEL REAWTNTLPE AFGHAVGANA VVA

> RXA00579 (1-1860, translated) 620 residues
MRVLIIDNYD SFTFNLATYV EEVTGQAPVV VPNDQEIDEM LFDAVILSPG PGHAGVAADF
GICAGVIERA RVPILGVCLG HQGIALAYGG DVDLAPRPVH GEVSQITHDG SGLFAGIPET
FEAVRYHSMV ATRLPESLKA TATSDDGLIM ALAHEVLPQW GVQFHPESIG GQFGHQIKN
FLNLARTYRW QLTEKTIPLS VDSAAVFETF FAHSSSHAFWL DDAQGTSYLG DASGPLARTK
THNVGEGDFF TWLKEDLAAN SVAPGQGFR L GWVGYVGYEL KAEAGARAAH TSSLPDALHI
FADRAIAVES DQVRLLALGE QDEWFEETIK KLHNLVAPRI PASGHLALQV RDSKDEYLDK
IRRAQELITR GESYEICLTT KLQGTDDVAP LAAYLALRGA NPTAYGAYLQ LGDTSILSSS
PERFITIDSA GYVESKPIKG TRPRGRTAQE DQEIILAE LRS NPKDRAENLM IVDLVRNDLA
RGALPTTVKT SKLFDVETYA TVHQLVSTVS AELGPRSPIE CVRAAFPGGS MTGAPKLRTM
EIIDELEAAP RGIYSGGLGY FSLDGAVDLS MVIRTLVIQN NHVEYGVGGA LLALSDFEAE
WEEIRVKSRP LLNLFGEVEF

> RXA00580 (1-1302, translated) 434 residues
MTDAHQADDV RYQPLNELDP EVAAAIAGEL ARQRTLEMI ASENFVPRSV LQAQGSVLTN
KYAEGYPGRR YYGGCEQVDI IEDLARDRAK ALFGAEFANV QPHSGAQANA AVLMTLAEFG
DKIMGLSLAH GGHLTHGMKL NFSGLYEVV AYGVDPETMR VDMDQVREIA LKEQPKVIA
GWSAYPRHLD FEAFQSIAAE VGAKLWVDMA HFAGLVAAGL HPSPVPYSDV VSSTVHKTLG
GPRSGIILAK QEYAKKLNS VFPQQGGPL MHAVAAKATS LKIAQTEQFR DRQARTLEGA
RILAERLTAS DAKAAGVDVL TGGTDVHLVL ADLRNSQMDG QQAEDLLHEV GITVNRNAV
FDRPPMVT S GLRIGTPALA TRGFDIPAFT EVADIIGTAL ANGKSADIES LRGRVAKLAA
DYPLYEGLED WTIV

> RXA00581 (1-969, translated) 323 residues
MAEQNAASTT GVKPSRTPD FSPYLDFOA QWRELNSMP QVLTQKEVIE LRGIGENIDL
AEVAEVYLPL SRLIHLQVAA RQQLTAATET FLGTSPSISV PFVIGVAGSV AVGKSTTARL
LQVLLQRWNS HPRVDLVTTD GFLYPGAELI RRGMLSRKGF PESYDQRALL RFVTDVKSCK
LEVNAVPYSH TAYDRVPGEF TTVRQPDILI VEGNLVLQTG PTLMVSDLFDF FSVYVDARTE
DIEKWYIDRF LKLRDTAFRR PGAHFSHYAD MADPESIAVA RELWQSINLP NLVENILPTR
VRASLVLLKKG SDHLVERVRM RKI

> RXA00584 (1-1125, translated) 375 residues
MHSPEQEK M SSPVSLNAA STSNKRVAFA HELPSPTDLI AANPLTPKQA SKVEQDRQDI
ADIFAGDDDR LVVVVGPCSV HDPEAAIDYA NRLAPLAKRL DQDLKIVMRV YFEKPTITVG
WKGLINDPHL NETYDIPEGL RIARKVLIDV VNLDLPVGCE FLEPNSPQYY ADTVAWGAIG
ARTTESQVHR QLASGMSMPI GFKNGTDGNI QVAVDVAVQAA QNPFFFGTS DDGALS SVET
AGNSNSHIIL RGGTSGPNHD AASVEAVVEK LGENARLMID ASHANSKGDH IRQEVVREI
AEQISGGSEA VAGIMIESFL VGGAQNLDPA KLRINGGEGL VYGQSVTDKC IDIDTTIDLL
AELAAAVRER RAAK

> RXA00618 (1-534, translated) 178 residues
MSFGRPLATA HQFSKNAIV GTLSKYFSMT GWRVGWIIIP DELVTPIENL QASLSLCAPA
IGQAAGRAAF TLEAGAE L DA HVEAYREARE VFVDKLPEIG LGTFADPDGG LYLWVDVSAY
TDDSEEWALR LLDEAGVAVA PGVDFDPEEG HKWIRLSLCA SKEDTIEGVR KIGEFIKK

> RXA00619 (1-1428, translated) 476 residues
VADKKKIANV LSNRYASAE L SNLWSAEEKI IMERQLWIAV MKAQKDLGVE IPAEAIESYE
AVIDQVDLAS IADRERVTRH DVKARIEEFN ALAGHEHIHK GMTSRDLTEN VEQLQIHRS L
ELVRNKGIAV VAAIGSRAAQ YQSLVMAGRS HNVAAQATTL GKRFATAADE MLVALERVTE
LLNRYPLRGI KGPMGTAQDM LDLMEGDEAR LSDLETRIAA HLGFDREVFS VGQVYPRSLD
FDAVSALVQL GSGPSSLSHT IRLMAGTETV TEGFKEGQVG SSAMPHKMNA RSCERVGG LQ
VILRGYLT MV ADLSGQQWNE GDVFCSVIRR VALPD AFFAI DGMFETFLTV LDEF GAFFAM
IERELERYLP FLATTRILMA AVRAGVGRET AHEVIKENAV AVALNMRENG GDQDLIQRLA

ADERLPMSEA DLEAALADRH AFIGAAESQV SRVLDRIQVL VDAHPGAADY RPGEIL

> RXA00620 (1-891, translated) 297 residues

MRPELSQYKH LSAGKVIETIY EIDDKHILMV ASDRISAYDF ILDTETPKG RVLTAMSQFF
FDTIDFPNHL AGPADDPRIIP EEVLGRAMVC KKLNMPLPFEC VVRGYLTGSG LVEYKQTSSV
CGVELPEGLV ESSQLPEPIF TPAKADIGD HDINVSFDVV EERLGEARAN QLRDASIAIY
KAAAEIARDR GVILADTKFE FGIDEDGTLV LGDEVLTPTS SRYWPLEGYE AGSVQPSFDK
QFVRNWLTPG KSGWDKDSGL EPPALPGSVV EATRERYIEA YELISGQKFC QWIGSCV

> RXA00624 (1-687, translated) 229 residues

MSGRLVSVS SIFDQTRSAA DRLISDLRAD GIEVSLVAP RIDGDWRLAK DKGTALWMEQ
QERGHLEIL NGFDQAVQGR RSEFANLERH EARLRLTGAI RQMKGIGFEF QIFAPPRWRM
SEGTFVAVLPE FDFNVAASTR GLHNLDGTEF LACRNLSVGE GFGAAKWWRK NVIKAVTRGA
EKGNTVRLSA SARNLTPNKV AADFREAALA ALDLGAQVQT YSQAAAQLA

> RXA00626 (1-780, translated) 260 residues

DRAAARAHVD AVLEGGNPVL LESFLDGPEV SLFFLVDPGET VVPLLPAQDH KRAYDNDEGP
NTGGMGAYAP LPWLPEDGVQ RIVDEVCPV AREMVARGCA YSGLLYAGIA WGAEGPAVVE
FNCRFGDPET QAVLALLKTP LAVLLNAVAT GTLAEQPALE WEDAYALTIV LASYNPEAP
RTGDVIRNAD ADNVLHAGTA LNAEGELVSA GGRVLNVIGV GETLEAARDN AYTTIKDIEL
EGSHYRSDIA LAALEGRISI

> RXA00627 (1-285, translated) 95 residues

MQMLDRVHRR RREGKDTLMF CAGQPSTGAP EAVIEEAEIA LRSGPLGYTE VIGDREFRER
IADWHSATYD VDTNPDPVIV TTGSSGGFVA SFIAT

> RXA00629 (1-264, translated) 88 residues

MRILVIGSGA REHALLRGLS TDPATTELHV APGNAGLGI ATVHPGIKAD DPEAVTALAK
ELNSDLVIG PEIPLVAGVA DALRAAGI

> RXA00632 (1-672, translated) 224 residues

MPFLFVSGTG TGVGKTFTA VLVRYLADQG HDVLPVKLVQ TGELPGEEDI FNIERLTGIA
GEEFARFKDP LAPNLAARRE GVEPIQFDQI ISWLRGFDDP DRIIVVEGAG GLLVRLGEDF
TLADVASALN APLVIVTSTG LGSLNAAELS VEAANRRGLT VLGVLGGSIP QNPDLATMLN
LEEFERVITGV PFWGALPEGL SRVEGFVEKQ SFPALDAFKK PPAR

> RXA00633 (1-1269, translated) 423 residues

MENPSLRELD HRNIWHPYAA PGVRNRLVTK TDGVFLTLED GSTVIDAMSS WWSAIHGHGH
PRLKAAAQKQ IDTMSHVMFG GLTHEPAIKL THKLLNLTGN SFDHVFYSDS GSVSVEVAIK
MALQASKGQG HPERTKLLTW RSGYHGDFT AMSVCDPENG MHSWLKGTLP EQIFAPAPPV
RGSSPQAISE YLRSMELLID EAVSAIIIEP IVQGAGGMRF HDVALIEGVA TLCKKHDRFL
IVDEIATGFG RTGELFATLS NGLQPDIMCV GKALTGGFMS FAATLCTDKV AQLISTPNGG
GALMHGPTFM ANPLACAVSH ASLEIIETGM WQKQVKRIEA ELIAGLSPLQ HLPGVADVRV
LGAIGVIEE QNVNVEEATQ AALDHGVWIR PFGRLLYVMP PYITTSEQCA QICTALHAAV
KKG

> RXA00688 (1-543, translated) 181 residues

MRLVLLGPPG AGKGTQAAIL SEKLGIPHIS TGDLEFRANIG EGTPLGIEAK QYIDAGKLVV
TDVTARMVAS RLAESDAAEG FLLDGFPRTV EQADILANLL SEAGQTLGTV VNYQVSEDEV
VERMLSRGRA DDNEETIRTR LGVYRDETAP LIDHYGDKII NIEAEGEVEE INARTLKALG
K

> RXA00708 (1-672, translated) 224 residues

TVGKAVRESG VPREELIVTS KLPGRFHARD LGRVRIEESL YRLNLDYIDL LLIHWPNSK
DLYVEAWETL IEVRDAGLVK HIGVSNFLPN HIDRLRRETG ELPAVNQIEL HPYFPQVEQV
DFHDELGIIT EAWSPLSNGR GLVEEPLLKE IGERYGVGSG EIALAWHAR GIVPIPRSTN
PARQRSNLEA VKISLIDEDV QAITALARKN GRIKDQDPAV YEEF

> RXA00717 (1-960, translated) 320 residues

VTPPARRDGT PDKKQSNRSG GYRSSVRGYK PGSSRPNTRQ QPQKKDEILL SNAKPAKKQN

VKSDDDWSMG FLNRNDSDBG RLQKVLAAQAG VASRRHAEIL IDQGRVEVND RIVTTQGVVRV
 DPNNDVIRVD GVRIHINEDL EYFVLNKPRG MHSTMSDELG RPCVGDLVSE KTASGQRLFH
 VGRLDADTEG LLLLTNDGEL ANRLMHPKYE VSKTYLATVR GEATNKLVS A LRDGVELEDG
 PAKADFAQII DVFQGKSLR IEIHEGRKHI VRRFLDELGF PVERLVR TKL HTVQLGDQKP
 GSLRALNSSE LTSLYKVVQL

> RXA00718 (1-708, translated) 236 residues
 VTEISNMPAG GLIVAIDGPS GTGKSTTSRA LATRLSAKYL DTGAMYRVAT LHVNLQGIDP
 ADSAAVIAAT AVLPLSISDD PASTEVLLAG VDVQKDIRGP EVTQNVSAVS AIPVRENLV
 ALQRALAAKA HRCVVEGRDI GTAVLVDAPL KAFLTASAEV RAQRRFDQDT AAGRVDVDFDA
 VLADVVRDE LDSTRAASPL KPADDAHIVD TSDMTMDQVL DHLIHLVEAS AERSNQ

> RXA00727 (1-912, translated) 304 residues
 LRFPKIPKRA VAATVGIVAT SFTLASCVTN EEQGNPDGWE QIVPDPVPEI QAMVPEALAQ
 RGVLTAGANP PFPFPEFKDS DGQIIGVEMD LVRAMAGVMG LEFSPQE QDF SLILPSVQAG
 TLDIGASGFT DNEERRENF D FIDFLFAGVQ WAQATDRETP IDPENACGLT VAVQRTTVAE
 TDDVRPRSAQ CEAEQKEPIT ILSYETADTA ATALILGRAD ALAADSPVSA WAAERSEGR I
 EVVGD MYLAA PFGFAFPLES DLTPAAAAAF QHLIDTGDYQ RIMAQWGIEE GLLDEALINE
 QPLN

> RXA00766 (1-843, translated) 281 residues
 MVFWDDAALT RGDGIFETLL IRDGHCNVR RHGERFKASA ALLGLPEPIL EDWEKATQMG
 IESWYSHRNA GEASCTWTLS RGRSSTGLAS GWLTITPVSS DKLAQREHGV SVMTSSRGYS
 IDTGLPGIGK ATRGELSKVE RTPAPWLTVG AKTLAYAANM AALRYAKSNG FDDVIFTDGD
 RVLEGATSTV VSFKGDKIRT PSPGGDILPG TTQAALFAHA TEKGWRCKEK DLSIDDLFGA
 DSVWLVS SVR GPVRVTRLDG HKLRKPDNEK EIKALITKAL G

> RXA00770 (1-315, translated) 105 residues
 VTGGGLAGNL ERVVEGLVA EMSRATWTPG QIFRTISSVG KVSREEMEKT FNMGVGMVAV
 VAEKDRDRAL AMLTARHIDC WEIGTVRNGE EGEPRVILNG EHPGY

> RXA00779 (1-933, translated) 311 residues
 MGNVYNNITE TIGHTPLVKL NKLTEGLDAT VLVKLESEFP ANSVKDRIGL AIVEDAEKSG
 ALKPGGTIVE ATSGNTGIAL AMVGAARGYN VVLTMPETMS NERRVLLRAY GAEIVLTPGA
 AGMQGAKDKA DEIVAERENA VLARQFENEA NPRVNRDTTA KEILEDTDGT VDIFVASFGT
 GGTVTGVGQV LKENNADVQV YTVEPEASPL LTAGKAGPHK IQGIGANFIP EVLDRKVLDD
 VLTVSNE DAI AFSRKLATEE GILGGISTGA NIKAAALDLAA KPENAGKTIV TVVTDFGER Y
 VSTVLYEDIR D

> RXA00780 (1-546, translated) 182 residues
 MIREDLANAR EHDPAARGDL ENAVVYSG LH AIWAHRVANS WWKSGFRGPA RVLAQFTREFL
 TGIEIHPGAT IGRRFFIDHG MGIVIGETAE IGEGVM LYHG VTLGGQVLTQ TKRHPTLCDN
 VTVGAGAKIL GPITIGESGA IGANAVVTKD VPAEHIAVGI PAVARPRGKT EKIKLVDPDY
 YI

> RXA00838 (1-900, translated) 300 residues
 MKIAIVGAGA VGGYFGALLQ ESGADITMVA RGR TLEALKS KGLHINDARG ERYVPIPAVA
 SVQELKDADV VMIATKALSR SLDLAELLGG IPANSVVAIT QNSIESADLA AKSIGADRVW
 PGVVRGFFVH EGPASVS YKG GPLSYTFGDS GELSRQFAST LEQAGIDGVL HPDILVDVWE
 KAMFVEVFGG LGAFVEKQLG TLRTHFRASL EALMEEVAEV ARAAGVALPS DAVERTM NFA
 DRMPENSTSS MQRDLAAGVA SELEAQTGAI VRAAHKVG VK TPLHDLIYAG LKLKEEENSL

> RXA00863 (1-744, translated) 248 residues
 MGIKVGVLGA KGRVGQTIVA AVNESDDLEL VAEIGVDDDL SLLVDNGAEV VVDFTTPNAV
 MGNLEFCINN GISAVVGTG FDDARLEQVR DWLEGKDNVG VLIAPNFAIS AVLTVMVFSKQ
 AARFFESA EV IELHHPNKLD APSGTAIHTA QGIAAARKEA GMDAQPDAT E QALEGSRGAS
 VDGIPVHAVR MSGMVAHEQV IFGTQGGTIL IKQDSYDRNS FAPGVLVGVR NIAQHPGLVV
 GLEHYLGL

> RXA00864 (1-750, translated) 250 residues
 VAEQVKLSVE LIACSSFTPP ADVEWSTDVE GAEALVEFAG RACYETFDKP NPRTASNAAY

LRHIMEVGHT ALLEHANATM YIRGISRSAT HELVRHRHFS FSQLSQRFVH SGSESEVVVPT
 LIDEDPQLRE LFMHAMDESR FAFNELLNAL EEKLGDEPNA LLRKKQARQA ARAVLPNATE
 SRIVVSGNFR TWRHFIMGRA SEHADVEIRE VAVECLRKLQ VAAPTVMGDF EIETLADGSQ
 MATSPYVMD

> RXA00865 (1-903, translated) 301 residues
 MSTGLTAKTG VEHFGTVGVA MVTPFTESGD IDIAAGREVA AYLVDKGLDS LVLAGTTGES
 PTTTAAEKLE LLKAVREEVG DRAKLIAGVG TNNTRTSVEL AEAAAASAGAD GLLVVTPYYS
 KPSQEGLLAH FGAIAAAATEV PICLYDIPGR SGIPIESDTM RRLSELPTIL AVKDAKGDV
 AATSLIKETG LAWYSGDDPL NLVWLALGGS GFISVIGHAA PTALRELYTS FEEGDLVRAR
 EINAKLSPLV AAQGRLLGVS LAKAALRLQG INVGDPRPLI MAPNEQELEA LREDMCKAGV
 L

> RXA00867 (1-627, translated) 209 residues
 FGDMDFKVAG TADFITALQL DTKLDGIPSK VLSDALEQAR DARLTILNTM ADVINGPDEM
 SKFAPRITTV KIPVAKIGEL IGPKGKNINA LTEETGANIS IEDDGTVFIS AADGASAEAA
 IEKINALANP QLPKVGREFL GTVVKTAFAG AFVSLLPGRD GLVHISKLGK GKRVEKVVDDV
 VKVGEKIQVE IADIDNRGKI SLVPVVEED

> RXA00873 (1-756, translated) 252 residues
 TAQWGIFLRN HDELTLEMVS DEERSYMYSQ FASEPRMRAN VGIRRRRLSPL LEGDRNQLEL
 LHGLLLSLPG SPVLYYGDEI GMGDNIWLHD RDGVRTPMQW SNDRNGGFSK ADPERLYLPA
 IQNDQYGYAQ VNVESQLNRE NSLLRWLRNQ ILIRKQYRAF GAGTYREVSS TNESVLTFLR
 EHKGQTILCV NNMSKYPQAV SLDLREFAGH TPREMSSGQL FPTIAEREWI VTLAPHGFFW
 FDLTADEKDD ME

> RXA00884 (1-1140, translated) 380 residues
 MSVFGVYIHV PFCSTRCGYC DFNTYTAGEF GSTAGPDYTL DSLEVELEMA VASLDNPRQA
 ETIFIGGGTP SLIGADGLAR VLGAVRNTFG IADGAEVTTT SNPESTSPEF FDGLREAGYN
 RISLGMQSAS SSVLKVLDRT HTPGRPVAAA KEAREAGFEH VNLDMIYGTP TETDDDVVKT
 LNAVLEANVD HVSAYSLIVK DGTAMARKVH KGELPAPDED VYADRFELID ARLRSAGFDW
 YEVSNNWAKPG GECKHNMGYW VDGDWWGAGP GAHSHIGDRR FYNIKHPARY SAQIAAGELP
 IKETERLTAE DHHTERVMLG LRLKQGVPLN LFAPAARPVI DRHIAGGLLH VNALGNLAVT
 DAGRLADGI IADILLSEED

> RXA00891 (1-1002, translated) 334 residues
 VLQTSWHFSI LAGMTDTSPL NSQPSADHHP DHAARPVLDA HGLIVEHESE EFPVPAPAPG
 EQPWEKKNRE WYKDAVFYEV LVRAFVDPEG NGVGSLLKGLT EKLDYIQWLG VDCIWIPPFY
 DSPLRDGGYD IRNFRILPE FGTVDVFVEL VDHAHRRGLR VITDLVMNHT SDQHAWFQES
 RRDPTGPYGD FYVWSDPPTL YNEARIIFVD TEESNWTYDP VRGQYFWHRF FSHQPDLYND
 NPAVQEAMLD VLRFWLDLGL DGFRLDAVPY LFEREGTNGE NLKETHDFLK LCRSVIEKEY
 PGRILLAEAN QWPQDVVEYF GEKDKGDECH MAFH

> RXA00952 (1-840, translated) 280 residues
 MSRYDDLAFAR LDTAGEGAFV PFIMLSDFSP EERAFQIISTA IEAGADALEL GVPFSDPVAD
 GPTVAESHLR ALDGGATVDS ALEQIKRVRA AYPEVPIGML IYGNVPFTRG LDRFYQEFAR
 AGADSILLPD VPVREGAPFS AAAAAAGIDP IYIAPANASE KTLEGVSAAS KGYIYAIRSD
 GVTGTERESS TDGLSAVDN IKKFDGAPIL LGFGISSPQH VADAIAAGAS GAITGSAITK
 IIAHCEGEH PNPSTIRDMD GLKKDLTEFI SAMKAATKKV

> RXA00954 (1-588, translated) 196 residues
 FLFAPAYNPA IAHVQPVQRQA LKFPTIFNTL GPLLSPARPE RQIMGVANAN HGQLIAEVFR
 ELGRTRALVV HGAGTDEIAV HGTTLVWELK EDGTIEHYTI EPEDLGLGRY TLEDLVGGGLG
 TENAEAMRAT FAGTGPDAGR DALAASAGAM FYLNGDVDSL KDGAQKALS LADGTTQAWL
 AKHEEIDYSE KESSND

> RXA00955 (1-1422, translated) 474 residues
 MTSNNLPTVL ESIVEGRRGH LEEIRARIAH VDVDALPKST RSLFDSLNOG RGGARFIMEC
 KSASPSLGM REHYQPGEIA RVYSRYASGI SVLCEPDRFG GDYDHLATVA ATSHLPVLCK
 DFIIDPVQVH AARYFGADAI LLMLSVLDDE EYAALAAEAA RFDLDILTEV IDEEEVARAI
 KLGAKIFGVN HRNLHDLSD LDRSRRLSKL IPADAVLVSE SGVRDTETVR QLGGHNSNAFL

VGSQLTSEQEN VDLAARELVY GPNKVCGLTS PSAAQTARAA GAVYGGLIFE EASPRNVSRE
 TLQKIIAAEP NLRVAVSRR TSGYKDLLVD GIFAVQIHAP LQDSVEAEKA LIAAVREEVG
 PQVQVWRAIS MSSPLGAEVA AAVEGDVDKL ILDAHEGGSG EVFDWATVPA AVKAKSLLAG
 GISPDNAAQA LAVGCAGLDI NSGVEYPAGA GTWAGAKDAG ALLKILATIS TFHY

> RXA00956 (1-1131, translated) 377 residues
 MTEKENLGGS TLLPAYFGEF GGQFVAESLL PALDQLEKAF VDATNSPEFR EELGGYLRDY
 LGRPTPLTEC SNLPLAGEGK GFARIFLKRE DLVHGGAHKT NQVIGQVLLA KRMGKTRIIA
 ETGAGQHGTAL TALACALMGL ECVVYMGAKD VARQQPNVYR MQLHGAKVIP VESGSGTLKD
 AVNEALRDWT ATFHESHYLL GTFAGPHFPF TIVREFHKVI SEEAKAQMLE RTGKLPDVVV
 ACVGGGSNAI GMFADFIDDE GVELVGAEPG GEGLDGSKHG ATITNGQIGI LHGTRSILMR
 NSDGQVEESY SISAGLDYPG VGPQHAHLHA TGRATYVGIT DAEALQAFQY LARYEGIIIPA
 LESSHAFAYA LKRAKTA

> RXA00957 (1-1128, translated) 376 residues
 DFLETFETLP AVEESVNTYP DYQFVLAIEV LDINHQQDQTA KLAGVSNAPG ELEAEELNKLK
 LLIDAALPAT EHAYQTTPHD GDTLRVVADI PDAQFRTQIN ELKENIYNGD IYQVVPARTF
 TAPCPDAFAA YLQLRATNPS PYMFYIRGLN EGRSYELFGA SPESNLKFTA ANRELQLYPI
 AGTRPRGLNP DGSINDELDI RNELDMRTDA KEIAEHTMLV DLARNDLARV SVPASRRVAD
 LLQVDYRSRV MHLVSRVTAT LDPELDALDA YRACNMNGTL TGAPKLRAE LLRGVEKRRR
 GSYGGAVGYL RGNMGDMNCI VIRSAFVQDG VAAVQAGAGV VRDSNPQSEA DETLHKAYAV
 LNAIALAAGS TLEVIR

> RXA00958 (1-624, translated) 208 residues
 MTHVVLIDNH DSFVYNLVDA FAVAGYKCTV FRNTVPVETI LAANPDLICL SPGPGYPADA
 GNMMALIERT LGQIPLLIGC LGYQALIEYH GSKVEPCGPV HGTTDNMILT DAGVQSPVFA
 GLATDVEPDH PEIPGRKVPI GRYHSLGCVV APDGIESLGT CSSEIGDVIM AARTTDGKAI
 GLQFHPESVL SPTGPVILSR CVEQLLAN

> RXA00970 (1-927, translated) 309 residues
 MAIELNVGRK VTVTVPGSSA NLGPGFDTLG LALSVDYDVE VEIIPSGLEV EVFGEQGEV
 PLDGSHLVVK AIRAGLKAAD AEPVGLRVVC HNNIPQSRGL GSSAAAAGV VAAANGLADF
 PLTQEQIVQL SSAFEGHPDN AAASVLGGAV VSWTNLSIDG KSQPPYAAVP LEVQDNIRAT
 ALVPNFHAST EAVRRVLPTE VTHIDARFNV SRVAVMIVAL QQRPDLLWEG TRDRLHQPYR
 AEVLPIITSEW VNRLNRGYA AYLSGAGPTA MVLSTEPIPD KVLEDAESG IKVLELEVAG
 PVKVEVNQP

> RXA00972 (1-1377, translated) 459 residues
 PAPGWRFRITG EDVTMATVEN FNELPAHVWP RNAVRQEDGV VTVAGVPLPD LAEEYGTPLF
 VVDEDDFRSR CRDMATAFGG PGNVHYASKA FLTKTIARWV DEEGLALDIA SINELGIALA
 AGFPASRITA HGNNKGVEFL RALVQNGVGH VVLDSAQELE LLDYVAAGG KIQDVLIRVK
 PGIEAHTHEF IATSHEDQKF GFSLASGSFA EAKAANNAE NLNLVGLHCH VGSQVFDAEG
 FKLAARVLG LYSQIHSELG VALPELDLGG GYGIAYTAAE EPLNVAEVAS DLLTAVGKMA
 AELGIDAPTV LVEPGRATAG PSTVTIYEVG TTKDVHVDDE KTRRYIAVDG GMSDNIRPAL
 YGSEYDARVV SRFAEGDPVS TRIVGSHCES GDILINDEIY PSDITSGDFL ALAATGAYCY
 AMSSRYNAFT RPAVSVVRAG SSRLMLRRET LDDILSLEA

> RXA00974 (1-393, translated) 131 residues
 MTSASAPSFN PGKGPSSAVG IALLGFGTVG TEVMRLMTEY GDELAHRIGG PLEVRGIAVS
 DISKPREGVA PELLTEDAFA LIEREDVDIV VEVIGGIEYP REVVLAALKA GKSVVVTANKA
 LVAHSAELA D

> RXA00981 (1-630, translated) 210 residues
 MSENLPAPEN LLDAERIQMI KNFRNELTGF MLNYQFGIDE ILTKINILKT EFSQLHEYAP
 IEHVSSRLKT PESIVKKVIR KGDELSLAAI KDTVFDIAGI RIVCSFLKDA YAIADMLTNQ
 KDVTVIEAKD YIANPKPNGY KSLHLILQVP VFLSNSVEKV NVEVQIRTIA MDFWASLEHK
 IYYKFEQEVQ QSILDELSED GKNPRGSEVT

> RXA00989 (1-1533, translated) 511 residues
 GIGLVANNDG IFDSENDDIT VGDVTLGETG LSLPIDLAGE VEAPASEEIT QEDLLRLAQV
 EAELDQRWLE TKIDPTFRRM SYMMDLMGQP QNSFPAIHVA GTNGKTSTTR MIESLLRAFH

RRTGRTTSPH LQLVTERIAI DGKPIHPRDF VRIYEEIKPY MEMTDAWSEA EGGPKMSKFE
 ALVALAYAGF ADAPVDVAVV EVGLGGRWDA TNVINAASV ITPVGMDHVD RLGNTIGEIA
 GEKAGIIKAR PASEDGTEPE GNVVIVGKQE PEAMNVILQQ AVDVDAVAR LNMEFGVVES
 AIAVGGQQLT LKGLGGEYTD IFLPLSGAHQ ADNAAVALAA VEAFFGASAG RPLDIDTVRE
 GFAQVQSPGR LERLRSAPT V FIDAANPHG AAALGAALDR DFEFRRLIGV IGVLCDDKAR
 GILESLEPYL HEIVCTQTAS ERALDAYDLA EYAREIYGDE RVHVQEDLAG AVELAIELAE
 DTDVQSGSGV VITGSIVTAG DARTLFGKEP A

> RXA00997 (1-582, translated) 194 residues
 MTTWKELTDN NPAHSENYAQ RWRNLAAAGN DIYGEARLID AMAPRGAKIL DAGCGQGRIG
 GYLSKQGHV LGTDLPILI DYAKQDFPEA RWVVGDLSD QISETDFDLI VSAGNVMGFL
 AEDGREPALA NIHRALGADG RAVIGFGAGR GWVFGDFLEV AERVGLELEN AFESWDLKPF
 VQGSEFLVAV FTKK

> RXA01009 (1-1230, translated) 410 residues
 LALKGYTNFD GEFIEFGSVQ AKEEEKRAFD NDRAHVHFSW SAQDKISPKV WAAAEGSTLY
 DFDGNAFIDM GSQVLSANLG HNNPRLVEAI QRQAARLTNI NPAFGNDVRS DVAAKIVSMA
 RGEFSHVFFT NGGADAIEHS IRMARLHTGR NKILSAYRSY HGATGSAMML TGEHRRILGNP
 TTDPIYHFW APFLHSSFF ATTQEEECER ALKHLEDVIA FEGAGMIAAI VLEFVVGSSG
 IILPPAGYLN GVRELCNKHG ILFIADVMV GFGRTGKLFA YEHAGDDFQP DMITFAKGVN
 AGYAPLGGIV MTQSIRDFTG SEAYSGGLTY SGHPLAVAPA KAALEIYAEG EIIPRVARLG
 AELIEPRLRE LAENVAIAD VRGIGFFWAV EFNADATAMA AGAAEFKERG

> RXA01019 (1-990, translated) 330 residues
 TLAHSLSPFD SLRDGPTVGD LGFEFVIRVI TEQAGSSLNG DDAAVLRHAS PNSRAVVTTD
 MLVAGRHFQL DWSTPEQIGQ KAIVQNFADI EAMGARPVAA LLAISAPHT PVEFVRGLAR
 GMNQRLLEYS AELVGGDITS GDLSVIAVTA IGQLGGSLEPE LTLGRARPGQ TLVAHGKIGY
 SAAGLALLQH FGPDNVPEHL RPLVDAHCAV VLTTPGRGMVA RAAGATAMTD NSDGLIVDLN
 QMAMKSGVRI DVDSCSISPD ELLSEAAVSL GTDAWRWILS GGEDHTLLST TFGDAPSGFR
 TIGQVTKTRH EDLVTVDKKT PAFSDGWRSF

> RXA01024 (1-657, translated) 219 residues
 MANKNNKPHE VDKDQDSAML INGRLLQIPA RPTEEFTRPT LAAGAVLWRG DITNPDSIEV
 AVIHRPHYDD WSLAKGVDP GESIPTTAAR EILEETGYDI RLGKLIGKVT YPVLDRTKVV
 YYWTAQVLGG EFVPNDEVDE IRWLSVDEAC ELLSYQVDTE VLAKAAKRFR TPSTTRVLYV
 RHAHAHGRQT WGGDDNKRPL DKKGRRQAEM LVPMLLPFK

> RXA01026 (1-1602, translated) 534 residues
 VWRDHVVSKE ENGEPLLYI DLQLLHEVTS PQAFDGLRMT GRKLRHPELH LATEDHNVPT
 EGIKTGSLLE INDKISRLQV STLRDNCEEF GVRLHPMGDV RQGIVHTVGP QLQATQPGMT
 IVCGDSHTST HGAFGSMAFG IGTSEVEHVM ATQTLPLKPF KTMAIEVTGE LQPGVSSKDL
 ILAIIAKIGT GGGQGYVLEY RGEAIRKMSM DARMTMCNMS IEAGARAGMI APDQTTFDYV
 EGREMAPKGA DWDEAVAYWK TLPTDEGATF DKVVEIDGSA LTPFITWGTN PGQGLPLGES
 VSPEDFTND NDKAAAEKAL QYMDLVPGTP LRDIKIDTVF LGSCTNARIE DLQIAADILK
 GHKIADGMRM MVVPSSTWIK QEAEALGLDK IFTDAGAERW TAGCSMCLGM NPDQLKPGER
 SAFTSNRNFE GRQGPGRTH LVSPAVAAAT ESADPVLTCR YLRKARKQWK NLPPTPALAF
 HCSDPWTPT RSSQPSTSSA SPGPASKTDC FPTGAKTTPT LSSTPTPTRT APFS

> RXA01027 (1-234, translated) 78 residues
 TDPEACKKRF TDVVAQGGVP MIVGQGDIIIP EMIKWFSENG TLPIDEKIKI KKGSVWVLSF
 HDGVFTGADY LASSLPVK

> RXA01073 (1-831, translated) 277 residues
 MTNTQTEIIN ELKVSPAIDV AKEVEFRVQF LVDYLRASHT KGFVLGISGG QDSTLAGRLT
 QLAVERIRAE ENSTDYVFYA VRLPYAIQAD EDDAQVALEF IAPDKSVTVN VKDATDATEA
 TVAAALELPE LTDFNRGNIK ARQRMVAQYA IAGQLGLLVI GTDHAAENV T GFTFKFGDGA
 ADLLPLAGLS KRQGAAIEH LGAPSSTWTK VPTADLEEDR PALPDEEALG VSYADIDNYL
 ENKPDVSEKA QQRIEHLWKV GQHKRHLPAT PQENWWR

> RXA01079 (1-690, translated) 230 residues
 MDFHALNALL NLYDDNGKIQ FEKDREANQ YFLQHVNT VFFHNLQEKI DYLVENKYYD

PIVLDKYDFQ FIKDLFKRAY GFKFRFQSFL GAYKYYTSYT LKTFDGRRYL ERFEDRVCMV
 ALTLDAGDRA LAENLVDEIM SGRFQPATPT FLNSGKAQRG EPVSCFLLRI EDNMESIGRS
 INSALQLSKR GGGVALLLSN LREAGAPIKK IEIQSSGVIP VMKLLEDAFS

> RXA01080 (1-444, translated) 148 residues
 MLIVYFSSAT DNTHRFVQKL DLPNVRIPLT RVEEPLKINE PYVLITPTYG GGVSMGTGENS
 RPVPPQVIRF LNDEHNRSFI RAVVAGGNSN FGSDFGGLAGE IISKCKKVPY VYRFELMGNE
 EDVSILRGGI TQNAQALGLE PQEPVTSR

> RXA01084 (1-1341, translated) 447 residues
 SFLDTKRENA DEKIRIKTLS LGVVIPDITF ELAKRNDDMY LFSPYDVERI YGKPFADVSI
 TEHYDEMVD DRIKTKINA RQFFQTLAEI QFESGYPIY YEDTVNASNP IEGRITHSNL
 CSEILQVSTP SEFNDDLTIA EVGEDISCNL GSLNVAMAMD APNFEKTXET EIRGLTAVXE
 QTSIDSVPSI RKGNEAAHAI GLGQMNHLGY FGREHMHYGS EEALDFTNAY FAAVLYQCLR
 ASNQIATERG ERFKNFENSK YATGEYFDDF DANDFAPKSD KVKELFKSN IHTPTVEDWA
 ALKADVMEHG LFNRLQAVP PTGSISYINN STSSIHPIAS KIEIRKEGKI GRVYYPAPHM
 DNDNLEYFED AYEIGYEKII DTYAVATKYV DQGLSLTLFF KDTATTRDIN RAQIYAWRKG
 IKTLYYIRLR QVALEGTEVD GCVSCML

> RXA01087 (1-876, translated) 292 residues
 MQTLAAIVRA TKQPFETITI DLDAPRPDEV QIRVIAAGVR HTDAIVRDQI YPTFLPAVFG
 HEGAGVVAV GSAVTSVKPD DKVVLGFNSC GQCLKCLGGK PAYCEKFYDR NFACTRDAGH
 TTLFTRATKE QAEAIIDTLD DVFYDADAGF LAYPATPPEA SGVSVLVVAA GTSDLPQAKE
 ALHTASYLGR STSLIVDFGV AGIHRLLSYE EELRAAGVLI VAAGMDGALP GVVAGLVSAF
 VVALPTSVGY GAGAGGIAPL LTMLNACAPG VGVVNIDNGY GAGHLAAQIA AR

> RXA01095 (1-783, translated) 261 residues
 MVATENRMLM EIAAEISARE ATLGFEQEVKT KRSRAGLTAA FDIASVFFSS GCNVVVAFDR
 FASNWDHSD HVDYAAQVAG FGASMLAYTV RRGQFDTAVR DIRDIKSEVD IPILLHDPII
 DPYQIHEARV MGIDALQFPV WAMEQARLES LVDRTESLGM TAIVSVRNHE EAHRAVDAGA
 TVVAIDITGY TGSLTLPEAF SGITQFMPKE VARIVLGGCS SPKELMRFR HSADAIFVPH
 ADLATTKSLV TAGMHPACPS R

> RXA01097 (1-354, translated) 118 residues
 MSDNPQEYEL DWDVEKRLKL NDAGLVPAIV QADGTNEVLM MAWMDTHALA YTLATRRGTY
 FRSRNEYWI KGLTSGNVQE VTGLALDCDG DTVLLTVKQT GGACHTGAHT CFDNDVLL

> RXA01098 (1-774, translated) 258 residues
 MGVAIRVIP LDVDNGRVVK GVNFEENLRDA GDPVELAKRY DEEGADELTF LDVTSKHGR
 GTMLDVVRR ADQVFIPITV GGGVRSEEDV DQLLRAGADK VSVNTSAIAR PELLSELSKR
 FGAQCIVLSV DARRVPEGGT PQPSGFVTT HGGSKSAELD AIEWAKRGE LGVGEILLNS
 MDGDGTKNF DLELLEKVRA AVSIPVIASG GAGKAHFPP AVAAGANAVL AATIFHFREV
 TIAEVKGAIK DAGFEVRK

> RXA01100 (1-738, translated) 246 residues
 MTFTILPAVD VVNGQAVRLD QGEAGTEKSY GTPLESALKW QEQGAWLHF VDLDAAFNRG
 SNHEMMAEIV GKLDVDVELT GGIRDDESLE RALATGARRV NIGTAALEKP EWIASAIQRY
 GEKIAVDIAV RLEDGEWRTR GNGWVSDGGD LWEVLERLDS QGCARFVVD VSKDGTLSGP
 NVELLREVAA ATDAPIVASG GISVLEDVLE LAKYQDEGID SVIIGKALYE HKFTLEEALA
 AVEKLG

> RXA01101 (1-633, translated) 211 residues
 MTKTVALLDY GSGNLRSAQR ALERAGAEVI VSSDPEVCTN ADGLLVPGVG AFDACMKGLK
 NVFGHRIIG RLAGGRPVMG ICVGMQILFD EGDEHGIKSA GCGEWPCKVE RLQAEILPHM
 GWNTLEMPN SPMFEGISPD ERFYFVHSYG VRKWTLETDD LTTPPEVVWA KHENDRFVAA
 VENGTWATQ FHPEKSGDAG AQLLRNWINY I

> RXA01104 (1-606, translated) 202 residues
 MTVAPRIGTA TRTTSESDIT VEINLDGTGK VDDITGLPFF DHMLTAFGVH GSFDLKVHAK
 GDIEIDAHHT VEDTAIVLGQ ALLDAIGDKK GIRRFASCQL PMDEALVESV VDISGRPFV
 ISGEPDHMIT SVIGGHYATV INEHFFETLA LNSRITLHVI CHYGRDPHHI TEAEYKAVAR

ALRGAVEMDP RQTGIPSTKG AL

> RXA01105 (1-1098, translated) 366 residues

MTKITLSLDP LREELRGEHA YGAPQLNVDI RLNTNENPYP PSEALVADLV ATVDKIATEL
 NRYPERDAVE LRDELAAYIT KQTGVAVTRD NLWAANGSNE ILQQLLQAFG GPGRTALGFQ
 PSYSMHPILA KGTHTEFIAV SRGADFRIDM DVALEEIRAK QPDIVFVTTT NNPTGDVTSL
 DDVERIINVA PGIVIVDEAY AEFSPSPSAT TLLEKYPTKL VVSRTMSKAF DFAGGRLGYF
 VANPAFIDAV MLVRLPYHLS ALSQAAAIVA LRHSADTLGT VEKLSVERVR VAARLEELGY
 AVVPSESFV FFGDFSDQHA AWQAFLDGRV LIRDVGIAGH LRTTIGVPEE NDAFLDAAAE
 IIKLNL

> RXA01106 (1-1326, translated) 442 residues

MLNVTDLRGQ TPSKSDIRRA LPRGGTDVWS VLPVQPVVE DVQNRGAEAA LDYGEKFDHI
 RPASVRPAE VIAAAENTLD PLVRESIEES IRRVRKVHAE QKPSEHTTEL SPGGTVTERF
 MPIDRVGLYV PGGNAVYPSS VIMNTVPAQE AGVNSLVVAS PPQAEHGGWP HPTILAACSI
 LGVDEVWAVG GGQAVALLAY GDDAAGLEPV DMITGPGNIF VTAARKLVRG VVGTDSEAGP
 TEIAVLADAS ANAVNVAYDL ISQAEHDVMA ASVLITDSEQ LAKDVNREIE ARYSITRNAE
 RVAEALRGAQ SGIVLVDDIS VGIQVADQYA AEHLEIHTEN ARAVAEQITN AGAIFVGDFF
 PVPLGDYSAG SNHVLPTSGS ARFSAGLSTH TFLRPVNLIE YDEAALKDVS QVVINFANAE
 DLPAGHAIR ARFENLPTTD EA

> RXA01132 (1-303, translated) 101 residues

MKLAVIGGDG IGPEVTAEAL KVLNAVRDDI ETTDYDLGAR RYLKNGELLT DEDLASLREH
 DAILLGAIGA PGSVPPGILE RGLLLKMRFA LDHHVNLRPS K

> RXA01145 (1-456, translated) 152 residues

MAIELLYDAD ADLSLIQGRK VAIVGYGSQG HAHSQNLDRS GVEVVIGLRE GSKSAEKAKE
 AGFEVKTTAE AAAWADVIML LAPDTSQAEI FTNDIEPNLN AGDALLFGHG LNIHFDLIK
 ADDIIVGMVA PKGPGHLVRR QFVDGKGVPC LI

> RXA01162 (1-1245, translated) 415 residues

MYIVGICLQL VVMSQPMSAP DSAPGTERGH ERTHFAVVDG SQDPAQATAP RAPAESITLI
 GIGTDGFEGL GLKAQQALQR ASVVIGSWRQ LNLVPDAIKA ERRPWPNGTK HPDLDALEKE
 FLGRHVAVLA SGDPLFYGVG TAMVHVLGMD RLTVIPGPSS ASLACARLGW TVNRTVRVYL
 GQEPITLIP IIESGAQFLV LGKDEFSTAQ VATLLNELGL GETPLTVLSD LGSTDEEITQ
 GTASHPPAAV SVLNVIAGVA RTAMPKPHFE GDVSNEDLRA LTVAALEPTQ QMLWTFGDI
 GAALACDWLR AAGNKAHAIS FASMVEQSQR NARKLGVSTL SVKETLSPKT LKDIRYVQGP
 ESASPFAIFM NKGLGIDLVP ETAWMLLRPG GKLIQASTE DNIACLHTLQ EQHGG

> RXA01208 (1-804, translated) 268 residues

VANSFLDSL T LVRQNTPLVQ CLTNSVVMQF TANVLLAAGA TPAMVDTPAE SAEFAAVANG
 VLINAGTPSA EQYQGMTKAI EGARKAGTPW VLDPVAVGGL SERTKYAEGI VDKQPAAIRG
 NASEVVALAG LGAGGRGVDA TDSVEVALEA AQLLAKRTGG VVAVSGAEDL IVSADRVTLW
 RSGDPMQLV IGTGCSLGL TAAYLGATVD SDISAHDAVL AAHAHVGAAG QIAAQKASAP
 GSFAVAFIDA LYDVDAQAVA SLVDVREA

> RXA01209 (1-1428, translated) 476 residues

MCERPEKYVT DFSLYLVTDV VLGGGPKKVA GIVDSAISGG VSVVQLRDKN SGVEDVRAAA
 KELKELCDAR GVALVNDYL DIAVELGLHL HIGQGDTPYT QARELLPAHL ELGLSIENLD
 QLHAVIAQCA ETGVALPDVI GIGPVASTAT KPDAAPALGV EGIAEIAAVA QDHGIAVAI
 GGVGLRNAAE LAATPIDGLC VVSEIMTAAN PAAAATRLRT AFQPTFSPET QTELSQTELQ
 GAFVNSPSAP RVLSIAGTDP TGGAGIQADL KSIAAGGGYG MCVVTSLSAQ NTHGVNTIHT
 PPLTFLEEQL EAVFSDVTVD AIKLGMLGSA DTVDLVASWL GSHEHGPVVL DPVMIATSGD
 RLLDASAEES LRRLAVHVDV VTPNIPELAV LCDSAPAITM DEAIAQAQGF ARTHDTIVIV
 KGGHLTGALA DNAVVRPDGS VFQVENLRVN TTNSHGTGCS LSASLATKIA AGESVE

> RXA01215 (1-975, translated) 325 residues

MTAHWKQNK NLMLFSGRAH PELAEAVAKE LDVNVTPMTA RDFANGEIYV RFEESVRGSD
 CFVLQSHTQP LNKWLMEQLL MIDALKRGS KRTAILPFY PYARQDKKHR GREPISARLI
 ADLMLTAGAD RIVSVDLHTD QIQGFDDGPV DHMHAMPILT DHIKENYNLD NICVSPDAG
 RVKVAEKWAN TLGDAPMAFV HKTRSTEVAN QVVANRVVGD VDGKDCVLLD DMIDTGTTIA

GAVGVLKKAG AKSVVIACHT GVFSDFPARER LSACGAEEVI TDTLPQSTE GWSNLTVLST
APLLARTINE IFENGSVTTL FEGEA

> RXA01239 (1-2433, translated) 811 residues

MARPISATYR LQMRGPQADS AGRSFGFAQA KAQLPYLKKL GISHLYLSPI FTAMPDSNHG
YDVIDPTTIN EELGGMGLR DLAAATHELG MGIIIDIVPN HLGVAVPHLN PWWWDVLKNG
KDSAFEFYFD IDWHEDNGSG GKLGMPIG AEGDEKLEFA ELDGEKVLKY FDHLPFIAPG
TEEGTPQEVY KRQHYRLQFW RDGVINFRFF FSVNTLAGIR QEDPLVFEHT HRLRLRLVAE
DLIDGVRVDH PDGLSDPFGY LHLRLDLIGP DRWLIIEKIL SVDEPLDPR L AVDGTGTGYDA
LRELDGVFIS RESEDKFSML ALTHSGSTWD ERALKSTEE LKRVVAQOEL AAEILRLARA
MRDNFSTAG TNVTEDKLSE TIELVAAMP VYRADIYSL RTTATVIAEM SKRFPSRRDA
LDLIAAALLG NGEAKIRFAQ VCGAVMAKGV EDTTFYRASR LVALQEVGGA PGRFGVSAE
FHLLQEERSL LWPRTMTTSL THDTRGEDT RARIISLSEV PDMYSELVNR VFAVLPA PDG
ATGSFLLQNL LGVWPADGVI TDALRDRFRE YALKAIREAS TKTTWVDPNE SFEAAVCDWV
EALFDGPSTS LITEFVSHIN RGSVQISLGR KLLQMVGAGI PDTYQGTFL EDSLVDPDNR
RFVDYTAREQ VLERLQTDWV TQVNSVEDLV DNADIAKMAV VHKSLELRAE FRASFVGGDH
QAVFGEGRAE SHIMGIARGT DRNHLNIAL ATRRPLIED RGGWYDITVT LPGGWEDRL
TGQRFSGVVP ATDLFSLHPV SLLVLVPDSE F

> RXA01253 (1-750, translated) 250 residues

MTTLNIGLIL PDVLGTGDD GNALVLRQRA RMRGINAEIQ RVTLD DAVPS TLDLYCLGGG
EDTAQILATE HLTKDGLQT AAAAGRPIFA VCAGLQVLGD SFRAAGRVID GLGLIDATTV
SLQKRAIGEV ETTPTRAGFT AELTERLTGF ENHMGATLLG PDAPLGRVV RGEENTDVWA
ASENTDDQORQ QFAEGAVQGS IIATYMHGPA LARNPQLADL MLAKAMGVAL KDLEPLDIDV
IDRLRAERLA

> RXA01321 (1-537, translated) 179 residues

VAENDYPMEV VAVVGNHENL RYIAENHNVP FFHVFPKDA VGKRKAQDQV AEIVNGYDPD
AIVLARFMQI LPPDLCEMWA GRVLNIHHSF LPSEFMGARPY HQAYSRGVKL IGATCHYATG
DLDDGPIIEQ DVIRVTHKDT PTEMQRLGRD AEKQVLARGL RFHLEDRLV YGNRTVVFD

> RXA01352 (1-606, translated) 202 residues

VFENRFDLRC YVVTGAGSVD EVVHTASAAA RGGAGVVQVR SKPISPEAMR ELASKVALEV
ARCSPTTRVL IDDLHLVASS LMREGLPIHG VHLGQDDMSV LEARELLGPE AIIGLTGTGL
ELVAAANELS DVLDIYAGP FRKTPKDSG RPPIGLAGYP PLVELSKVPI VAIGDVPAD
VRALSATGVA GVAMVRAFSE SD

> RXA01360 (1-159, translated) 53 residues

MLHIADKTFD SHLIMGTGGA TSQALLEESL VASGTQLTTV AMRRHQATTS SGE

> RXA01361 (1-606, translated) 202 residues

ADAVISIDGH DPCLTVTMNS GVRVASKSVV VLAAGLGAAS IPGWFEKANP LQLRPVYGDI
VRVRVPERLQ PMVTKVVRGF VEDRQIYIIP RTDGTLAGA TSREDHPQPR TGAVDHLRD
AIRLIPGIEE TEFIEVTCGA RGPDPDDL PY LGWVGSNVIA STGYFRHGIL LSALGARA
DMATNQPLFP TLDVCDPFRH QI

> RXA01371 (1-1296, translated) 432 residues

MAQVMDFKVA DLSLAEAGR QIRLAIEYEMP GLMQLRKEFA DEQPLKGARI AGSIHMTVQT
AVLIETLTAL GAEVRWASCN IFSTQDEAAA AIVVGSQTVE EPAGVPVFAW KGESLEEYWW
CINQIFSWGD ELPNMILDDG GDATMAVIRG REYEQAGLVP PAEANDSDEY IAFGLMLREV
LAAEPGKWK IAEAVKGVTE ETTTGVRHLY HFAEEGVLPF PAMNVNDAVT KSKFDNKYGT
RHSLIDGINR ATDMLMGGKN VLVCGYGDVG KGCAEAFDQ GARVKVTEAD PINALQALMD
GYSVVTVDEA IEDADIVITA TGNKDIISFE QMLKMKDHAL LGNIGHFDNE IDMHSLLRD
DVTRTTIKPQ VDEFTFSTGR SIIVLSEGR LNLGNATGHP SFVMSNSFAD QTIAQIELFQ
NEGQYENEVY RL

> RXA01381 (1-921, translated) 307 residues

SAGVGTITVI DDDTVDISNI HRQILFGASD VGRPKVEVAA ERLKELQPD TVNALHERIT
PENACELLNS VDLVLDGSDS FSTKYLVS DA AEITGTPLIW ATVLRFHGEL ALFNSGPDHR
GVGLRDVFP QPSADFVPC ATAGVLGATT ATIGALMATH AIGFLTEIGD VQPGTILSYD
AFPAATRSFR VSADPARLV TRLRASYEAA RTDTTSLIDA TLNGSLTALD IREPHEVLLK

DLPEGATSLK LPLSQITSDS DILEALSGID GDILVYCASG IRSSDFIDNY SHLGHKFVN
P
GGVNAL

> RXA01393 (1-870, translated) 290 residues
MNPIQLDTLL SIIDEGSFEG ASLALSISPS AVSQRVKALE HHVGRVLVSR TQPAKATEAG
EVLVQAARKM VLLQAETKAQ LSGRLAEIPL TIAINADSLS TWFPVFNEV ASWGGATLTL
RLEDEAHTLS LLRRGDVLGA VTREANPVAG CEVVELGTMR HLAIATPSLR DAYMVDGKLD
WAAMPVLRFG PKDVLQDRDL DGRVDGPVGR RRVSVIPSAE GFGEAIRRGL GWGLLPETQA
APMLKAGEVI LLDEIPIDTP MYWQRWRLES RSLARLTDV VDAIEGLRP

> RXA01394 (1-699, translated) 233 residues
MEIFITGLLL GASLLSIGP QNVLVIKQGI KREGLIIVLL VCLISDVFLF IAGTLGVDLL
SNAAPIVLDI MRWGGIAYLL WFAVMAAKDA MTNKVEAPQI IEETEPTVPD DTPLGGSABA
TDTRNRVRVE VSVDKQRVWV KPMLMAIVLT WLNPNAYLDA FVFIGGVGAQ YGDTGRWIFA
AGAFAASLIW FPLVGFGAAA LSRPLSSPKV WRWINVVAV VMTALAIKLM LMG

> RXA01416 (1-630, translated) 210 residues
AGASENVVNR VKDGAPAPTE KIVSDGLEAA KPFIDILCRA QEGLAQRVGN AAKEFPLFPP
YTDEVYSAVE RKVSKKLASL LTLKAKQERD DATNAYMEEI EAELLPKFEA SYSSAAEASK
EIRAGYNAV M KAIVRRMILT DHFRIDGRGV TDIRDLAVEV ELIPRAHGSS LFERGETQIL
GVTTLDMLKM EQQIDSLAPG DAKRYMHYHN

> RXA01442 (1-1224, translated) 408 residues
MYIPESIGTP LTPNATKVML LGSSELGKEV AIAFQRLGLE VHAVDRYEHA PAHQVAHFSY
VIDMTDAAQV RELVERVRPD FVIPEIEALA TDELVKIEEE GLATIVPTAR AAKLTMNREG
IRKLAAEELG LPTSNYEFCS TFEEFSAAA KLGYPNVVVP VMSSSGKGQS VLRSSDDLQA
AWDYAMSGAR VANSRVIVEA FVEFDYEITL LTVRSIDPTT SKPATWFCEP IGHRQEDGDY
VESWQPMEMT PRALENARSV AARITNALGG RGVFGVELFV SGDDVYFSEV SPRPHDTGLV
TLATQRFSEF ELHAKAILGL PVDVTLISPG ASAVIYGGIE SEGVSYTGLA EALAVAETDL
RIFAKPEAFT KRRMGVAVST AEDVAAARDR ATLAAAIAKV HPGNSAEA

> RXA01446 (1-1290, translated) 430 residues
MAAIVIVGAQ WGDEGKGKAT DILGGLVDYV VKPNGGNNAG HTVVVGGEKY ELKLLPAGVL
SETATPILGN GVVINLEALF EEIDGLEARG ADASRLRISA NAHLVAPYHQ VMDRVQERFL
GKRAIGTTGR GIGPTYADKV SRVGIRVQDI FDESILRQKV ESALDYKNQV LVKMYNRKAI
VAEEIVQYFL SYADRLRPMV IDATLVLENA LDQGHVLEME GGQATMLDVD HGTYPFVTSS
NPTAGGASVG SGIGPTKITS SLGIIKAYTT RVGAGPFPT LFDKWGEYLO TVGGEVGVNT
GRKRRRCGWYD SVIARYASRV NGFTDYFLTK LDVLTGIGEI PICVAYDVDG VRHDEMPLTQ
SEFHATPIF ETMPAWDEDI TDCKTFEDLP QKAQDYVRRL EELSGARFSY IGVGPGRDQT
IVLHDVLADN

> RXA01483 (1-1272, translated) 424 residues
MYPYSDADAF RRQPERAKSS QLRTSAVDTR SAFADRARV LHSALRRLA DKTQVVGPN
GDTPTRLTH SLEVAQIARG IGAGLDLDPD LCDLAGLCHD IGHPPYGHNG ENALNEVAAA
CGGFEGNAQT LRILTRLEPK IVSDEGESFG LNLRAALDA ACKYPWAKTN ADGSVNKKYS
AYDEDAEILA WIRQGHEDLR PPIEAQVMDF SDDIAYSVDH VEDGIVSGRI DLKVLWDLVE
LAALADKGA AFGGSPAELI EGAASLREL VVAAAADFDF SLRSYAALKA MTSELVGRYV
GSTIESTKKT HAGIDVGRMH GDLIIPETAA SEVKLLKTLA VLYVMDDPGH LARQNRQRDR
IFRVFDYLV GAPGSLDPMY RQWFIEADSE SEQIRVIVDQ IASMTESRLE RLARNAADIS
GFLG

> RXA01486 (1-657, translated) 219 residues
MSDVKDFEDT EFGLEAVAT IDNGDFGTRT IRFETGQLAR QADGAVTTYL DDDTMLLAT
TASNQPREGF DFFPLTVDVE ERMYAAGRIP GSFFRREGRP STEAILACRL IDRPLRPTFV
KGLRNEVQIV VTVMNPNED YYDVVAINGA SAATRISGLP VSGAVGGVRM ALVGDEKHPE
GQWVAFPTA QHEQSVFEIV VAGRLVERKR GNKTFSOVA

> RXA01489 (1-1023, translated) 341 residues
VDIWSGLDSV PADLQGSVVT IGVFDGLHRG HQSLIGEAKK QAEELGVPCV MVTDFPHPIA
VFLPGKEPTR LAPLDYRLNL AAECGVDAAL VIDFTKELAG LSAEEYFTTM IVDTLHARSV
VVGENTFTGV NGAGTESTMR ELGQKFGVNV TIAPLLHDDD QRICSTLVRD YLDQGEVERA

NWALGRRYAV RGEVVRGAGR GGKELGYPTA NLYLPTSVAL PADGVYAGWF TITDDREIDK
EISRDIDGTM VPGVRYQTAI SVGTNPTFGD ERRSVEAFIL DQEADLYGHH VMVEFVGHLLR
DMVKFNGVDE LLDAMARDVT NARDILAKDK LLLDADTQPS A

> RXA01491 (1-651, translated) 217 residues
MLDESLFPNS AKFSFIKTGD AVNLDHFHQL HPLEKALVAH SVDIRKAEFG DARWCAHQAL
QALGRDSGDP ILRGERGMPL WPSSVSGSLT HTDGFRAAVV APRLLVRSMD LDEAPAEPLP
KDVLGSIARV GEIPQLKRLE EQGVHCADRL LFCAKEATYK AWFPLTHRWL GFEQAEIDLR
DDGTFVSYLL VRPTVPFIS GKWLRLDGYV IAATAVT

> RXA01508 (1-1539, translated) 513 residues
MSDLGPIWRW LLLVSVSICA ASGLVYELAL VSLSTSLNGG GIVETSLIVA GYVAALGLGA
LLVKPFLNWP AQTFILGVETL LGLIGGCSAL VLYFTFATIG QSLWILVIAT AAIGILVGAE
LPLLMTMIQQ GRLADAKTTG SLVATLNAAD YLGALLGGLA WPFVLLPWLG MMRGAAAAGM
INLVAALFVG CVLLRHLLPR THFFVSVVAL LLAIAALATV LVKSDGIVAT ARAQLYRDPV
IYSHQSDYQD IVVTERGKDR RLYLNGGLQY STRDQHRYTE SLVYPSLNPE AESVLIIGGG
DGLAARELLR FPSMQITQVE LDPEVIEVAN TVLRSDNGGA MEDPRVSIIV DDAFTWLRSG
GNNGETYDSI IIDLPDPNND TMARLYSEEF YTLARARLNE QGRMVVQSSS AYTTDPVFWR
VGATLKSAGC EQVIPYHVHV PTFGDWGFQL CGPADMELEL REDTPPLTFL NDEVLVAAGV
FGLDNQPREL EPSTLDHPRV VEDLRKGYRE SGD

> RXA01512 (1-600, translated) 200 residues
MSNNVEMADH KDLNVPANPY GTDIESVLIS EEKLRQRIAE MAKRVSEEFK DAEEDLILVC
VLKGAFYFLA DFSRMLDIPT QSEFMAVSSY GNSTSSSGVV RILKDLDEI EGRDVLIVED
IIDSGLTSLW LMRNLKNRNP KSLNVITLLR KPERLTTNID MFDIGFDIPN EFVVGYYGLDF
AERYRDLPPYV GTLEPHVYSD

> RXA01514 (1-588, translated) 196 residues
VDNHAHVREF DEERATAAIR ELLIIVGEDP DREGLLETPA RVARAYKETF AGLHEDPTTV
LEKTFSEGHE ELVLVREIPI YSMCEHHLVP FFGVAHIGYI PGKSGKVTGL SKLARLADMF
AKRPQVQERL TSQIADALVE KLDAQAVAVV IEAEHLCMAM RGIRKPGAVT TTSAVRGGFK
NNAASRAEVF SLIRGH

> RXA01515 (1-852, translated) 284 residues
MNVSSLTIPG RCLVMGIVNV TEDSFSDGGK YIDVDQAIHA AKELVAAGAD MIDVGGESTR
PGAVRVDAVS ERDRVVPVIK ALHDAGIHTS VDTMRASVAQ AAAGAGVSMI NDVSGGLADP
EMFSVMAEAQ IPVCLMHWRT LQFGDAAGQA DHGGDVVADV HAVLDDLVAR ATAAGVAENQ
IVLDPGLGFA KSREDNWRLL QALPEFISGP FPILVGASRK RFLAGVRKDR GLDVTPIADAD
PATAAVTAVS AHMGAWGVRV HDVPVSRDAV DVAALWRSRG THHG

> RXA01516 (1-390, translated) 130 residues
MADRIELKGL ECFGHHGVFD FEKEQGQFFI VDVTCWMDFD AAGASDDLSD TVDYGALALL
VAEIVEGPSR DLIETVATES ADAVMAKFDA LHAVEVTIHK PKAPIRPTFA DVAVVARRSR
KSMAAGRSNA

> RXA01517 (1-477, translated) 159 residues
MHAVALSIGSN MDDRYALLNT VIEEFKDEIV AQSAIYSTPP WGIEDQDEFL NAVLVVEVEE
TPIELLRRGQ KLEEAERVR VRKWGPRTLD VDIVQIIKDG EEILSEDPEL TLPHPWAWQR
AFVLIPWLEA EPDAVLHGTT IAEHVDNLDP TDIEGVTKI

> RXA01521 (1-798, translated) 266 residues
LSFTHGQGRV FDTVEQIRMF GSALRKTGKP VVLVPLGNGL HAGHIALIRA AKRIPGAVVV
VAYAGPESDH ARLREELIDA IFPFNPETLW PHGIRVEVTG GPTLTPQGAE VTKVLGLLGI
TGATDVVLGE KDYELVVLVQ RALNDLHIPV KLHSVPTVRM PDGLAISLRN ISVPEDSRET
ALSLAAALTA GAHSAEHGEA VVKETVTQVL KAAGVTPDYV EIRGLDLGPA PEIGDARLFA
AITLGDVQLH DNVGLPLGIG FKNIEG

> RXA01528 (1-528, translated) 176 residues
VNQAWQQSRL VTSDETSAGG LUVSGLAEAV NANNEVDLSK IYVALIGRLD RRGRLWSMP
KGHVEPGEDK AATAEREVWE ETGIGHGEVFT ELGVIDYWV SEGKRIHKTV HHHLLRYVDG
DLNDEDPEVT EVAWIPANQL IEHLAFADER KLRQAHDLL PEFALKEKAE GRSTPR

> RXA01551 (1-1875, translated) 625 residues

LKAVPTGARA RAEIALIAAR APFEPVRLAP AKEERNGAMT PTQNEIHPKH SYSPIRKDGL
 EVPETEIRLD DSPSPGNEPF RIYRTRGPET NPKQGLPRLR ESWITARGDV ATYQGRERLL
 IDDGSRAMRR GQASAEWKGO KPAPLKALPG KRVTMQAYAR AGVITREMEF VALREHVDAAE
 FVRSEVARGR AIIPNNVNHP ESEPMIIGRK FLTGINANIG NSAVTSSIEE EVSKLQWATR
 WGADTVMDLS TGDDIHTTRE WIIRNSPVPI GTVPIYQALE KVNQVAADLN WEVFRDTIIE
 QCEQGVDMYT IHAGVLLAYI PLTTRRVGTI VSRGGSIMAG WCLAHHRESF LYEHFDELCE
 IFAQYDVAFS LGDGLRPGSL ADANDAAQFA ELKTIGELTQ RAWEDVQVM VEGPGHVPLN
 MIQENNELEQ KWAADAPFYT LGPLVTDIAP GYDHITSAG AAHIAMGGTA MLCYVTPKEH
 LGLPNRDDVK TGVITYKLAA HAADVAKGHP GARAWDDAMS KARFEFRWND QFALSLEPDT
 AIAYHDETLP AEPAKTAHFC SMCQPKFCSM RISQDIRDMF GDQIAELGMP GVGDSSSAVA
 SSGAREGMAE KSREFIAGGA EVYRR

> RXA01561 (1-930, translated) 310 residues

MLTLNDVITA QQRTPHVRRL TPLFEADPID GTQIWIKAEF LQKCGVFKTR GAFNRQLAAS
 ENGLLDPTVG IVAASGGNAG LANAFAAASL SVPATVLVPE TAPQVKVDRL KQYGATVQQI
 GSEYAEAFEA AQTFESETGA LFCHAYDQPD IAAGAGVIGL EIVEDLPDND TIVVAVGGGG
 LYAGIAAVVA AHDIKVVAVE PSKIPTLHNS LIAGQPVDVN VSGIAADSLG ARQIGREAFD
 IATAHPPIGV LVDDEAIIAA RRHLWDNYRI PAEHGAAAAAL ASLTSGAYKP AADEKVAVIV
 CGANTDLTTL

> RXA01599 (1-1662, translated) 554 residues

MTSSRKVRPT KHIFVTGGVV SSLGKGLTAA SLGQLLIARG LSVTMQKLDL YLNVDPGTMM
 PFEHGEVFTV EDGAETDLDL GHYERFLDRN LGLNANVTG KVVSTVIAKE RRGEYLGKTV
 QVIPHITDEI KARILSMGEP DAHGNAPDVV ISEVGGTVGD IESQPFLEAA RQVRHEIGRE
 NCFEIHCSLV PYLATSSELK TKPTQHSVAE LRGIGILPDA LVLRCREVP QGLKDKIAMM
 CDVDYEGVVS CPDSSSIYNI PDVLYREHL TFIIRRLGLP FRDWDSTWH DLLERVNNPR
 HELTVGIVGK YIDLDPAYLS VVEAVRAAGY ANWTRTNIKW ITSDDCETPS GAMKALSGLD
 AIVVPGGFGI RGIEGKIGAI TFAREHKIPL LGLCLGLQCT VIEAARQAGL EQASSTEFDP
 AATQPVIAATM EEQKAAVSSE ADLGGTMRLG AYPATLEEGS LVAELYGTTE VSERHRHRYE
 VNNAYRAQIA EGSGLVFSGT SPDGHLVEFV EYPKEVHPYL VATQAHPEYK SRPTHAPPLF
 YGLVKTALEL RVHP

> RXA01617 (1-615, translated) 205 residues

ANQIEAATAA HDLDVVKIGM LGTPATIDTV ATALEENSFK HVVLDPVLIC KGQEPGAALD
 TDTALRAKVL PQATVVTNN FEATTLGLD KLETIDDLKE AARLIHQGP QYVVVKGGID
 FPGDNAVDVL FDGTDYHVS EPKIGDERVS GAGCTFAAVI TAELAKGNSA VDAVTTAKRV
 VTRAVKDAVA SNAPFTSVWL AEDNK

> RXA01657 (1-501, translated) 167 residues

VIVGVVLAQG GVEEHLTALE ALGATTRKVR VPKDLGLEG IVIPGGESTV LDKLARTFDV
 VEPLANLIRD GLPVFATCAG LIYLAKHLN PARGQOTLAV VDVVVRNNAF GAQRESFDTT
 VDVSFDGATF PGVQASFIRA PIVTAFGPTV EAIAALNGGE VVGVRQG

> RXA01660 (1-552, translated) 184 residues

MSSNSINAEA RAELAELIKE LAVVHGEVTL SSGKKADYYI DVRRATLHAR ASRLIGQLLR
 EATADWDYDA VGGLTLGADP VATAIMHADG RDINAFVVRK EAKKHGMQRR IEGPDLTGKK
 VLVVEDTTTT GNSPLTAVAA LREAGIEVVG VATVVDRTG ADEVIAAEGE PYRSLGLSLD
 LGLN

> RXA01678 (1-528, translated) 176 residues

MLKCAVDEAA GGRAQAFVSS GDNIGSPFQ SSILGDEPTL EALNQMGLEY SAVGNHEFDK
 GYADLSSRVA DLADFDYLG NVEGENPDLA PYGISHLDGV KVAFVGTVSQ ETPMLVNSEG
 IEGITFTDPL EATNRVADEL VGSGAADVVV ALYHEGITGT EAWSENIDVV FAGHTH

> RXA01679 (1-1236, translated) 412 residues

MQSGNYGHAL ADVDFSFNHD TGELTVDDAR MLGVDDINAC ENPDDTIADI VAQAELDAGE
 AGKEVVATID GDFLRASDEG AESGSNYGAE SQLVNMIAA VRWSMSTNTA TTADIGLMNA
 GGLHTDLFSG DVTYAEAFEI QPFSGEDSFV TLKGSVFKDA LDQQWEEGSA RPVAALGVSD
 NVSYTYDINR PIGDRVTSVT IDDTPLDPER DYVVAASLYL QSGNEGMTAL TRGTAPAQGT

IVDVQSTIGY LSNNNVTPRT GQAQISITPS GEFNAGETIT LDMAGLRYTQ GDTATEVTVS
 LREEIVSAPI DPQLGEAGFG EAGTATVSLD IPATLSGTQN LVVTTDTGTR ISMPVEIVGA
 EQPAPQPAGS SVLGTGVLSG LLGIVVGILG MVGLVNWIDP SFIQQIQQQI FA

> RXA01690 (1-1053, translated) 351 residues
 PDRLKEILAA PKFGKFFTDH MVTIDWNESE GWHNAQLVPY APIPMDPATT VFHYGQAIFFE
 GIKAYRHSDE TIKTRPDEN AERMQRSAAR MAMPQLPTED FIKALELLVD ADQDWVPEYG
 GEASLYLRPF MISTEIGLV SPADAYKFLV IASPVGAYFT GGIKPVSVWL SEDYVRAAPG
 GTGDAKFAGN YAASLLAQSQ AAEGKCDQVV WLDAIEHKYI EEMGGMNLGF IYRNGDQVKL
 VTPELSGSLP PGITRKSLLQ VARDLGYEVE ERKITTTEWE EDAKSGAMTE AFACGTAAVI
 TPVGTVKSAH GTFEVNNNEV GEITMKLRET LTGIQQGNVE DQNGWLYPLV G

> RXA01692 (1-750, translated) 250 residues
 MTISQENQPI IQPVSLIGGG PGAWDLITVR GMNRLQEADV ILADHLGPTD ELEKLCDISS
 KTVVDVSKLP YGRQVTQERT NEMLVEYAAQ GLKVVRKGG DPYVFGRGFE ELEFLGEHGI
 ECEVIPGVTS AVSVPAAAGI PITNRGVVHS FTVVSGHLPP GHPKSLVDWA ALAKSGGTLS
 IIMGVKNAGA IAQALMDGGL DADTPAAVIQ EGTDAQRSV RCTLGTLGAV MVEEEIKPPA
 VYVIGQVAGL

> RXA01698 (1-990, translated) 330 residues
 GNTEWDKWTI IMSSDALDME DPDNVAAMSS GRGAKLTRPR PGHADYAGML KYGFDDARNV
 LERSSARETA ARVAAATVAR SFLRETIGVE VLSHVISIGA SEPYTGAEPT FADIQAIDDS
 PVRAF GKDAE ESMIAEIEAA KKAGDTLGGI VEVIVEGLPI GLGSHISGED RLDAQIAAAL
 MGIQAIKGV IGDGFEEARR RGSEAHDEVF LDDNGVYRNT NRAGGLEGGM TNGETLVRRA
 GMKPISTVPR ALKTIDMENG KAATGIHQRS DCAVPAAGV VAEAMVTLVL ARAVLQKFGG
 DSLSETKSN I DTYLKNIEER MKFEGLEDGA

> RXA01699 (1-570, translated) 190 residues
 MERNEVNDQI HLDHQSDDTI ECSCPIVVLV GLPGAGKSTI GRRLARALNT ELVDSDELIE
 RATGKACGAV FSELGEPAFR ELEAIHVAEA LKSSGVVSLG GGSVLTESTR ELLKGQDVVW
 IDVPVEEGIR RTANERSRPV LQAADPAEHY RNLVKVRTPL YEEVATYRLR TNNRSPQQVV
 AAVLHHLEID

> RXA01712 (1-501, translated) 167 residues
 VKAENYGGVE VSPEIQKQRQ ELGQEAIPPI AVMSGSLNFD VDTRFFLEAE VPPIIITDNS
 DQAKQORLVD AGAQVIEVET LTAEVGVEKL RSLGYARIDC EGGATLYGQM LAADLVVDVW
 HTIDPTLSGS VERPTVKGGD DAPRRFALEH VFVDDDDSTLF LRYKRAK

> RXA01719 (1-561, translated) 187 residues
 MNIIILAGGE GKRMGGVDKA AVAVDGRITL DILLSQLDPE DDVVVVSPA I IDGITTVCEE
 PPLGGPVAGI EAGLNSFEHA HEFTAILAVD APYSAAMLPL LQAQIGKADV AVTLAADGWV
 QPLCALWRSG SLEAVIHS LG ETRNRPAKAL LKQAGHIVEV GGDGTEKD YD TVAELEV LGN
 VTLPKAH

> RXA01720 (1-1209, translated) 403 residues
 VAQQRSVDDY LSILIDSVAP LPPVKTPILG AHPLSHLAED VVATIPKPF TNSAVDGYAI
 LKEDIHSGSP WTLVGGDTP AGSAPASINN GKAIRVMTGG PVPSTNKDMI VVPVELTNAP
 VDHS LPT EIT INELPGERNN IRHAGEHLKE GEIAVAAGTA FDAGTVSTVI SVGHDTVKAH
 PCPRVAVITT GDELNQGNPW GIPNSNGPML VAELKRVGIK DPQHFHSDDS ETALRETLDK
 PAEVADVIIT VGGISAGAFD VVKAVGKTG GFEFFPIAMK PGKPQGHGQW GDAKVVCPLG
 NPVAAWVSFR LFVVPVIERL GGGKRLASIS ELPVVALRSN RALKAREGPV LAIPVAIDWE
 KRMANSQAHR SHMVGALAGS GGIALVTSSI AEDGLVDVVL GRM

> RXA01746 (1-753, translated) 251 residues
 MTAPRPDFFP ADLSIRASAE PIEIQRGLI DYQEAWDYQA ELATRRANDE IPDQLLILEH
 PSVYTAGKRT QPEDLPNTGL PVINADRCGR ITWHGPQQLV IYPIIKLADP IDVVDYVRRL
 EEALIQVVG D MG VAGAGRID GRSGVWVPAH DGWVDSKVAA IGIRITRGVA MHGVAINC NN
 TLDFYEH IIP CGIADAGLST LSRELKRDVS VEELVEPSIR ALDDALAGRL VVSDHSFGSA
 PDPTKNL PKR G

> RXA01747 (1-1044, translated) 348 residues

VTIAPEGRRL LRVEARNSET PIETKPRWIR NOVKNGPEYQ DMKERVAGAS LHTVCQEAGC
 PNIHECWESR EATFLIGGAN CSRRCDFCMI NSARPEPLDR GEPLRVAESV REMQLNYSTI
 TGVTRDDLDD EGAWLYSEVV RKIHELNPHT GVENLVPDFS GKDLLQEVF ESRPEVFAHN
 VETVPRIFKR IRPAFRYERS LDVIRQARDF GLVTKSNLIL GMGETKEEIT EALQDLHDAG
 CDIITITQYL RPGPLFHPIE RWVKPEEFLE HADAAKEMGF AAVMSGPLVR SSYRAGRLYA
 QAMEFRGEEI PAHLAHLKDT SGGSTAQEAS TLLERYGASE DTPVVSFN

> RXA01757 (1-801, translated) 267 residues
 MPTASPIYDV VVVGAGISGL IATQLLDLAG LNIKCFEACS RVGGRAVSQV QSDLFLDLGA
 TWFWLNEPLV QQLVNNLGLG TFPQAIEGDA LFETLVDAPS RLRGNPIDAA SGRFQAGASS
 LALGLAAQLK PGVLELGDV HSLSEEDGEI VVKSSKQIVR AKHVIIAVPP ALAAELIGFT
 LDLPADVKA AHPQHIAVMN WAKEKYTLPT QAASAGGFGH ELFQQPLGHG RIHWASTEVA
 TEFGGHLEGA VRAGIQAALQ TGFNLKS

> RXA01807 (1-792, translated) 264 residues
 MPSAGEEILE QRAQLEFDQR RADVVMIGSQ VVYGSVGLSA AIPVMHNEGL RVVAVPTVVL
 SSMRYASSH RQPMSDQWLA DALQDLVDLG IIDEVSTIST GYFTSASQVR VVAWLQKIR
 ETHPHVRIV DPIMGDSVVG IYVADEIATA ICQDLCLPLAT GIIPNAFELS HMGSGDPRS
 LLGPFGEWII ITSATETVGT TVTRIVTRDS VQEIASATVD TTAKGAGDVY AAALIAALHK
 DFLSIDAASH ASNTVCAGLQ TKAL

> RXA01821 (1-378, translated) 126 residues
 RNSQGWKCP TRSPKNTSIE DNGDHVVIQA GEETTIVDRV IVTGSWTSE LVPSTIAPLE
 VRRVLVTWFL PNNPVDFQPE NLPCFIRDR GFHVFGAPCV DGYSIKIAGL DEWGVPLSLD
 PPMCPR

> RXA01835 (1-531, translated) 177 residues
 MNTAAWAHRH HVRKGGGIPY VSHLYSVMYL LASVTNDEDV LIAGLLHDTL EDVPPEEYNSA
 QLEADFGPRV RELVEELTKQ PLKSWKARAD AYLLHLSAGA SLEAVLISTA DKLHNLMSIL
 DDLEIHGEDL WQRFNAGKEQ QIWWYSEVYQ ISLQRLGFNE LNKQLGLCVE KLLKQSA

> RXA01850 (1-1347, translated) 449 residues
 MAISVVDLFS IGIGPSSSHT VGPMRAALTY ISEFPSSHVD ITHGSLAAT GKGHCTDRAV
 LLGLVGWEPT IVPIDAAPSP GAPIPAKGSV NGPKGTVSYS LTFDPHPLPE HPNAVTFKGS
 TTRTYLSVGG GFIMTLEDER KLDDIGSGVS TIHPEAEVPC PFQKSSQLLA YGRDFAEVMK
 DNERLIHGDG GTVDAHLDRV WQIMQECVAQ GIATPGILPG GLNVQRRAPQ VHALISNGDT
 CELGADLDAV EWNVLYALAV NEENAAGGRV VTAPTNGAAG IIPAVMHYAR DFLTGFGEAQ
 ARTFLYTAGA VGIIKENAS ISGAEVGCQG EVGSASAMAA AGLCAVLGGS PQQVENAAEI
 ALEHNGLTLC DPVGGVLQIP CIERNAIAAM KSINAARLAR IGDGNNRVSL DDVVVTMAAT
 GRDMLTKYKE TSLGGLATTL GFPVSMTEC

> RXA01878 (1-879, translated) 293 residues
 MEEPSGAQLL GPVEIRALAE KLDVTPTKKL QGNFVHDPNT VRRIVAAAEL TPNDHVVEVG
 PGLGSLTLAL VESAASVTAV EIDPRLAAEL PETFQWRAPA LAHKLSIVLK DALKVQQSDM
 AVQPTALVAN LPYNVSVPLV LHMMEEFPTI NKVLVMVQAE VADRLAADPG SKIYGVPSVK
 ASFYGPVTRA GSIGKNVFWP APKIESGLVK IVREDTAWKQ DDETRKKVWP IIDAAFLQRR
 KTLRAALSGH YGSGQAEEA LRAADIDPTL RGEKLDVTDY VRLAGVLQOK DEK

> RXA01892 (1-729, translated) 243 residues
 VTTSSQPRPT GYKRVMLKLE GEMFGGGKVG VDPDVVDNVA RQIAEVAKTG AEIAVVIGGG
 NFFRGAEQQ RGMDRARSY MGMLGTVMNC LALQDFLGQH GVECRVQTAI NMAQVAEPYL
 PLRAERHLEK GRVVIFGAGM GMPYFSTDDT AAQRALEIGC DVLLMAKAVD GVYSDDPRTN
 PDAELFTEIT PKEVIEKGLK VADATAFSLC MDNKMPIVLF NLLTEGNIAR AISGERIGTL
 VES

> RXA01894 (1-855, translated) 285 residues
 MPKPKNNAGR DLKAAIAVGI GLGVLVLLGI VLSPWGWYIL VAGFMAAATW EVGSRLKEGG
 YHLPLPIMII GGQAIWLSW PFGTMGILAS FVATVLVLMY FRIFYNGTEK EARNYLRTDS
 VGIFVLTWIP LFGSFAAMLS LMQNNISIPGT YFILTFLMLCV IASDVGGYIA GVFFGSHPM
 PLVSPKKSWE GFAGSIVLGS VTGALSVMFL LDHWWMGVI LGCALVVCAT LGDLVESQFK
 RDLGIKMSN LLPGHGGLMD RLDGMLPAAM VTWLILSVIS SSYPS

> RXA01920 (1-414, translated) 138 residues

ADVIRLIIRD EAVHGYIIGY KYQKAVAKET PERQEELKEY TFDLLYDLYD NETQYSEDLY
DDLGWTEDEVK RFLRYNANKA LNNLGYEGLF PADETKVSPN ILSALSPNAD ENHDDFFSGSG
SSYVIGKAEN TEDDDWDF

> RXA01928 (1-837, translated) 279 residues

MQVATTKQAL IDALLHHKSV GLVPTMGALH SGHASLVKAA RAENDTVVAS IFVNPLQFEA
LGDCDDYRNY PRQLDADLAL LEEAGVDIVF APDVEEMYPG GLPLVWARTG SIGTKLEGAS
RPGHFDGVAT VVAKLFNLVR PDRAYFGQKD AQQVAVIRRL VADLDIPVEI RPVPIIRGAD
GLAESSRNQR LSADQRAQAL VLPQVLSGLQ RRKAAGEALD IQGARDTLAS ADGVRDLHLE
IVDPATLEPL EIDGLLTQPA LVVGAIFVGP VRLIDNIEL

> RXA01929 (1-807, translated) 269 residues

MSGIDAKKIR TRHFREAKVN GQKVSVLTSY DALSARIFDE AGVDMLLVGD SAANVVLGRD
TTLSITLDEM IVLAKAVTIA TKRALVVVDL PFGTYEVSPN QAVESAIRVM RETGAAAVKI
EGGVEIAQTI RRIVDAGIPV VGHIGYTPQS EHSLGGHVVQ GRGASSGKLI ADARALEQAG
AFAVVLEMVP AEAAREVTEDE LSITTIGIGA GNGTDGQVLV WQDAFGLNRG KKPRFVREYA
TLGDSLHDAA QAYIADIHAG TFPGEAESF

> RXA01940 (1-579, translated) 193 residues

RVTLVSTGPL TNIALAVRKE PRIAERVKEV VLMGGGYHVG NWTAVAEFNI KIDPEAAHIV
FNEKWPLTMV GLDLTHQALA TPEIEAKFNE LGTDVADFV ALFDAFRKNY QDAQGFDPNP
VHDPICAVAYL VDPTVFTRK APLDVELYGA LTTGMTVADF RAPAPADCTT QVAVDLDFDK
FWMNMVIDAVK RIG

> RXA01970 (1-1206, translated) 402 residues

PEPVRIIAIE ALGLMCAEEV QASRALPGFA QAAIDGYAVR AVDVGGEKSF SQQLPVAPPE
KSLPVVGEVA AGSQQLRLRQ PKQAVMVHTG APLPMLADAV LPMWSDRGR KRVTAQRPVR
SGEFVRKEGD DIQPGDIAVS AGAVLGPAQI GLLAAVGRSK VLVYPRPRMS VISVGAELVD
IDRQPGLGQV YDVNSYSLAA AGREAGADV RYGLAAGEPR RIKEIIESQM LRSEIIVITG
AVGGAGSAGV RQVLNELGDI DTERVAMHPG SVQGFLLGE NKIPCFLLPS NPVASLVIFE
TFVRPVVRMS LGKSNAARRV VRARALNHVV SVAGRKGFI SRMLMRDAETQ DYLVEALGGA
TGAPSHLLAG LSEANGMIRI PEDVTEIRPG DVVDVIFLAQ GR

> RXA02022 (1-1107, translated) 369 residues

VNSELKPGLD LLGDPVILTQ RLVDIPSPSG QEQIADIEIE DALRNLNLPG VEVFRFNNNV
LARTNRGLAS RVMLAGHIDT VPIADNLPSR VEDGIMYCG TVDMKSGLAV YLHTFATLAT
STELKHDLT L IAYECEEVAD HLNLGLHIRD EHPEWLAADL ALLGEPTGGW IEAGCQGNLR
IKVTAHGVRA HSARSWLGDN AMHKLSPIS KVAAYKAAEV NIDGLTYREG LNIVFCESGV
ANNVIPDLAW MNLNFRFAPN RDLNEAIEHV VETLELDGQD GIEWAVEDGA GGALPGLGQQ
VTSGLIDAVG REKIRAKFGW TDVSRFSAMG IPALNFGAGD PSFAHNRDEQ CPVEQITDVA
AILKQYLSE

> RXA02024 (1-759, translated) 253 residues

MSSLPVIMAI VNRTPDSEFYD KGATFEDTAA LNRAAEVIEQ GAGIVDIGGV KAGPGDFVSA
EEEIDRVVPI IAAVRERFPD IDISVDTWRA SVADVAVAHG ATLINDTWAG HDHELVQVAG
QHKVGYVCSH TGGVIPRTRP YRVHFDDIVA DVITETTKLA EQAVRAGVPE ERVFIDPTH
FGKNTFHGLE LLRRIDEVVA TGWPVLMALS NKDFIGETLE RGVDKRVAGT LAATAWAAAR
GVAAFRVHEV AET

> RXA02027 (1-495, translated) 165 residues

MSQTKQELRT KLREARTNMD EASRTRENAA IIANVSYIIR SKQPKRIAAY VPVRTEPGGR
LLLDALHAET SALILPVSLE DRRLDWALYE GPTSLVPGAF GIQEPGGTRL GPEALNFCDL
VIAPALACTP SGIRLGKGGG FYDRALATGV KADVITLLFN GEIRD

> RXA02031 (1-474, translated) 158 residues

MTEEREILTY EMFGTAMREL AQEIIDDYQP DCVLSIARGG LLIGGALGYA LGIKNVSVIN
VEFYTDIGEH LEEPMLPPT PKAVDLSGMR VLVADDVADT GKTLELVDRF LGDQVVEVRT
AVIYHKPNV FKPEYVWRET DKWINFPWST LPPVEPSK

> RXA02072 (1-1341, translated) 447 residues

MTVDEQVSNY YDMLLKRNAG EPEFHQAVAE VLESCLKIVLE KDPHYADYGL IQRLCEPERQ
LIFRVPWVDD QGQVHVNRGF RVQFNSALGP YKGGRLRFHPS VNLGIVKFLG FEQIFKNSLT
GLPIGGGKGG SDFDPKGKSD LEIMRFCQSF MTELHRHIGE YRDVPAGNIG VGGHEIGYLF
GHYRRMANQH ESGVLTGKGL TWGGSLVRTE ATGYGCVYFV SEMIKAKGES ISGQKIIVSG
SGNVATYAIE KAQELGATVI GFSDSSGWVH TPNGVDVAKL REIKEVRRAR VSVYADEVEG
ATYHTDGSIW DLKCDIALPC ATQNELNGEN AKTLADNGCR FVAEGANMPS TPEAVEVFRE
RDIRFGPGKA ANAGGVATSA LEMQQNASRD SWSFEYTDER LQVIMKNIFK TCAETAAEYG
HENDYVVGAN IAGFKKVADA MLAQGVV

> RXA02085 (1-1800, translated) 600 residues

MTSNFSSTVA GLPRIGAKRE LKFALEGYWN GSIEGRELAQ TARQLVNTAS DSLSGLDSVP
FAGRSYYDAM LDTAAILGVL PERFDDIADH ENDGLPLWID RYFGAARGTE TLPAQAMTKW
FDTNYHYLVP ELSADTRFVL DASALIEDLR CQQVRGVNAR PVLVGPLTFL SLARTTDGSN
PLDHLPALFE VYERLIKSF TEWVQIDEPA LVTDVAVEVL EQVRAGYTTL AKRDGVFVNT
YFGSGDQALN TLAGIGLGAI GVDLVTHGVT ELAAWKGEEL LVAGIVDGRN IWRTDLCAAL
ASLKRLAARG PIAVSTSCSL LHVPYTLAE NIEPEVRDWL AFGSEKITEV KLLADALAGN
IDAAAFDAAS AAIASRRTSP RTAPITQELP GRSRGSFDTR VTLQEKSLLEL PALPTTTIGS
FPQTPSIRSA RARLRKESIT LEQYEEAMRE EIDLVIKQE ELGLDVLVHG EPERNDMVQY
FSELLDGFLS TANGWVQSYG SRCVRPPVLF GNVSRPAPMT VKWFQYQSL TQKHVKGMLT
GPVTILAWSF VRDDQPLATT ADQVALALRD EINDLIEAGA KIIQVDEPAT RELLPATRRR

> RXA02086 (1-480, translated) 160 residues

MSLRFVNCCP LRDVDKPAYL QWSVDSFRLA TAGAPDDVQI HTHMCYSEFN EVISSVIALD
ADVTTIEAAR SDMQVLAALK SSGFELGVGP GVWDIHSPRV PSAQKVDGLL EAALQSVDP
QLWVNPDCLG KTRGWPEVEA SLKVLVESAK QAREKIGATI

> RXA02093 (1-804, translated) 268 residues

MVNYVDRETT LCISLAARPS NHGVRFNHNL YAEGLNLYLY KAVAPADITA AVAGIRGLNI
RGAGVSMYPK SDVIPLIDEL HPSAERIRSV NTIVNNDGHL VGYNTDYTAV YHLEEHRVN
PNARVAIKGS GGMANAVVAA LAEYGLSGTV VARNHTTGSA LASRYGWEYS ATPVEDAKIL
VNVTPMGNG PDQDVVSFGE DEVDRADVIF DCVAFPVETP LIKLAKEKKG QTIDGGEVAA
LQAAEQFHLY TGVLPNTDQI IAAEEFSK

> RXA02106 (1-1056, translated) 352 residues

MNNHFELKVP GGKLVVVDVT TDLDSIADV ISGDFPLEPD EAFFALGRAL QGASVGDNTD
RLQAKLDAAL AEYDDVELHG FSTADIALAV RRAVTGAQDF TDYEWEILHP GVLPTPLNVA
LDELLLDQVA SGQRGPTMRI WDWDRTATVI GSFQSYVNEI NQEGVNEHGV TVVRRMSGGG
AMFMEGGNCI TYSLYAPESL VAGLSYEQSY EYLDWRVIAA LKTHDVDAWY VPINDITSTG
GKIGGAAQKR RSGAVLHHVT MSYDIDADMM TQVLRIGKVK ISDKGLRSK KRVDPPLRRQT
GASREQIIDT LKSTFSARYG AQEVELSDED FAAGHDLVKT KYATEEWTKR VQ

> RXA02111 (1-1284, translated) 428 residues

MTTSITPSVN LALKNANSCN SELKDGPFWL DQPGMPDVYG PGASQNDPIP AHAPRQQVLP
EEYQRASDDE LHRRIREAKD TLGDKVVILG HFYQRDEVIQ HADFGVDSFQ LARAAKTRPE
AEAIVFCGVH FMAETADLLS TDEQSVILPN LAAGCSMADM ADLDSVEDCW EQLTSIYGDD
TLIPVTYMN SAALKGFVGE HGGIVCTSSN ARSVLEWAFE RGQRVLFPPD QHLGRNTAKA
MGIGIDQMPL WNPKNPLGGN TVSELENKAV LLWHGFCSVH KRFTVEQINK ARAEYDPVHV
IVHPESPMPV VDAADSSGST DFIVKAIQAA PAGSTFAIGT EINLVQRLAA QYPQHTIFCL
DPVICPCSTM YRIHPGYLAW ALEELVAGNV INQISVSESV AAPARVALER MLSVVPAPV
TPSSSKDA

> RXA02112 (1-837, translated) 279 residues

MTHIDRIVG AALSEDAPWG DITSDFIFP SAQLSAKVVA REPGVFSGQA LLDASFRLVD
PRINASLKVA DGDSFETGDI LGTITGSARS ILRSERIALN FIQRTSGIAT LTSCYVAEVK
GTKARIVDTR KTPGLRIIE RQAVRDGGGF NHRATLSDAV MVKDNHLAAI ASQGLSITEA
LSNMKAKLPH TTHVEVEVDH IEQIEPVLAA GVDTIMLDNF TIDQLIEGVD LIGGRALVEA
SGGVNLNTAG KIASGTGVDVI SVGALTHSVH ALDLGLDIF

> RXA02134 (1-921, translated) 307 residues

MSGKAGFTPE DPEDSDNRHG NPLFEGIFTA LNWMTVLPVP GASVFDRTTG ARVMASLPFV

GFVFGMFTAI IMWAIGPISG VIHVDGLLVA VLIVAFWELL NRFMHLDLGLA DVSDALGSYA
 APPRAREILA DPRTGLFGLA TAMLSVLLQV AAVASLVDDST VWMICFIPV LGRIAGQVTA
 LKNHNAFSPT GFGALVIGTV KFWWIALWLL VTAALAFWCA ELISPLSPLT SVNTPFVAGP
 FPAAINPAWL GGWVAITAVV ACVFAALFSR RLSRSFGGLN GDCIGACIHL GASISAVMFA
 VVANAMV

> RXA02135 (1-1074, translated) 358 residues

MVPAELFARV EFPDHLKILAQ TKDFHDSLTK PPGSLGKLEQ IGCFFISACQG QIPPRPLNNS
 KIVVFAGDHG VATKGVSAYP SSVSLQMAEN ITNGGAINV IARTTGTSVR LIDTSLDHEA
 WGDERSRSC GSIDVEDAMT QEQVERALKI GKRIADQEV D AGADILIPGD LGIGNTTTAA
 ALVGTFTLAE PVVVVGRGTG IDDEAWKLKV SAIRDAMFRA RDLRQDPIAI ARKISSPDLA
 AMAAFIAQAA VVRTPVLLDG VVVTAALLA NKLPAGARRW FIAGHRSTEP AHSVALNALA
 LDPILELGMS LGEGSGAATA LPLVKIAVDL MNDMSTFSSA GVDGPLNASS EAEQNTE

> RXA02136 (1-522, translated) 174 residues

MRTLVLGGAR SGKSAFAESL VGSGPVLYVA TARPSGDDPE FAERIAVHAE RRPTSWVLDE
 EGDVDKLLAS PPAMPVLVDD LGTWLTHATD ACDGWEASSA QLEAKMDLLI DAILHFQGED
 LVIVSPEVGM GIVPEYKSGR LFRDRIGTLN QRVAACICERV VFVVGAPLE LKTF

> RXA02139 (1-1839, translated) 613 residues

MRHRGPDDAG TWHADAAAFG FNRLSIIDIA HSHQPLRWGP ADEPDYAMT FNGEIYNYVE
 LRKELSDLGY AFNTSGDGEP IVVGFHHWGE SVVEHLRGMF GIAIWDTKK SLFLARDQFG
 IKPLFYATTE HGTVFSSEKK TILEMAEEMN LDLGLDKRTI EHYVDLQYVP EPDTLHAQIS
 RLESGCTATV RPPGKLEQKR YFKPQFPVQK VVKGKEQDLF DRIAQVLEDS VEKHMRAVDT
 VGSFLFGGID STAI AALAKR HNPDLTFTT GFEREYSEV DVAAESAAAI GAEHIVKIVS
 PEEYANAIPK IMWYLDPAV DPSLVPLYFV AAEARKHVKV VLSGEGADEL FGGYTIYKEP
 LSLAPFEKIP SPLRKGLGKL SKVLDPGMMK KSLLESGSMT MEERYGNAR SFNFEQMQRV
 IPWAKREWDH REVTAPIYAO SRNFDPVARM QHLDLFTWMR GDILVKADKI NMANSLELRV
 PFLDKEVFKV AETIPYDLKI ANGTTKYALR RALEQIVPPH VLHRKKLGFP VPMRHWLAGD
 ELFGWAQDTI KESGTEDIFN KQAVLDMLNE HRDGVSDHSR RLWTVLSFMV WHGIFVENRI
 DPQIEDRSYP VEL

> RXA02153 (1-780, translated) 260 residues

MIMHNVYGVMT MTKVAIAGA SGYAGGEILR LLLGHPAYAS GELEIGALTA ASTAGSTLGE
 LMPHIPQLAD RVIQDTTAET LAGHDVVFLG LPHGFSAEIA LQLGPDVTVI DCAADFRQLN
 AADWEKFYGS EHQTWPYGI PEMPGHREAL RGAKRVAVPG CFPTGATLAL LPAVQAGLIE
 PDVSVVSITG VSGAGKKASV ALLGSETMGS LKAYNTSGKH RHTPEIAQNL GEVSDKPVKV
 SFTPVLAFLP REFSPLQPHL

> RXA02154 (1-291, translated) 97 residues

LKEGVTAEQA RAVYEEFYAQ ETFVHVLPEG AQPQTQAVLG SNMCHVQVEI DEEAGKVLVT
 SAIDNLTKGT AGAAVQCMNL SVGFDEAAGL PQVGVP

> RXA02155 (1-1164, translated) 388 residues

MAEKGITAPK GFVASATTAG IKASGNPDMA LVVNQGPES AAVFTRNRV FAAPVKVSRE
 NVADGQIRAV LYNAGNANAC NGLQGEKDAR ESVSHLAQNL GLEDSDIGVC STGLIGELLP
 MDKLNAGIDQ LTAEGALGDN GAAAAKAIMT TDTVDKETVV FADGWTVGGM GKGVGMMAPS
 LATMLVCLTT DASVTQEMAQ IALANATAVT FDTLDIDGST STNDTVFLLA SGASGITPTQ
 DELNDVYAA CSDIAAKLQA DAEGVTKRVA VTVVGTTNNE QAINAARTVA RDNLFKCAMF
 GSDPNWGRVL AAVGMADADM EPEKISVFFN QQAVCLDSTG APGAREVDLS GADIDVRIDL
 GTSSEGQATV RTTDLSEFSY EINSAYSS

> RXA02156 (1-951, translated) 317 residues

MNDLIKDLGS EVRANVLAEA LPWLQHFRDK IVVVKYGGNA MVDDDLKAAF AADMVFLRTV
 GAKPVVHHG GPQISEMLNR VGLQGEFKGG FRVTPEVMD IVRMVLFQV GRDLVGLINS
 HGPYAVGTSG EDAGLFTAQK RMVNIDGVPT DIGLVGDIIN VDASSLMDII EAGRIPVST
 IAPGEDGQIY NINADTAAGA LAAAIGAERL LVLTNVEGLY TDWPKSSLV SKIKATELEA
 ILPGLDSGMI PKMESCLNAV RGGVSAAHVI DGRIASVLL ELLTMGGIGT MVLDPDVFDR
 NYPEGTVFRK DDKDGEL

> RXA02157 (1-1173, translated) 391 residues

MSTLETWPQV IINTYGTTPV ELVSGKGATV TDDQGNVYID LLAGIAVNAL GHAPPAIEA
 VTNQIGQLGH VSNLFASRPV VEVAEELIKR FSLDDATLAA QTRVFFCNSG AEANEAAFKI
 ARLTGRSRII AAVHGFHGRV MGSALTGQP DKREAFLEMP SGVEFYYPYGD TDYLRKMMVET
 NPTDVAAIFL EPIQGETGVV PAPEGFLKAV RELCDEYGIL MITDEVQTVG GRTGDFFAHQ
 HDGVVPDVVT MAKGLGGGLP IGACLATGRA AELMTPGKHG TTFGGNPVAC AAAKAVLSVV
 DDAFCAEVAR KGELFKELLA KVDGVVDVRG RGLMLGVVLE RDVAKQAVLD GFKHGVILNA
 PADNIIRLTP PLVITDEEIA DAVKAI AETI A

> RXA02158 (1-957, translated) 319 residues

MTSQPQVRHF LADDDLTPAE QAEVLTAAK LKAAPFSERP LEGPKSVAVL FDKTSTRTRF
 SFDAGIAHLG GHAIIVDSGS SQMGKGESLQ DTAAVLSRYV EAIWRTYAH SNFHAMAETS
 TVPLVNSLSD DLHPCQILAD LQTIENLSP EEGPAGLKGK KAVYLGDDN NMANSYMIGF
 ATAGMDISII APEGFPRAE FVERAEKRGQ ETGAKVVVTD SLDEVAGADV VITDTWVSMG
 MENDGIDRTT PFVPYQVNDE VMAKANDGAI FLHCLPAYRG KEVAASVIDG PASKVFDEAE
 NRLHAQKALL VWLLANQPR

> RXA02159 (1-513, translated) 171 residues

MSLGSTPSTP ENLNPVTRTA RQALILQILD KQKVTSQVQL SELLLDEGID ITQATLSRDL
 DELGARKVRP DGGRAYYAVG PVDSIAREDL RGPSEKLRRM LDELLVSTDH SGNIAMLRTP
 PGAAQYLASF IDRVLKEVV GTIAGDDTVF VLARDPLTGK ELGELLSGRT T

> RXA02160 (1-1203, translated) 401 residues

MTNRIVLAYS GGLDTTVAIP YLKKMIDGEV IAVSLDLGQG GENMDNVRQR ALDAGAAESI
 VVDAKDEFAR EYCLPTIKAN GMYMKQYPLV SAISRPLIVK HLVEAGKQFN GTHVAHGCTG
 KGNDQVRFEV GFMDTDPNLE IIAPARDFAW TRDKAIAFAE ENNVPIEQSV KSPFSIDQNV
 WGRAIETGYL EDLWNAPTKD IYAYTEDPAL GNAPDEVIIS FEGGKPVSID GRPVSVLQAI
 EELNRRAGA QGVRLDMVED RLVGIKSREI YEAPGAIALI KAHEALEDVT IERELARYKR
 GVDARWAEV YDGLWFGPLK RSLDAFIDST QEHVTGDIRM VLHAGSITIN GRRSSHSLYD
 FNLATYDTGD TFDQTLAKGF VQLHGLSSKI ANKRDREAGN N

> RXA02161 (1-783, translated) 261 residues

MEQHGTNEGA LWGGRFSGGP SEAMFALSVS THFDWVLAPY DVLASKAHAK VLHQADLLSD
 EDLATMLAGL DQLGKDVAAG TFGPLPSDED VHGMERGVV DRVGPEVGGR LRAGRSRNDQ
 VATLFRMWVR DAVRDIALGT TELVDALSAQ AKAHAGAIMP GKTHFQAAQP VLLAHQLLAH
 AQPLLRLDIDR IRDLKRLAV SPYSGALAG SSLKLNPEAI AEELGFDSAA DNSIDATSSR
 DFASATAFVL AQLAXGYVPL G

> RXA02162 (1-663, translated) 221 residues

MSRLAEIIIA WCTPEFGYIT LSDSWSTGSS IMPQKKNPDV AELTRGKSGR LIGNLTGLLA
 TLKAQPLAYN RDLQEDKEPI VDSVAQLNLL LPAMTGLVST LTFNTERMRE LAPAGFTLAT
 DLAEWMVRQG VPFREAHEAS GACVRIAESR GVDLIDLTDE ELSGVDARLT PEVREVLITD
 GAVASRATRG GTAGVRVAEQ RARVDAASTA HAEWARAGVR R

> RXA02176 (1-1128, translated) 376 residues

MTDFPTLPSE FIPGDGRFGC GPSKVRPEQI QAIVDGSASV IGTSHRQPAV KNVVGSIREG
 LSDLFSLPEG YEIILSLGGA TAFWDAATFG LIEKKSGLHS FGEFSSKFAK ASKLAPWLDE
 PEIVTAETGD SPAPQAFEGA DVIAWAHNET STGAMVPVLR PEGSEGSLVA IDATSGAGGL
 PVDIKNSDVY YFSPQKCFAS DGGLWLAAMS PAALERIEKI NASDRFIPEF LNLQTAVDNS
 LKNQTYNTPA VATLLMLDNQ VKWMNSNGGL DGMVARTTAS SSALYNWAEA REEASPYVAD
 AAKRSLVVG TIDFDDSIDAA VIAKILRANG ILDTPEYRKL GRNQLRIGMF PAIDSTDVEK
 LTGAIDFILD GGFARK

> RXA02189 (1-738, translated) 246 residues

VDAADYHERH PSYLGTDASH GEFYWCPEML HEKDVRLGTT PAALSGKKIL EIGCGSAPCA
 RWLANDVPNA FVTAFDISSQ MLKYAGHDHN VHLVQADAMS LPYADSSFDV VFSVFGAIPF
 VEDSAALMKE IARVLKPGGR LIFSITHPMR WIFLDDPGPA GLTAITSYFD QRGYVEEDED
 TGALSYAEQH RTMGARINEL IDASLHLDHL IEPEWPDELE ENWGQWSPLR GKLFPGTAIF
 LATYRP

> RXA02193 (1-1578, translated) 526 residues

MSKTSNKSSA DSKNDAKAED IVNGENQIAT NESQSSDSAA VSERVVEPKT TVQKKFRIES

DLLGELQIPS HAYYGVHTLR AVDNFQISRT TINHVPDFIR GMVQVKKAAA LANRRLHTLP
 AQKAEAIWVA CDQILIEERC MDQFPIDVFQ GGAGTSLNMN TNEVVANLAL EFLGHEKGEY
 HILHPMDDVN MSQSTNDSYP TGFRLGIYAG LQTLIAEIDE LQVAFRHKGN EFVDIIKMGR
 TQLQDAVPMS LGEEFRAFAH NLAEEQTVLR EAANRLLEV N LGATAIGTGV NTPAGYRHQV
 VAALSEVTGL ELKSARDLIE ATSDTGAYVH AHSIAKRAAM KLSKICNDLR LLSSGPRAGL
 NEINLPPRQA GSSIMPAKVN PVIPEVNVQV CFKVFGNLDT VTMAAEAGQL QLNVMPEVIG
 ESLFQSLRIL GNAAKTLREK CVVGITANAD VCRAVDNSI GIITYLNPFL GHDIGDQIGK
 EAAETGRPVR ELILEKKLMD EKTLEAVLSK ENLMHPMFRG RLYLEN

> RXA02194 (1-843, translated) 281 residues
 MLKIAVPNKG SLSERAMEIL AEAGYAGRGD SKSLNVFDEA NNVEFFFLRP KDIAIYVAGG
 QLDLGITGRD LARDSQADVH EVLSLGFGSS TFRYAAPADE EWSIEKLDGK RIATSYPNLV
 RDDLAARGLS AEVLRLDGAV EVSIKLGVAI AIADVSTGR TLRQQGLAPF GEVLCTSEAV
 IVGRKDEKVT PEQQILLRRI QGILHAQNFL MLDYNVDRDN LDAATAVTPG LSGPTVSPLA
 RDNWVAVRAM VPRRSANAIM DKLAGLGAEA ILASEIRIAR I

> RXA02195 (1-270, translated) 90 residues
 MYRVKTFDSL YEELLNRAQT RPEGSGTVAA LDKGIHHLGK KVIEEAGEVW IAAEYETDEE
 LAGEISQLIY WTQVIMVARG LKPEDIYKNL

> RXA02197 (1-528, translated) 176 residues
 AERMRFSPFR QQRGRFLCIA DFIRPREQAV KDGQVDVMPF QLVTMGNPIA DFANELFAAN
 EYREYLEVHG IGVQLTEALA EYWHRSVRSE LKLNDGGSVA DFDPEDKTKF FDLDYRGARF
 SFGYGSCPD L EDRAKLVELL EPGRIGVELS EELQLHPEQS TDAFVLYHPE AKYFNV

> RXA02198 (1-2478, translated) 826 residues
 MSTSVTSPAH NNAHSSEFLD ALANHVLIGD GAMGTQLQGF DLDVEKDFLD LEGCNEILND
 TRPDVLRQIH RAYFEAGADL VETNTFGCNL PNLADYDIAD RCRELAYKGT AVAREVADEM
 QPGRNGMRFR VVGS LGPGTK LPSLGHPYA DLRGHYKEAA LGIIDGGGDA FLIETAQDLL
 QVKA AVHGVQ DAMAELDTFL PIICHVTVET TGTMLMGSEI GAALTALQPL GIDMIGLNCA
 TGPDEMSEHL RYLSKHADIP VSVMPNAGLP VLGKNGAEYP LEAEDLAQAL AGFVSEYGLS
 MVGCCCGTTP EHIRAVRDAV VGVPEQETST LTKIPAGPVE QASREVEKED SVASLYTSVP
 LSQETGISMI GERTNSNGSK AFREAMLSGD WEKCVDIKQ QTRDGAHMLD LCVDYVGRDG
 TADMATLAAL LATSSTLPIM IDSTEPEVIR TGLEHLGGRS IVNSVNFEDG DGPESTRYQRI
 MKLVKQHGAA VVALTIDEEG QARTAEHKVR IAKRLIDDIT GSYGLDIKDI VVDCLTFPIS
 TGQEETRDRG IETIEAIREL KKLYPEIHTT LGLSNISFGL NPAARQVLNS VFLNECIEAG
 LDSAIAHSSK ILPMNRIDDR QREVALDMVY DRRTEYDPL QEFMQLFEGV SAADAKDARA
 EQLAAMPLFE RLAQRIIDGD KNGLEDDLEA GMKEKSPIAI INEDLLNGMK TVGELFGSGQ
 MQLPFVQLQA ETMKTAVAYL EPFMEEEAEA TGSAQAEKGK KIVVATVKGD VHDIGKNLVD
 IILSNNGYDV VNLGIKQPLS AMLEAAEEHK ADVIGMSGLL VKSTVV

> RXA02208 (1-1002, translated) 334 residues
 LGVVDGVAPL NRTMEKIIAV HDDSLSQEVF GVTFFRPLGL AAGFDKNASM ADAWGAVGFG
 YAELGTVTAF PQPGNPTPRL FRLPADKAIL NRMGFNNLGA AEVAKNLRNR KSTDVIGINI
 GKTKVPAEH AVDDYRRSAS LLGDLADYLV VNVSSPNTPG LRDLQAVESL RPILA AVQES
 TTVPVLVKIA PDLSDDEDIDA VADLAVELKL AGIVATNTTI SREGLNTPSG EVEAMCAGGI
 SGAPVAARSL EVLKRLYARV GKEMVLISVG GISTPEQAW E RITSGATLLQ GYTPFIYGGP
 DWIRDIHLGI AKQLKAHGLR NIADAVGSEL EWKN

> RXA02229 (1-825, translated) 275 residues
 LTIPFAKGHA TENDFIIIPD EDARLDLTPE MVVTLCRRRA GIGADGILRV VKAADVEGST
 VDP SLWFMDY RNADGSLAEM CGNGVRLFAH WLYSRGLVDN TSFDIGTRAG VRHVDILQAD
 QHSAQVRVDM GIPDVTGLST CDINGQVFAG LGVDMGNPHL ACVVPGLSAS ALADMELRAP
 TFDQEFFPHG VNVEIVTELE DDAVSMRVWE RGVGETRSCG TGTVAACAA LADAGLGEGT
 AKVCVPRGEV EVQIFDDGST LTGPSAIIAL GEVQI

> RXA02234 (1-3198, translated) 1066 residues
 GSNPATIMTD PEMADHTYVE PIEPEYIDKI FAKEIEQGHP IDAVLATLGG QTALNAAIQL
 DRLGILEKYG VELIGADIDA IERGEDRQKF KDIVTTIGGE SARSRVCHNM EEVHETVAEL
 GLPVVVRPSF TMGGLGSGLA YNTEDLERIA GGGLAASPEA NVLIEESILG WKEFELELMR
 DTADNVVVIC SIENVDALGV HTGDSVTVAP ALTLT DREFQ KMRDQGI AII REVGVDTGGC

NIQFAINPVD GRIITIEMNP RVSRSSALAS KATGFPIAKM AAKLAIGYTL DEITNDITGE
 TPAAFEPTID YVVVKAPRFA FEKFGVGGDDT LTTTMSKSVGE VMSLGRNYIA ALNKALRSLE
 TKQQGFWTKP DEFFAGERAT DKAHVLEDLK RPTGRLYDV ELAMRLGASV EELYEASSID
 PWFLAELEAL VQFRQKLVDL PFLNEDLLRE AKFMGLSDLQ IAALRPEFAG EDGVRTLRSL
 LGIRPVFKTV DTCAAEFEAK TPYHYSAYEL DPAAESEVAP QTEREKVLIL GSGPNRIGQG
 IEFDYSCVHA ALELSRVGYE TVMVNCPNPET VSTDYDTADR LYFEPLTFED VMEVYHAEAQ
 SGTVAGVIVQ LGGQTPLGLA DRLKKAGVPV IGTSPEAIDM AEDRGEFGAL LNREQLPAPA
 FGTATSFEEA RTVADEISYP VLVRPSYVLG GRGMEIVYDE ASLEDYINRA TELSSDHPVL
 VDRFLDNAIE IDVDALCDGD EVYLAGVMEH IEEAGIHSGD SACALPPMTL GAQDIEKVRE
 ATKKLALGIG VQGLMNVQYA LKDDILYVIE ANPRASRTVP FVSKATGVNL AKAASRIAVG
 ATIKDLQDEG MIPTDYDGGG LPLDAPIAVK EAVLPFNRF RPDGKTLDTL LSPKMKSTGE
 VMGLANNFGA AYAKAEAGAF GALPTEGTVF VTVANRDKRT LILPIQLRAL MGYKILATEG
 TAGMLRRNGI ECEVVLKASD IREGVEGKSI VDRIREGEVD LILNTPAGSA GARHDGYDIR
 AAAVTVGVPL ITTVQGVTA VQGIEALREG VVSVRALQEL DHAVKA

> RXA02235 (1-834, translated) 278 residues

MTFGEKLLNA ASTRGRCLVG IDPHESLLTS WGLPVNVDGL AEFSRACVEA FADTVALVKP
 QVAFYERFGS AGFAILEETI QTLRERGCLV VSDAKRGDIG STMAGYASAW LDPASPLSSD
 AVTVSPYLG FSLDPVFELA EQHGRGVFVL AATSNPEARE LQDQQNADGV SISQQIVDQA
 AALNAPYMAQ GKAGNIGVVI GATLSKPPRL STLGGAILMP GVGAQGGTAS DVDEIAGDMA
 HLAFPNVRS ILATGPDIAE MKNSVAKNAA DFPGFPRS

> RXA02237 (1-570, translated) 190 residues

VSGDNQLGRL VILAGPSAVG KSTVVDRLRN DVPNLYFSVS MTTRAPRPGE VDGRDYFYVT
 AQEFQDKIDC GEMLEWADIIH GGLQSRGTPA GPVNARQNG RPLVVEVDLA GARNIASLIP
 DAETIFLAPP SWEVLVERLT GRGTESEDI ARRLETAREE LAAQSEFKHV IINDVDVTA
 KAIEDVLLGA

> RXA02239 (1-1266, translated) 422 residues

VPMTHVSSPS APRNVVVGVA GGIAAYKACH IVRAFKEAGD NVRVVPTEA LKFVGKATFE
 ALSGNPVSTT VFDAVDSVQH VKVGQEADLI VIAPATADLM ARVVAGLGDD LLAATLLVAT
 CPVVIAPAMH TEMWFNPATV ANVATLRQGR ITVIEPAHGR LTGKDTGPGR LPDPEQIVDL
 ANAVHAGARL PQDLAGKKVL ITAGGTHEHI DPVRFIGNSS SGRQGFALGE IAAQRGAHVS
 IVAGNAAELP TPAGAEIVPV VSTQDMFQAV QERAGQSDFI VMAAAVADFT PASQATSKLK
 KGSDSDDAL STISLVENPD ILATTVKRRE AGELDSNPVI VGFAAETGDE HTTALEYARK
 KLQKKGCDLL MCNEVGMGKV FGQKHNEGWI LDAHGGVVDV EHGSKIEVAA QIWDAAALAYR
 EV

> RXA02240 (1-1221, translated) 407 residues

VAQPTAVRLF TSESVTGHP DKICDAISDT ILDALLEKDP QSRVAVETVV TTGIVHVVG
 VRTSAYVEIP QLVRNKLIEI GFNSSEVGF DRTCGVSVSI GEQSQEIADG VDNSDEARTN
 GDVEEDDRAG AGDQGLMFGY ATNETEYMP LPIALAHRLS RRLTQVRKEG IVPHLRDPGK
 TQVTFAYDAQ DRPSHLDTVV ISTQHDPEVD RAWLETQLRE HVIDWVIKDA GIEDLATGEI
 TVLINPSGSF ILGGPMGDAG LTGRKIIVDY YGGMARHGGG AFSGKDPKSV DRSAAYAMRW
 VAKNIVAAGL ADRAEVQVAY AIGRAKPVGL YVETFDTNKE GLSDEQIQAA VLEVFDLRPA
 AIIRELDLLR PIYADTAAYG HFGRTDLPLP WEAIDRVDEL RAALKLA

> RXA02246 (1-984, translated) 328 residues

MDVAHALDLA HHVSDQVRGT TSPNPPVGAV ILDADGEVVG VGATAPPGGP HAEVVALAAA
 GVRANGGTAV VTLEPCNHYG RTGPCSKALL DAGIAHVIFYA NADFFPSAAG GGAFLAEAGV
 DTHFLDERIR ALEPWLVAIR LGRPHVTLKF ASTVDGFAGA TDGTSQWITG PDARAFVHED
 RSKRDAIIVG TGTALTDNPS LTARTDTGLY ENQPRRVVIG SREVPADSNL ARLGYEQYAG
 IPEALSALWD KGCRDILIEG GPTLAGAALR LGIVDQVQAY VAPALLGAGR SVINWPQETT
 MDQIMRFDIT SVRQLGSDVL IEMMRKEH

> RXA02247 (1-633, translated) 211 residues

MFTGIVEELG SVAGVEHLGD SIRMQISAST VLEGVHLGDS ISVNGVCLTV ASFGEGHFTA
 DLMQETLDRS SLGALSTGSK VNLERAMAAD GRLGGHIMQG HVDATSLIK RTSSENWDVL
 RFELPADLAR YVVEKGSIAL NGTSLTVSSL GDDWFEVSLI PTTLRDTTHG ELAVGDIVNI
 EVDVIAKYVE RMMTRGVAGN TPNDYTDFTF D

> RXA02248 (1-1266, translated) 422 residues

VSEHEQAHSQ LDSVEEAIAD IAAGKAVVVV DDEDRENEGD IIFAAELATP ELVAFMVRYS
SGYICAPLTA KDAADRLDLP MTAHNQDARG TAYTVTVTDAN TGTTGISATD RAHTLRLLAD
PEADRTDFTR PGHVPLRAR EGGVLVRAGH TEAAVDLARA AGLRPAGVIC EVVSEEDPTG
MARVPELRRF CDEHDLKLIS IEQLIEWRRK NEILVERQVE TVLPTDFGTF KAVGYRSIID
GTELVAIVAG DVASDGGENV LVRVHSECLT GDVFGSRRCD CGQQLHESLR LIQEAGRGVV
VYMRGHEGRG IGLLAKLRAY QLQDEGADTV DANLALGLPA DAREFGTSAQ ILYDLGVRSL
NLISNNPAKK VGLEHGHSI ASRTPIPVAV HEDNVRYLKT KRDRMGHDL P DVALWEQEHF
EN

> RXA02249 (1-477, translated) 159 residues

MAKEGLPAVE LPDASGLKVA VVTARWNAEI CDRHLKHAVD AGRAAGATVS EYRVIGALEL
PVVVQELART HDAVVALGCV VRGGTPHFDY VCDVTEGLT RIALDTSTPI GNGVLTNTTE
EQAVERSNGE GSVEDKGAEA MVAALDTALV LSQIRATEG

> RXA02250 (1-579, translated) 193 residues

VTTNAPDGAT NNINNAHSGA VGKPKVQLSD AEIQEYTAAF AGTTTTPWE LEVTTKFLKK
IAWVAVVIM AVHIFMGAVV DVDFTGAAVT FVDTLAFPAL GIIFSVLVFL GLTRPRVRAN
EDGVEVRNFI GTRFYPWVVI YGMSFPKGSS VARLELPDFE FVPMWAFQSR DGEDVVRVA
TFRDLENKYM PED

> RXA02262 (1-1146, translated) 382 residues

MTATYTTTETA INFLFLSEPD MIAAGVKDVA QCVDVMEETL VLLAQGDYKM AGLNSNSHGA
MITFPENPEF EGMPKDGPD RFMAMPAYLG GRFKNTGVKW YGSNAENKAS GLPRSIHTFV
LNDTVTGAPK AIMSANLLSA YRTGAVPGVG VKHLAVADAT TLAVVGPVGM AKTITEACIA
ERPGITTIKI KGRSERGINA FATWALEKFP EIEVVAVGSE EDVVKDADIV IAATTTDAAG
SSAFPYFKKE WLKPGALLLL PAAGRFDAY LLDDARLVVD YMGLYEAWAE EYGPQAYQLL
GIPGTHWYDL ALQGKLDLAK ISQIGDICS KLPGRTNDEE IILYSVGGMP VEDVAWATQV
YENALEKGVG TTLNLWESPA LA

> RXA02263 (1-360, translated) 120 residues

MKIAVIGLGS TGSMALWHLN NIPGVEAIGF EQFGISHGYG AFTGESRLFR MAYHEGSTYV
PLLKRARALW SSLSEISGRE LFHNFGVLST GKEDEAPFQR LVESVERYEL PHERLTAAQM

> RXA02272 (1-1245, translated) 415 residues

VRITNAQVKN YAEVLDTIE GEKISSITPS SIRSEEDHRA DDYDAAGRLV APQFAEAHII
LDYANTAGIP RENSSGTLFE AIEIWADRKT QGFHIKEDIK AKALQAARRA AEHGVGFIRT
HVDVTDPTFA GFEAIAELRD EVREWCIDIQI VAFPPQNGIYA YEGGQKLISD AMSAGADVVG
GIPHLEPTRD DGVESVKWLF DLAEKHSAPI DIHTDEIDDP HSRFVEVLAA EAAKRDMAQ
TVVSHSVAMA YYSPGYMARL LPKLAASKVR FAVCPNENLH LQGLGFQGPV PRGVAPVKQL
TEWGIPVSFC QDSLNDPFYP MGDGDLRLIL DSGLHVSHML TASHLKNALS FITTNPAGNL
GLDNYDIAEN SPANLLVLDA SSEKEAVQRK ASVLLSIHRG KKVLSREPEQ VDWNI

> RXA02281 (1-1068, translated) 356 residues

VQKDSVVRME ATTIDDAIAK LIDIYDTSTK LAKETLNNED YAAYADVVP KLTVDVLEWK
PIDRTEPFY VDRAGRYSAT LSKPRVIERY LREQLERLTS NYPCKIYVSE SDIRIPPEYI
RGAPSATEAR RAGDVADIIP RPTLDEVHDA IIDGDWHAFN GPPLPLFHFG PQRFDIACAR
IEHYTGINVE HVQKYILFTN YAMHTTEFVH FAMSELTSED SRYVGLSLPN GQVIDRETAT
SLGTETDLT SRFQMPRYDL ITEAGDGITI INIGVGPSNA KTITDCLAVL RPEAWVMIGH
CAGMDARMRI GDLILGNAYQ REDHILNTRI PLGNPIPAIP EIQALESASV DEIYGS

> RXA02284 (1-3024, translated) 1008 residues

MTSMNLPIEL ATLSDAQVDK VRSWLEYSKK ESVPNADAKR LAAVLQDPNG LEFTVGFVDR
VVRTEDREAA AHALYELGKI APSTMSFLDR AQIQAGSLVG RALPQVVVPA ARARIRQMVG
HMIVDARDKQ FAKAVAEIQS DGHRLNINLL GEAVLGRKEA AKHLDDTVRL LRRPDVEYVX
XXXSSVASQI SMWGFEDTVN YVVEQLTPLY IEPARAPKGT KFINLDMEEY RDLRLTMEVF
KRLLSNPELH ELEAGIVLQA YLPDALGAIQ DLAQFGRERV NTGGAGVKVR LVKGANLPME
HVHAQITGWP VATEPSKQAT DANYKRVLYW TMRKENMEGL RLGAVAGHNL DIAFAHLLSV
ERGVADRVEF EMLQGMASDQ ARAVSVDVGE LLLYVPAVRP QEFDAISYL VRRLEENAAS
ENFMSAIFDL DADNPSFKRE ESRFRASISD LATLIDVPAP GPNHTQDRSK ETLLDAPLVP
FINEPDTPA LIQNQQWATK AVATAAEPGW LEKQTKPEVL EEGDVVKLIN DVRDAAEAWA

ARPAPERAEI LYKTAEILRV RRGHLISVTA AEVGKAVEQT DPEISEAIDF ARYYAHLALE
 LDDVDNAEFT PDRVVVVTPP WNFPIAIPAG STFAALAAGA GVIHKPSKPS QHCSAAVVEA
 LWEAGVPREV LHCIYPANRD VGCALISHEH VDRVILTGSS ETAAMFSSWR PELTINGETS
 GKNAIVVTPS ADRDLAVADL VKSAFGHAGQ KCSAASLGIL VGSVYESERF RKQLVDAASS
 LIVDWPTNPS ATVGPLTELP SDKLHHALT LEEGESWLLK PRQLDDTGRL WSPGIKEGVK
 PGTFHFLTEV FGPVLGLMKA TDLNEAIEFQ NGNDFGLTGG LQSLDADEV R TWLDHVDVGN
 AYVNRGITGA IVQRQSFGGW KKSSVGLGSK AGGPNYVMLM GTWADAPSHH APRETNPPLIS
 KLDLPGEELE WLEKANASDE TAWNTEFGSP RDPSGLDVEA NIFRYRPA

> RXA02299 (1-408, translated) 136 residues
 MLRTILGSKI HRATVTQADL DYVGSVTIDA DLVHAAGLIE GEKVAIVDIT NGARLETYVI
 VGDAGTGNIC INGAAHLIN PGDLVIIMSY LQATDAEAKA YEPKIVHVDA DNRIVALGND
 LAEALPGSGL LTRSRI

> RXA02311 (1-690, translated) 230 residues
 VAKADLDKDP FDVASMFDDV GKNYDLTNTV LSFGQDRVWR KRTRQRLDLK PGEKVLDLAA
 GTAVSTVELA KSGAFCVACD FSQGMLAAGK DRDVSQVVG D GMQLPFADNS FDAVTISYGL
 RNIHDFRAGL KEMARVTKPG GRLTVAEFST PVIPVFGTVY KEYLMRLLPQ AARAVSSNPE
 AYIYLADSIR AWPSQAEAR EINQNGWSDC GWQNLTFGIV ALHSAIKPEN

> RXA02315 (1-1629, translated) 543 residues
 MSSTPAQDLA RAVIDSLAPH VTDVVLCPGS RNSPLSLELL ARQDLRVHVR IDERSASFLA
 LSLARTQARP VAVVMTSGTA VANCLPAVAE AHAHIPLIV LSADRPALHV GTGASQTINQ
 TGIFGDLAPT VGITELDQVA QIAESLAQGA SQIPRHFNLA LDVPLVAPEL PELHGEAVGA
 SWTHRWINHG EVTVDLGEHT LVIAGDEAWE VEGLEDVPTI AEPTAPKPYN PVHPLAAEIL
 LKEQVSAEGY VVNTRPDHVI VVGHPTLHRG VLKLSMDPGI KLTVLSRTDI ITDPGRHADQ
 VGSTVKVTGT QEQWLKICS AASELAADGV RDVLNDQEFQ FTGLHVAAAV ADTLGTGDTL
 FAAASNSIRD LSLVGMPFDG VDTFSPRGVA GIDGSVAQAI GTSLAVQSRH PDEIRAPRTV
 ALLGDLNFLH DIGLLIGPD EPRPENLTIV VSNDNGGGIF ELLETGADGL RPNFERAFGT
 PHDASIADLC AGYGIEHQV DNLQDLIIAL VDTTEVSGFT IIEASTVRDT RRAQQQALMD
 TVH

> RXA02318 (1-279, translated) 93 residues
 MNSLFDVSPH WSSANAKLTA HFNTGKFSTG MKFVNLIADS AEEANHHPDI LLTYGFVEIT
 LTSHDVGEIT DRDVALAKVI DAHAKTLAIS AEA

> RXA02319 (1-957, translated) 319 residues
 MSNYSTDNPF DPTQWATVPG FEEFTDITYH RHVGTTRADG IVRIAFDRPE VRNAFRPHTV
 DELYQALDHA RRTPDVGTIL LTGNGPSEKD GGWAFCSGGD QRIRGRSGYQ YATEHARDDA
 TADVFTVDIA RTKVEGGRLH ILEVQRLIRT MPKVVIHAVN GWAAGGGHSL HVVCDLTIAS
 RQEARFKQTD ADVGSFDAGY GSAYLAKMVG QKNAREIFFL GRITYDAERMQ QMGAVNIVAD
 HGDLEKEAIQ AAREINTKSP TGQRMLKFAF NLTDGGLMGQ QVFAGEATRL AYMTDEAVEG
 KEAFLEKREP NWNEFPYYY

> RXA02345 (1-810, translated) 270 residues
 FAAIESVEDA VGFFEAVDQ VCLKARRGGY DGKGVWFPAD VAEQLQSLVAE LLDGGTPLMA
 EKKVALNREL SAMVARTPSG ETKAWPVVES VQKNGVCAEA IAPAPELSAE LQESTRGLAQ
 KIATELGVTG VLAVELFETL DQNGQPEIFV NELAMRSHNT GHWTQDGCVT SQFEQHLRAV
 LDYPLGATDT LADYTVMANV LGADTDPEMP MATRMVEVGR KYPDAKIHLY KGKHRPGRKI
 GHVNMVGS DL EKTRAEALAC AYFLVNARWD

> RXA02346 (1-123, translated) 41 residues
 VGPLVGLIMG SDSWDTVAP AAEVLAEFGI PFEVGVVSAH R

> RXA02350 (1-210, translated) 70 residues
 LDSLLSIVQM PGGVPVATVS IGGAKNAGLL AVRILGAGDP SLVTKMADYQ
 ENMAKEVEAK DEALKKRLLG

> RXA02373 (1-915, translated) 305 residues
 MSVVGTLFF GSPEEERDKL MQSLMDQKNK LSKSEGIPLV TLNDGKTIPQ LGFGVFKVDP
 DEAEVVTAE LEVGYRHIDT AAIYGNEEGV GRAIAKSGIP REELFITTKL WNDRLHDVEA

AFEESLQKLG LDYVDLYLVH WPAPKNDNYV AAWKGLEKLG DRARSIGVCN FLPEHLEKLL
 AEATTVPAIN QIELHPALQQ RDAVEASLAA GITVESWGPL GQGRFDLGAE EPIAAAAKNH
 GKTPAQVVIR WHLQNGFVVF PKTVTKSRMV ENIDVDFEL SDEEMAAITA LERNDRGGSH
 PNDLN

> RXA02375 (1-1227, translated) 409 residues

MAPVTGLPVT PYSQEASIGA SFPVDPDTK DSAAYGHESG MRERISNAKR VVVKIGSSSL
 TNDEDGHTVD PNRINTIVNA LQARMEAGSD LIVVSSGAVA AGMAPLGLST RPTELAVKQA
 AAAGVQVHLM HQWGRSFARY GRPIGQVLLT AADAGKRDRA RNAQRTIDKL RILGAVPIVN
 ENDTVATTGV NFGDNDRLLA IVAHLVSADA LVLLSDVDGL FDKNPTDPTA KFISEVRDGN
 DLKGVIAAGDG GKVGTGGMAS KVSARLASR SGVPVLLTSA ANIGPALEDA QVGTVFHPPK
 NRLSAWKFWA LYAADTAGKI RLDDGAVEAV TSGGKSLAV GITEIIGDFQ QGEIVEILGP
 AGQIIGRGEV SYDSDLQSM VGMQTQDLPD GMQRPVVHAD YLSNYASRA

> RXA02378 (1-609, translated) 203 residues

MSSTTLTDDQ IRDNERTVL AKATAAKNIV PDI AVLGTGP KNAILRAAAD ELVARSAEII
 EANASDIEAG RANGMEESMI DRLALDESRI EGIAGGLRQV AGLTDPVGEV LRGHVMENGI
 QMKQVRVPLG VMGMVYEARP NVTVDAGFLA LKSGNVALLR GSSTAVHSNT KLVEILQDVL
 ERFELPRETV QLLLAKPADP SKI

> RXA02380 (1-654, translated) 218 residues

MTTIVKRRAR IGIMGGTFDP IHNGHLVAGS EVADRFDL DL VVYVPTGQPW QKANKKVSPA
 EDRYLMTVIA TASNPRFMVS RVDIDRGGDT YTIDTLQDLS KQYPDAQLYF ITGADALAQI
 VTWRDWEKTF ELAHFVGVT R PGYELDGNII PEMHQDRVSL VDIPAMAISS TDCRERSSEE
 RPVWYLVDPG VVQYIAKRQL YRPEGSDKDM DPKGQNA

> RXA02382 (1-600, translated) 200 residues

PTIETGTGNC HFYIDAEAKL DQAIAMVING KTRRCSVCNA TETALLDAAL SDSDKLAVVQ
 ALQEAGVTIH GRVAELEAFD ATDVVEATET DWDSEYLSFD IAVAVVDGVD GALAHIAKYS
 TKHTEAIATQ NIETAQRFD RVDAAVAMIN ASTAYTDGEQ YGMGAIEIGIS TQKLHARGPM
 ALPELTSTKW ILQGTGQIRP

> RXA02400 (1-570, translated) 190 residues

MSISRTVFGI AATAALSAAL VACSPPHQD SPVQRTNEIL TTSQNPTSAS STSTSSATTT
 SSAPVEEDVE IVVSPAALVD GEQVTFEISG LDPEGGYAA ICDSVANPGN PVPSCGTGEMA
 DFTSQAWLSN SQPGATVEIA EDGTATVELE ATATGTGLDC TTQACVAKVF GDHTEGFRDV
 AEPVPTFAAA

> RXA02405 (1-771, translated) 257 residues

VNTNPSEFSS NRSTALLTDK YELTMLQAAL ADGSAERPST FEVFSRRLPN ERRYGVVAGT
 ARVLKAIRDF VFTEEQLADL DFLDDRTLEY LRNYRFTGQV DGYREGEIYF PQSPLLTVRG
 TFAECVILET VILSIMNADS AVASAAARMV TAADGRPIIE MGSRRTHEYS AVTASRAAYL
 AGFSTTSNLE AARYGIPAS GTSAHAWTLL HINDDGTPNE AAAFKAQVES LGVDTTLLVD
 TYDITQGVAT AIEVAGP

> RXA02432 (1-975, translated) 325 residues

MSKQHSTPLN NDEEHTSAPQ KVAVITTGGT IACTSDANGH LLPTVSGADL LAPIAPRFNG
 AQIAFEIHEI NRLDSSSMTF EDLDSIIATV HKVLEDPDVV GVVVTHGTDS MEESAIIVDT
 FLDDPRPVIF TGAQKPFDPH EADGPNNLFE ACLIASDPSA RGIGALIVFG HAVIPARGCV
 KWHTSDELAF ATNGPEEPER PDALPVAKLA DVSVEIIPAY PGATGAMVEA AIAAGAQLV
 VEAMGSGNVG SRMGDALGKA LDAGIPVMS TRVPRGEVSG VYGGAGGGAT LAAKGAVGSR
 YFRAGQARIL LAIAIATGAH PVTLY

> RXA02458 (1-1290, translated) 430 residues

MVFVSDSSIS LPIWDAPRAR GPIVSDLAIP GSKSITNRAL ILAALASTPS TIIDVLRSD
 TDLMTDGLRS LGITITEAV DRYRVEPGQL SAGSVECGLA GTVMRFLPPV AAFADGPVHF
 DGDPQARVRP MTSILDALRS LGVEVDNNNL PFTVNAGEVP EGGVVEIDAS GSSQFVSGLL
 LSAPRFKNGV TVKHVGGRLP SMPHIEMTV MLRSAGIEIE ESENQWVHP GEILGRTWRI
 EPDLNATPF LAAAATVGGT IKINHWPIKT TQPGDAIRSI LERMGCVEL VAQGEYDLS
 VTGPVALKGI EIDMSDIGEL TPTVAALAL ASTESRLTGI AHLRGHETDR LAALTAEINK
 LGGKCTELKD GLLEIPASLH GGVVHSYADH RMATAGAIIG LAVDGVQVED IKTSKTFPG

FENVWEEMVG

> RXA02469 (1-1431, translated) 477 residues

MRFLNNSNPP YELTYSDFVM VPSRSDVGSR MSVDLRTNDG TGTTIPLVVA NMTAVAGRRM
 AETIARRGGM AILPQDVPAD IAAETIANVK KADLVFDTPI TVKPHHTVGY ARNLIHKRAH
 GAAIVLEGDQ PVGIVTDKDL EGADNFTQVG TLMSTSLTL PEDISPEDAF GILHEHSRKL
 APVVAADGSL RGILTRTGAL RATMYKPAID ANGRLRVGAA IGINGDIEGR TKTLLDAGAD
 VLVVDTAHGH QSTMISALKR IRALDVNVPI VAGNVVTADG VRDLVEAGAN IIKVGVGPGA
 MCTTRMQTGV GRPQFSVLE CAAEARKLGA HVWADGGVRD PRDVALALAA GASNMVGSW
 FSGTYESPGD LRFESDGRMY KESFGMASRR AVESRNQKVE AFEKARRAMF EEGISTARIY
 IDKRHHGGVED LVDQIISGVR SSFTYAGADS IETFFERATV GVQSTEGYAE GKPRASR

> RXA02479 (1-390, translated) 130 residues

VTELIQNESQ EIAELEAGQQ VALREGYLPV VITVSGKDRP GVTAFFRVL SANQVQVLDV
 EQSMFRGFLN LAAFVGIAPE RVETVTTGLT DTLKVHGQSV VVELQETVQS SRPRSSHVVV
 VLGDVPDLDL

> RXA02497 (1-927, translated) 309 residues

VRGLVLDVGS NTVHLVAVDA RPPGGHPTMS NWRTPLRLVE LLDDSGAISE KGINKLTSVA
 GEAADLAKTL GCAELMPFAT SAVRSATNSE AVLHDVEKET GVRLSILSGE DEARQTFLLAV
 RRWYGSWAGR ITNLDIGGGS LELSSGTDES PDLAFSLDLG AGRLTHNWFD TDPARKKIN
 LLRDYIDAEI AEPARQMRITL GPARLAVGTS KTFRTLRLT GAAPSSAGPH VTRTLTAPGL
 RQLIAFISRM TAADRAELEG ISSDRSHQIV AGALVAEAAM RALDIDKVEI CPWALREGVI
 LTRIDKGLE

> RXA02499 (1-810, translated) 270 residues

MTTIAVIGGG QIGREALVSGI IANMNPQNI RVTNRSEERG QELDRYIGIL NMTDNSQAAD
 EADVVFCLVK PKFIVEVLSE ITGTLDNNSA QSVVVSMAAG ISIAAMEESA SAGLPVVRVM
 PNTPLMVKG MSTVTGGRYV DAEQLEQVKD LLSTVGDVLE VAESDIDAVT AMSSSPAYL
 FLVTEALIEA GVNGLGLPRAT AKKLAVASFE GAATMMKETG KEPSELRAGV SSPAGTTVAA
 IRELEESGIR GAFYRAAQAC ADRSEELGKR

> RXA02501 (1-1065, translated) 355 residues

MSSEGRNHNW DYAAIGTPED FLASWSASRG NLRRFFEDHA AAPINDAAQR QAGEAAATQA
 VAAIYGMELN EFNAGVDAVA GAIESAGAIH VSIPDPDVPQ DVGAAFFDV DNTLIQSSSL
 IVFAQGLFRK KFFTKEILP VVWKQVKFKL TGSENADDVS RGRQALEFI KGRPVQELVD
 LCEEIVDQRM ADKMWPQTKQ LADMHIAAGH QVWLVSATPV QLAQILAQRL FTGAIGTVA
 EAKDGVFTGR LVGDILHGPB KRHAVALAS IEQLDLTRCT AYSDSINDLP MLSMVGTAVA
 VNPDSKLRKE AETRQWDVRD FRSIRKATRE YGIPALVTAA FSVAGWSLRR RWRKQ

> RXA02503 (1-435, translated) 145 residues

MTLKIGTRGS KLATTQAGTI RDQLKHYGRD AELHIVTTPG DVNMSPVERI GVGVFQALR
 DVLHSGECDV AVHSMKDLPT ATDPRFHLV PTRADXRXP YRXXRXXFX SXQXXRWEL
 SAPRRISQLK AIRPDLEILP LARKH

> RXA02504 (1-438, translated) 146 residues

MLVMLAYAGL TRVGMQDRAT EVFDADIIMP APAQGALAIE CRADDTETVR ALNMLMHADT
 FVSAVAERTV LNRLEAGCTA PVAHAATLDG YSGDTMTLTA GVALDGSQ LVFSAEGDGA
 RPEELGELVA QQLIDAGAN LLGDRS

> RXA02516 (1-1263, translated) 421 residues

MSDFLNADGS LNVDKVREEF PILKRTVRDG KPLAYLDGA TSQRPERVWR AEEHFVLHTN
 APVHRGAYQL AEEATDAYEG AREKIAAFVG AEQHEIAFTK NATEALNLVA YTLGDDRSCK
 YRVQAGDTVV ITELEHHANL VPWQELCRRT GATLKWYKVT EDGRIDLDSL ELDETQVVA
 FTHQSNVTGA VADVPELVRR AKAVGALTVL DACQSVPHMP VNFHELDVDF SAFSGHKMLG
 PAGVGVVYAK SPILDELPPF LTGGSMIEVV TMEGSTYAAA PQRFEGTQM TSQVVGLGAA
 VDMLNEIGME AIAAHEHALT AYALEKLTAI KGLTIAGPLT AEQRGGAISF GVEGIHPHDL
 GQVLDDQGVN IRVGHHCAMP VHRSMNVQST ARASFYLYNT FEEIDRLAAA IEKAKQFFGV
 E

> RXA02517 (1-447, translated) 149 residues

MNLEQMYQEV ILDHYKNPQH KGLRDPFDAE VHHVNPSCGD ELTLRVKLSE DGSTVEDVSY
EAVGCSISQA STSVMAEEIV GQPVDKALEK LTEFEKMIVS RGQFVGDEDL IGDGVAFSGV
AKYPARVKCA LLGWKAFQAA TADAVAHAH

> RXA02532 (1-1047, translated) 349 residues

MNPPITLSST YVHDSEKAYG RDGNDGWGAF EAAMGTLDDG FAVSYSSGLA AATSIADLVP
TGGTVVLPKA AYYGVTNIFA RMEARGRLKV RTVDADNTEE VIAAAQGADV VVVESIANPT
MVVADIPAIV DGVRGLGVLT VVDATFATPL RQRPLELGAD IVLYSATKLI GGHSDDLGLV
AVCKSEHHAQ FLATHRHDHG SVPGGLEAFL ALRGLYSLAV RLDRAESNAA ELSRRLNAHP
SVTRVNYPGL PDDPQHEKAV RVLPSGCGNM LSFELDATPE RTDEILESLS LLTHATSWGG
VETAIERRTR RDAEVVAEVP MTLCRVSVGI EDVEDLWEDL NASIDKVLG

> RXA02536 (1-756, translated) 252 residues

MDNFALLRDA AEKAAEQGAR VLVFPEATSQ SFGTGRLDLQ AEELDGEFST AVRKLADELD
VVIVAGMFTP ADTVQRGEKT ISRVNNTVLI SGAGLHQGYN KIHTYDAFGY RESDTVKPGD
ELVVFEVDDI KFGVATCYDI RFPEQFKDLA RNGAQIIVVP TSWQDGPGL EQWEVLPRAR
ALDSTCWIVA CGQARLPEEL RDERKGPTGI GHSMVTNPHG EVIASAGYEP EMLIADIDVS
GLAKIREALP VL

> RXA02550 (1-1311, translated) 437 residues

VTTDKRKTSK TTDANKAVG ADQAARPTRR TTRRIFDQSE KMKDVLVEIR GPVAAEAERM
ELDGHNILKL NTGNPAVFGF DAPDVIMRDM IANLPTSQGY STSKGIIPAR RAVVTRYEVV
PGFPHFDVDD VFLGNGVSEL ITMTTQALLN DGDEVLPAP DYPLWTAATS LAGGKPVHVL
CDEEDDWNPS IEDIKSKISE KTKAIVVINP NNPTGAVYPR RVLEQIVEIA REHDLILAD
EIYDRILYDD AEHISLATLA PDLICITYNG LSKAYRVAGY RAGWMVLTGP KQYARGFIEG
LELLAGTRLC PNVPQAHAHQ VALGGRQSIY DLTGEHGRL EQRNMAWTKL NEIPGVSCVK
PMGALYAFPK LDPNVYEIHD DTQLMLDLLR AEKILMVQGT GFNWPBHDHF RVVTLPWASQ
LENAIERLGN FLSTYKQ

> RXA02559 (1-903, translated) 301 residues

MIPVLIDCDT GIDDALALIY LVALHKRGEI QLFGATTTAG NVDVKQTAIN TRWVLDQCGL
ADIPVLAGQP EPKHVPLVTT PETHGDHGLG YINPGHVEIP EGDWKQLWKE HLSNPETKLI
VTGPATNLAE FGPVENVTLM GGTLYLPGNT TPTAEWNTWV DPHGAKEAFA AAQKPITVCS
LGVTEQFTLN PDILSTLINT LGSQPIAEHL PEMLRFYFEF HEVQGEGLA QIHDLITCMI
ALDKIPFSGR EVTVDVEADS PLMRGTTVAD IRGHWGKPAN AFLVETADIE AAHAELLRAV
E

> RXA02622 (1-1560, translated) 520 residues

MSDDRKAIKR ALISVYDKTG LEDLAQALHR ENVEIVSTGS TAAKIAELGI PVTPEELTG
FPECLEGRVK TLHPKVHAGI LADTRKEDHL RQLKELEVAP FQLVVVNLYP FAETVASGAD
FDACVEQIDI GGPSMVRAAA KNHPSVAVVV SPNRYEDVQE ALKTGGFSRA ERTKLAAEF
RHTATYDVTV ATWMSEQLAA EDSETEFPGW IGTNTLSRS LRYGENPHQS AALYVGNTG
LAQAKQFHGK EMSYNNYTDS DAAWRAAWDH ERPCVAIIKH ANPCGIAVSD ESIAAAHREA
HACDSVSAFG GVIASNREVS VEMANQVAEI FTEVIIAPSY EEGAVEILSQ KKNIRILQAE
APVRKGFESR EISGGLLVQE RDLIHAEGDN SANWTLAAGS AVSPEVLKDL EFAWTAVRSV
KSNAILLAKN GATVGVGMGQ VNRVDSARLA VDRAGAERAT GSVAASDAFF PFADGFEVLA
EAGITAVVQP GGSIRDNEVI EAANKAGVTM YLTGARHFAH

> RXA02623 (1-591, translated) 197 residues

VNSDSTTIV VLSAGTGTL QSLIEAQGT SIVGVVSDVE CPALSRAADA GIDTAVVPLG
KDRAQWNHEL ADAVAVSDPD LVVSAGFMKI LGEGFLSRFP SRIINTHPAL LPSFPGAHAV
RDALAYGVKV SGSTVHLVDA GVDTGPIIAQ RAVPVEVNDD ESSLHERIKQ VERKLIVEVL
NSVEFSRQGG VQLNWRG

> RXA02629 (1-585, translated) 195 residues

MSKDPLGSLT DVVDTRVPLP DVEPDPEFLK ATEKEFHMAS QKRALVVLVG DHVAEADGTG
RLVTELLLES GFNVDAVSVS KSKKSQIRQA IETAVVGGAD LVLTIGGVGV GPRDKTPEAT
SAVLDQDVP IAQALRSSGL ACGAVDASVS RGVAGVSGST VVVNLAESRS AIRDGMATLT
PLVDFVVDQL RTSV

> RXA02645 (1-1830, translated) 610 residues

MLKDLTGLRE LVLREMCHSI SHLSSPTGSI FTSLVAMLT SFSVWAPLP HDVHLILNGE
 TLPMHKTEGS WWRAEIAPKA GDRYGFSLFD GSSWSKTLPD PRSTSQPDGV HGLSEVSDDS
 YLWGDQQWTG RILPGSVLYE LHVGTFS EDG TFEGVVDKLP YLRDLGVTAI ELLPVQPF GG
 NRNWGYDGV L WHAVHAGYGG PAGLKKLIDA SHQAGIAVYL DVVYNHFGPD GNYNGQFGPY
 TSGGSTGWGD VVNINGHDS EVRNYILDAA RQWFEDFHVD GLRLDAVHSL DDRGAYSLLA
 QLTMAEDVS AQTGIPRS LI AESELNDPKF VTSREAGGFG LDAQWVDDIH HALHALVSGE
 RNGYYSDFGS VDTLAKTLRE VFEHTGNYST YRGRNHGRPV HPDITPASRF VTYTTTHDQT
 GNRAIGDRPS TTLTPQQVL KAAIIYSSPY TPMLFMGEEF GATTPFAFFC SHTDPELNRL
 TSEGRKREFA RLGWNADDIP SPELESTFTS SKLDWEFTAE QRRINDAYKQ LLHLRHTLGF
 SQPNLLTLEV EHGENWLSMA NGRGRILANF SDDTITVPLG GELIYSFTSP TVTDTSTTLQ
 PWGFAILTRN

> RXA02646 (1-1269, translated) 423 residues

MASGAELIRA ADIQT AQARI SSVIAPTPLQ YCPRLSEETG AEIYLKREDL QDVR SYKIRG
 ALNSGAQLTQ EQRDAGIVAA SAGNHAQGVA YVCKSLGVQG RIYVPVQTPK QKRDRIMVHG
 GEFVSLVVTG NNFDEASAAA HEDAERTGAT LIEPFDARNT VIGQGTVAE ILSQLTSMGK
 SADHVMVPVG GGGLLAGVVS YMADMAPRTA IVGIEPAGAA SMQAALHNGG PITLETVDPF
 VDGA AVKRVG DLNYTIVEKN QGRVHMSAT EGAVCTEMLD LYQNEGIIAE PAGALSIAGL
 KEMSFAARSV VVCIISGGNN DVLRYAEIAE RSLVRRLKH YFLVNFQKP GQLRHFLDI
 LGPDDITLF EYLKRNNRET GTALVGIHLS EASGLDSLLE RMEESAIDSR RLEPGTPEYE
 YLT

> RXA02648 (1-525, translated) 175 residues

DAPDLAEAWD QINPEPSVKD YLDWIGTRID AINSAVKGLP KEQTRLHICW GSWHGHVHTD
 IPFGDIIGE LRAEVGGFSF EGASPRHAHE WRVWEENKLP EGSVIYPGVV SHSINAVEHP
 RLVADRIVQF AKLVGPENVI ASTDCGLGGR LHSQIAWAKL ESLVEGARIA SKELF

> RXA02653 (1-1998, translated) 666 residues

MIPKPDVTDL YLEDLLNEGS EKIRSAKDLS ELRTVLKEVS SQIQUERAGKK DEEWGMGATW
 RELYPSIVER ASYEGRDSLI GFDHLAREME RLAFGPPSES FEYLQELVKS GVVDITHLHR
 GREPLTDLVR ELEITVVIDA VLPPPGVVPG TLVHNLVKEG YARMRPGTRG LDVAADGT VQ
 GQRHLAAVGR MTEDVVLGND TSLRSLHDII PKWARRVIRD ASTYPDRVHG TPPLPARLEP
 WAEKLTS DPA TCRHLIEEFG SPVNVLHSGS MPRNINELVD AGIQMGVDTR IFFARKANKG
 LTFVDAVKDT GHGVDVASER ELSQVLNRGV PGERIILSAA IKPDRLLALA IENGVIISVD
 SRDELDRISA LVGDRVARVA PRVAPDPAVL PPTRFGERAA DWGNRLTEVI PGVDIVGLHV
 HLHG YAAKDR ALALQECCQL VDSLRECGHS PQFIDLGGGV PMSYIESEED WIRYQSAKSA
 TSAGYAESFT WKDDPLSNTY PFYQTPVRGN WLKDVLSKGV AQMLIDRGLR LHIEPGRSL
 DGCGVT LAEV AFVKTRSDGL PLVGLAMNRT QCRTTSDDFL IDPLHITDGD VGEEIEAYLV
 GAYCIEDELI LRRRIRFPRG VKPGDIIGIP NTAGYFMHIL ESASHQIPLA KNVVWPEGQL
 DDIDAD

> RXA02658 (1-684, translated) 228 residues

MSQNRIRTH VGSLPRTEPEL LDANIKRSNG EIGEEFFQI LQSSVDDVIK RQVDLGIDIL
 NEGEYGHVTS GAVDFGAWN YSFTRLGGLT MTDTDRWASQ EAVRSTPGNI ELTSFSDRRD
 RALFSEAYED PVSGIFTGRA SVGNPEFTGP ITYIQEETQ TDVDLLKKGM NAAGATDGFV
 AALSPGSAAR LTNKFYDTDE EVVAACADAL SQEYKIITDA GLTVQLDA

> RXA02687 (1-945, translated) 315 residues

MSDAPT VVAY LGPAGTFTEE ALYKFADAGV FGDGEIEQLP AKSPQEAVDA VRHGTAQFAV
 VAIENFVDGP VTPTFDALDQ GSNVQIIAEE ELDIAFSIMV RPGTSLADV K TLATHPVGYQ
 QVKNWMATTI PDAM YLSASS NGAG AQMVAE GTADAAAAPS RAAELFGLER LVDDVADV RG
 ARTRFVAVQA QAAVSEPTGH DRTSVIFSLP NVPGSLVRAL NEFAIRGV DL TRIESRPTRK
 VFGTYRFHLD ISGHIRDIPV AEALRALHLQ AEELVFVGSW PSNRAEDSTP QTDQLAKLHK
 ADEWVRAASE GRKLN

> RXA02717 (1-882, translated) 294 residues

MPPRDAAEE RLYRAAEVFH DLGASFVSVT YGAGGSTRETS TSRIARRLAK QPLTTLVHLT
 LVNHTREEMK AILREYLELG LTNLLALRGD PPGDPLGDWV STDGGLNYAS ELIDLIKSTP
 EFREFDLGIA SFPEGHFRAK TLEEDTKYTL AKLRGGAEYS ITQMFFDVED YLRLRDLVA
 ADPIHGAKPI IPGIMPITSL RSVRRQVELS GAQLPSQLEE SLVRAANGNE EANKDEIRKV
 GIEYSTNMAE RLIAEGAEDL HFMTLNFTRA TQEVLYNLGM APAWGAEHQ DAVR

> RXA02754 (1-486, translated) 162 residues
PTNTKIVVSS DLDEFIAIAGL RGEFVDVFGV GTSVVTGSGA PTAGLVYKIG EVAGHPVAKR
SRNKESYGGG KKAVRTHRKS GTAIEEIVYP FNAEAPDTGK LDTLSLTIPL MRDGEIVPGL
PTLEDSRAYL AKQLVSLPWE GLALSRDEPV LHTRFVGFPF AA

> RXA02758 (1-435, translated) 145 residues
MGYQTAVVSG GFIQVLEGLA EELELDYVRA NTLEIVDGKL TGNVTGKIVD RAAKAEFLRE
FAADSGLKMY QTVAVGDGAN DIDMLSAAGL GVAFNAKPAL KEIADTSVNH PFLDEVLHIM
GISRDEIDLA DQEDGTFHRV PLTNA

> RXA02759 (1-111, translated) 37 residues
VLRLYPTLIT GEVIEMLAAH AGKEAKVAAV TERAMRG

> RXA02768 (1-603, translated) 201 residues
LSFDPNTQGF STASIHAGYE PDDYYGSINT PIYASTTFAQ NAPNELRKGY EYTRVGNPTI
VALEQTVAAL EGAKYGRAFS SGMAATDILF RIILKPGDHI VLGNDAYGGT YRLIDTVFTA
WGVEYTVVDI SVVEEVKAAI KDNTKADLGG NPNQPSTLAL PDIEAXCKTS PERHQPOACC
LTPPSHSPYL QXPLKXXXHT Q

> RXA02771 (1-555, translated) 185 residues
VSEQALSTFD RAREALDKKT RYVQDFPEKG VLFEDLTPVL GDAESFVAVV DAMAEAAEKL
NAEIIIGLDA RGFLGSAVA YKLGLGVLA RKKGKLPFV VTQYELEYG TAALELPSEG
IDIAGKNIVL IDDVLATGGT LGAARKLIES CDGHVSGYVL AIEVPGLGGR DNLGDRPVIV
VRDPQ

> RXA02772 (1-780, translated) 260 residues
MSARLARSIT GNRVRTNPVL DPLLSIHRQF HPRADVQVLE RAYDTAERLH DGVIKSGDP
YITHPLAVAT IAAEIGMDTT TLVAALLHDT VEDTDYSLDD LTRDFGEEVA RLVDGVTKLD
KVALGAAAEA ETIRKMIVAM SQDPRVLVIK VADRLHNMRT MRFLPPEKQA KKAQTLEVI
APLAHRLGMA SVKWELEDLS FAILPKKYE EIVRLVADRA PSRDRYLKEI IDQVTGGLRE
NNIAAEVLGX XKHSGLSFKR

> RXA02773 (1-162, translated) 54 residues
MIVRGRDFDD IFDLVGIRXL XDNVNNWVRR XRCRALXXQC SXWXXQRLYF SPAL

> RXA02790 (1-1143, translated) 381 residues
MEPVYVKRRQ RFIAVTIASL ILIIGAIYI GVATSNRTPH DYEGSGNGVV QLVEIPEGSS
ISELGPELEE RDIVATNSAF QTAASNNPNA GSVQPGFYRL QEOMNAAAIV SALLDPDNQV
DLLDIHGAT LMDVTVVGGN TRAGIYSQIA AVTCTEGSAN CITAEDLQQV ASTVSPAELG
VPDWAIAAVE ARGTDPKRLE GLIMPGQYV DPSNDAQGIL TDLITRSANH FQETDITGRA
DAIGLTPYEL VTAASLIERE APAGDFDKVA RVILNRLAEP MQLQFDSTVN YGLSEQEVAT
TDEDRTQVTP WNTYAMDGLP QTPIAAVSTE ALQAMENPAE GNWLYFVTID TDGTTVFNDT
FEEHEADIEQ ALNSGVLDN R

> RXA02791 (1-828, translated) 276 residues
LGSHITHRAA VLGSPIEHSK SPVLHNTGYK ALGLDQWEYD RFECTGDMPL GIVSGADETY
CGFSVTMPK FAALEFADEV TERACAIGSA NTLRLTATGW RADNTDVGDI RGALGELLGG
ASLAGKHAIV IGSGETARPA IWALIEAGVA RITVLNRSR TAEQLTLFDE TPTTLAYAPL
EHLHIEADV VSTVPSAAIA GLEDTLAIAP VLDVIYDPWP TPLVEVTRAK GLKAVGGHVM
LAHQSYGQFE QFTGMDAPRD AMREALEESL GISEEH

> RXA02801 (1-435, translated) 145 residues
VGFDVARVRG LYTSLGDGWT YLNSHQIPQV PERVASGVAA AFRTHAQISE VTSQPIAVDQ
LEAAREAVAS LAGVDPDCVV LGPTRQFLAH TLARGLGGFV RRGAGVLSR ADADWLTAPF
RSLDGVFSWA EPDLGTGMLP DWQYQ

> RXA02802 (1-468, translated) 156 residues
MAMEALKIIT GVGTPLIQKL GYYSSLDGTW EYIPVVGSP VLERVLGSAG VSGISGGFGE
VLDVPRVSAL VDGVSILIDR EPSEFSAYSI PGAHNTPLSA IREGAIPPSV SAGKEVIVYC
AAGVRSQAQAI AILESAGYTG MSSLDGGIEG WLDSL

> RXA02805 (1-585, translated) 195 residues
 VFPGVVDGIS HYGNCGLPLN IGGETVFDD S YAGNPLVNAL CVGTLKVEDL KLAFASTGN
 KVILFGSRTG LDGIGGVSVL GSASFEEGEE RKLPAVQVGD PFAEKVLIEC CLELYKAGVV
 VGIQDLGGGG LACATSELAA AGDGGMRVNL DNVPLRAENM SAAEILASES QERMCAVVTP
 ENVERFLEIC AKWDV

> RXA02814 (1-471, translated) 157 residues
 AKNLEEHSYV VNHLRTILEP LCSQFDAPTV PELTKTNEMW HLATPIVGT L KYPHITALEL
 AIRTHPTPAI CGTPTDAAEA LIIEAESPRN FYAGAAGWCD STGDGEYMVA IRCAEVSEDG
 TWARAWAGGG IVAESDAQEE FDETTAKLQT IMRSLGL

> RXA02843 (1-891, translated) 297 residues
 MTTASATGIA TLTSTGDVLD VWYPEIGSTD QSALTPLEGV DEDRNVTRKI VTTTIDTDAA
 PTDTYDAWLR LHLLSHRVFR PHTINLDGIF GLLNNVVWTN FGPCAVDGEA LTRARLSRRG
 QVTVYSVDKF PRMVDYVVP S GVRIGDADR V RLGAYLADGT TVMHEGFVNF NAGTLGASMV
 EGRISAGVT V DDGTDVGGGA SIMGTLSGGG QHVISLGKRC LLGANS CGCI PLGDDCIIEA
 GLYITAGTKV LFDGSLHKAS TLAGSNGLIF RRDSVSGQV AVPNTKVV L NTALHSN

> RXA02857 (1-513, translated) 171 residues
 MDITIVNHPL VASRLTLRD ERSDNAAFRA AANDLGAMLI YEASRDLEVE HFDTKTPVAM
 AEGTRLKQPP IIVPIIRAGL GMIDPALSMI PDAQVGFIGL ARDEETHEPV PYLEALPQDL
 SNQPVFLVDP MLATGGSLLH AIRLLADRG A TDITAICMVS AQPGVDALAE S

> RXA02879 (1-861, translated) 287 residues
 ELADYIPELK SADPNPLAVA LCTVNGHIYS AGDDDIEFTM QSISKPFAYA LALQECGFDE
 VSASVALEPS GEAFNELSLD GENRPMNPMI NAGAIINQL INGS DSTVED RVEKIRHYFS
 ELAGRELTID RVLAESLAG ADRNLSIAHM LRNYGVIEDE AHDAVLSYTL QCAIKVTTTRD
 LAVMTATLAA GGTHPITGKK LLDARVCRLT LSVMASAGMY DEAGQWLSTV GIPAKSGVAG
 GLIGILPGQL GIATFSPRLN PKGNSVRGVK IFKQLSDDMG LHLMSTE

> RXA02903 (1-483, translated) 161 residues
 VSKLKGSRS L LDVSGSDHSF ADLAGRQVAH VDVVDPLINT TFEETFQPTQS YDAITFIASL
 HHMNAEEGLN KAVRILNPGG KLLIVGLAKN KTASDWIISG LQAFLSRPIS LINREQQIYP
 FPTKEPSESL HEIRQLTKQL LPHRRIRRG I HFRYLLEWTK P

> RXA02906 (1-498, translated) 166 residues
 MTQSAPEFIA TADLVDIIGD NAQSCDTQFQ NLGGATEFHG IITTVKCFQD NALLKSILSE
 DNPGGVLVID GDASVHTALV GDIIAGLGKD HGWSGVIVNG AIRDSAVIGT MTFGCKALGT
 NPRKSTKTGS GERDVVVSIG GIDFIPGHYV YADSDGIIVT EAPIKQ

>RXN00023 TRANSLATE of: rxn00023.seq check: 8571 from: 1 to: 3456
 MTSMLPIEL ATLSDAQVDK VRSWLEYSKK ESVPNADAKR LAAVLQDPNG LEFTVGFVDR
 VVRTEDREAA AHALYELGKI APSTMSFLDR AQIQAGSLVG RALPQVVVPA ARARIRQMVG
 HMIVDARDKQ FAKAVAEIQS DGHRLNINLL GEAVLGRKEA AKHLDDTVRL LRRPDVEYVS
 IKVSSVASQI SMWGFEDTVN YVVEQLTPLY IEAARAPKGT KFINLDMEEY RDLRLTMEVF
 KRLLSNPELH ELEAGIVLQA YLPDALGAIQ DLAQFGRERV NTGGAGVKVR LVKGANLPME
 HVHAQITGWP VATEPSKQAT DANYKRVLYW TMRKENMEGL RLG VAGHNL F DIAFAHLLSV
 ERGVADRVEF EMLQGMASDQ ARAVSVDVGE LLLYVPAVRP QEFDV AISYL VRRLEENAAS
 ENFMSAIFDL DADNPSFKRE ESRFRASISD LATLIDVPAP GPNHTQDRSK ETLLDAPLVP
 FINEPDTNPA LIQNQQWATK AVATAAEPGW LEKQTKPEVL EEGDV DKLIN DVRDAAEAWA
 ARPAREAEI LYKTAEILRV RRGHLISVTA AEVGKAVEQT DPEISEAIDF ARYYAHLALE
 LDDVDNAEFT PDRVVVVTPP WNFPIAIPAG STFAALAAGA GVIHKPSKPS QHCSAAVVEA
 LWEAGVPREV LHCIYPANRD VGCALISHEH VDRVILT GSS ETAAMFSSWR PELTINGETS
 GKNAIVVTPS ADRDLAVADL VKSAFGHAGQ KCSAASLGIL VGSVYESERF RKQLVDAASS
 LIVDWPTNPS ATVGPLTELP SDKLHHALTT LEEGESWLLK PRQLDDTGRL WSPGIKEGVK
 PGTFHHLTEV FGPVLGLMKA TDLNEAIEFQ NGNDFGLTGG LQSLDADEV R TWLDHVDVGN
 AYNVRGITGA IVQRQSF GGW KKSSVGLGSK AGGPNYVMLM GTWADAPSHH APRETNPLIS
 KLDLPGEELE WLEKANASDE TAWNTEFGSP RDP SGLDVEA NIFRYRPAEV VLRLDDSATP
 RETARALLAA RRAGVTPRVL QTPGVSEQVR EVLSAAGVSA ETVDDSVFIS NVLRGEYDEN
 SSVRVRYLGK VS DTVRERLS VRPEVLLDD AVTASGRVEL RYWLKEQAIS MTLHREGNPV

AAFHELAEEEL KR

>RXN00076 TRANSLATE of: rxn00076.seq check: 5232 from: 1 to: 1371
 MTTPLRVAVI GAGPAGIYAS DLLIRNEERE VFVDLFEQMP APFGLIRYGV APDHPRIKGI
 VKSLHNVLDK PRLRLGNIE IGKDITVEEL RDYYDAVVFS TGAVADRDNL IPGIEAEGSF
 GAGEFVGFDY GNPRFERSWD LSAQSVAVIG VGNVGLDVAR ILAKTGDELK VTEISDNVYD
 SLKENKATEV HVFGRRGPAQ VKFTPQELKE LDHSPTINVV VDPEDIDYDG ASEEARASK
 SQDLVCQILE QYAIREFPKDA PHTLQIHLFE NPVEVLQKDG KVVGLRTERT SLDGNGGVNG
 TGEFKDWPVQ AVYRAVGYS DPIDGVPFDE NKHVIPNDGG HVLTPGAEP VPGLYATGWI
 KRGPGLIGN TKSDAKETTD ILIKDAVAGV LEAPKHQGEI AIELLDSRN IPFTTWEGWY
 KLDAAERALG EAEGRRKKI VDWEEMVRQA REAPAIV

>RXN00116 TRANSLATE of: rxn00116.seq check: 3330 from: 1 to: 1161
 MSNDFVVSRL RPFGETIFAT MTQRAVEAGA INLQGQFPDE DGPRRMLEIA SEQILGNNQ
 YSAGRGDASL RAAVARDHLE RFDLEYNPDS EVLITVGATE AITATVLGLV EPGDEVIVLE
 PYYDAYAAAI ALAGATRVAV PLQEVENSWD VDVKLHAAV TKKTRMIIVN SPHNPTGVSF
 SKKALKQLAG VARAYDLLVL SDEVYHLVF DDQKHVSVAK LPMWDRVT VSSAAKTFNV
 TGWKTGWALA PEPLLEAVLK AKQFMSYVGA TPFQPAVAHA IEHEQKWVSK MSKGLLEKRD
 ILRTALDKAG LKTHDSMGTY FIVADIGDRD GAFCFELIE KVGVAIPVQ AFVDHPKWS
 SKVRFAFCKK EETLREAAER LKGIKKL

>RXN00132 TRANSLATE of: rxn00132.seq check: 6992 from: 1 to: 1434
 MAQVMDFKVA DLSLAEAGRH QIRLAIEYEMP GLMQLRKEFA DEQPLKGARI AGSIHMTVQT
 AVLIETLTAL GAEVRWASCN IFSTQDEAAA AIVVGSQTV EAPAGVPVFAW KGESLEEYWW
 CINQIFSWGD ELPNMILDDG GDMATMAVIRG REYEQAGLVP PAEANDSDEY IAFGLMLREV
 LAAEPGKWKI IAEAVKGVTE ETTTGVHRLY HFAEEGVLPF PAMNVNDAVT KSKFDNKYGT
 RHSLIDGINR ATDMLMGKGN VLVCYGDVG KGCAEAFDQG GARVKVTEAD PINALQALMD
 GYSVTVDEA IEDADIVITA TGNKDIISFE QMLKMKDHAL LGNIGHFDNE IDMHSLLHRD
 DVTRTTIKPQ VDEFTFSTGR SIIVLSEGR LNLGNATGHP SFVMSNSFAD QTIAQIELFQ
 NEGQYENEVY RLPKVLDEKV ARIHVEALGG QLTELTKQA EYIGVDVAGP FKPEHYRY

>RXN00198 TRANSLATE of: rxn00198.seq check: 9286 from: 1 to: 549
 MYPNLFRTAT AHEEGEYIIT GDESADEIAA LGLAERAAGS TLGERKFAVN TVEFHGNNH
 VTGLTGNQIR VVNGKREPIE GTEFPFEADL VLVALGFTGA EQGGLAHELG VGFDGRIL
 RDSEYRSPTN SRVYIAGDNG RGQSLIVWAI AEGRACAAI DADLMGETAL PVAVAPQDVP
 LAV

>RXN00262 TRANSLATE of: rxn00262.seq check: 6430 from: 1 to: 1074
 MLYLDNAATT SVRNEALEAM WPYLTGAFGN PSSPHEVGRL ASAGLEDART RVARIIGGRP
 TQVTFSTGGS EANNLAIKGA CLANPRGRHL ITTPIEHDSV LETAAYLERF HDFEITYLSP
 DHTGLISPEG LRKAVRPDTH LISIGYANNE VGTIQPIAEL AAVSSTPFHT DAVQAAHLTF
 DLGVDALSLS GHKFGAPKGI GVLWSKPLE PVIHGGQEK GRRSGTENVA GAIAFATALE
 LARAESYPDL GEFIEEVLT IGAHLTGHP MRIDGHASFL FDSIGSETVL LELERQGIVC
 SPGSACSGSE VSHVLLALGL EEDQARTAVR CTFSTTHSRE DALVAASALK SAVALIRG

>RXN00351 TRANSLATE of: rxn00351.seq check: 7296 from: 1 to: 1455
 MDDNSFVVV ANRLPVDMTV HPDGSYSISP SPGGLVTGLSPVLEQHRGCWV GWPGTVDVA
 PEPFRTDTGV LLHPVVLTA DYEGFYEGFS NATLWPLFHD LIVTPVYNTD WWHAFFREVNL
 KFEEAVSQVA AHGATVWVQD YQLLLVPGIL RQMRPDLKIG FFLHIPFPSP DLFRQLPWRE
 EIVRGMLGAD LVGFHLVQNA ENFLALTQQV AGTAGSHVGQ PDLQVSGEA LVREIGAHVE
 TADGRRVSVG AFPIIDVEM FGEASKSAVL DLLKTLDEPE TVFLGVDRDL YTKGILQRL
 AFEELLESQA LEADKAVLLQ VATPSRERID HYRVSRSQVE EAVGRINGRF GRMGRPVVHY
 LHRSLKNDL QVLYTAADV LVTPEKDG MN LVAKFVANH RDGTGALVLS EFAGAATELT
 GAYLCNPFV ESIKQMVAA VHDLKHPES AATRMKTNSE QVYTHDVNVW ANSFLDCLAQ
 SGENS

>RXN00355 TRANSLATE of: rxn00355.seq check: 5514 from: 1 to: 1020
 MHLGKLDQDS ATTILEDYKN MTNIRVAIVG YGNLGRSVEK LIAKQPDMDL VGIFSRATL
 DTKTPVFDVA DVDKHADDV VLFLCMGSAT DIPEQAPKFA QFACTVDTYD NHRDIPRHRQ
 VMNEAATAAG NVALVSTGWD PGMFSINRVY AAAVLAHQH HTFWGPGLSQ GHSDALRRIP

GVQKAVQYTL PSEDALEKAR RGEAGDLTGK QTHKRQCFVV ADAADHERIE NDIRTMPDYF
 VGYEVEVNFI DEATFDSEHT GMPHGGHVIT TGD TGGFNHT VEYILKLDNRN PDFTASSQIA
 FGRAAHRMKQ QGQSGAFTVL EVAPYLLSPE NLDDLIARDV

>RXN00365 TRANSLATE of: rxn00365.seq check: 223 from: 1 to: 627
 MILSPSKTFF LEIVEKAFRE GWVQPVIPSM STGLSVAVVG SGPAGLAAAQ QLTRAGHSVT
 VFERDDRLGG LMRYGVPEYK MENRWIDRRI EQMEAEGTTF QVGTSPRAAE LALFDAILLA
 TGTPVARELS VPGHDLNGIH AAMDYLTAQN RINEGDGEVS PINAKGKKVV IIGGGDTGTD
 CFGTALRQGA ESVTQFDIRP RAPFQRADS

>RXN00367 TRANSLATE of: rxn00367.seq check: 6400 from: 1 to: 4530
 MKPQGLYNPA HEHDACGVAF IADHGRPSR SIVDRALEAL RNIDHRGAAG AEKNTGDGAG
 ILMQIPDGFY REVSGIELPE AGEYATGIAF LPRGRMAMMD AQKEIERIAK QEGADVLGWR
 MVPFDSRD LG SMAEEAMPSF AQIFLTVPGK SGEDLDRVMF FIRKRCEREL GTTNGRDTVY
 FPSLSRTII YKGMTTLTQL EGFFEDLGDA RLESAIAIVH SRFSTNTFPS WPLAHPYRFV
 AHNGEINTVR GNENWMRARE ALIKNDKLG N LSSVLPICTP EGSDTARFDE ALELLHLGGY
 SLPHAVAMMI PQAWEHNKTL SPELRDFY EY HSCLMEPWDG PAALAF TDGR FVGAVLDRNG
 LRPGRITITD SGLVVMASES GVLDLREESV VKRTRVQPGR MFLVDTAAGR IVEDEEIKQK
 LSEAQPYGEW IRDNFVHLDR LPQTRYNYMA HSRAVLRQRV FGITEEDVDL LLLPMARQGA
 EAIGSMGSDT PIAALSQRPR MLYDFFAQRF AQVTNPPLDS IREKPVTSMF TLLGAQSDVL
 NPGPDAAARRI RLESPIIDNH ELATLINANA HGEWDSFGAA VISGLYPVAH HGAGMKA AIA
 RVRREVSEAI RNGKTLIVLS DRESDERMAP IPALLLTS AV HQYLVQQRTR TQCSLVVESG
 DAREVHHLAM LIGFGADAIN PYMAFETIDE LRMKGQLGDL SLDEASRNYI KAATTGVLKV
 MSKMGIATVS SYRGAQLADV TGLHQDLLDN YFGGIASPI S GIGLDEVAAD VEARHRS AFL
 PRPEEHAHRE LDLGGEYKWR REGEYHLFNP ETIFKLQHAT RSGSYEIFKD YTRKVDDQST
 RLGTIRGLFE FSTDRKPISV SEVEPVSEIV KRFSTGAMSY GSISAEAEHV LAIAMNRLGG
 MSNSGEGGED ARRF DVEPNG DWKRS AIKQV ASGRFGVTSH YLNNCTDIQI KMAQGA KPGE
 GGQLPPNKVY PVWAEVRIT PGVGLISPPP HHDIYSIEDL AQLI HDLKNA NPRARIHVKL
 VAEQGVGTVA AGVSKAHADV VLISGH DGGT GASPLTSLKH AGGPWELGLA ETQQTLLNG
 LRDRIRVQCD GQLKTGRD VV IAALLGAEEF GFATAPLVVE GCIMMRVCHL DTCPVGIATQ
 NPDLSKFTG KAEHVVNFFT FIAQEVREYL AQLGFRSIDE AVGQAQVLRK RSGIPADSRA
 AHLDSLPIFH RPETPHFPTQ DVRCTKTQEH SLEKALDN AF IDKASDTITR AAAGVETSIV
 IDSSISNVNR SVGTMLGSAV SRVAGAQGLP DGTITLNLQG CAGNSFGAFI PRGITINLTG
 DANDFVGKGL SGGKIVIKPS AQAPKQLKNN PNIIAGNVLG YGATSGELFI RGQVGERFCV
 RNSGATAVVE GIGNHGCEYM TGGRVLVLGP VGENFGAGMS GGIAYLANSP DLNQKINGEL
 VDVVPLSADD LTWADEL IAR HRELTGSETK LRAQDLVKIM PRDFQKVLNI IETAHAEGQD
 PAIKIMEAVS

>RXN00371 TRANSLATE of: rxn00371.seq check: 9489 from: 1 to: 1794
 MTIAHKPEMA ETTGIETNQV SETIGVESLT HG NLRPVSSF EGQHEGQTEE LLPGKVIFVG
 AGPGNPDLLT VRAREVLGNA VRAITDEQVL SGVRAFVATE IPVPEDKLQA AEDEYERICI
 EAKENGARRK PPRPAPPTAA EITEVSEATP AQIVELVQDA LSYGGDVIRL VTGNPLSSDA
 TLAEISAVSE AGLEFQVVP G MSLPATVPAF AGIALGSTYT ETDVNGQNL D WQLASAPQP
 LVLQARVDDL SRIAQELKAR NMSLET PVS V TANGTTRLQR TYDTTLG L LH KLD AELSGPL
 VVTLGKGVDD RSKYSWWENR ALYGWRVLVP RAREQAASMS ARLSSHGAIP QEVPTISVEP
 PRNPAQMER A IKGIVEGRYQ WVVLTSVNAV KAVWEKITEF GLDSRSFAGV RIAAVGEKTA
 AEIRALGITP ELLPARTRQN AQGLVDVFPE YFEELDPVGR VLLPRADIAT DVLVDGLTHL
 GWEVEDVVAY RTVRAAPPSA DIRDMIKTGG FDAVAFTSSS TVKNLVGIAG KPHPRTIVAC
 IGPMTAATAE ELGLRVDVMP EIAEVP ELID ALAEHVADLR AKGELPPPRK KRRRRKAS

>RXN00383 TRANSLATE of: rxn00383.seq check: 2070 from: 1 to: 1344
 MRFAIIGAGL AGLTAAEIH KADPTAQIDV LEAGERIGGK LFTVPFASGP TDIGAEAF LA
 ARSDAVEFFT ELGLADSLVS PSAAKSQYFA GGALHAF PAG GVMGIPSNPP AGAQDTAFDW
 TPGQDISVGA LVRRQY GDEI VDTVVSSLLG GVSSTADDL GVRASVPALA AALDQLAEAG
 EPVTL SAAVK AVEAQREAAK TTSETRPVFQ TFKGGYAE LY EALAEQCGAD IHLDSFVSAI
 TKDGEGFAIK GGEGTYDKV ILAVPAPTAA VLLRDLAPAA APHLRAIKLA S SAVVGMRF D
 SSEGLPDNSG VLVAVNEPGI TAKAFTFSSK KWP HLEARGG ALVRASFGRL GDEASARMDE
 DLLVDAALDD LLTITGFDGR AAGLGEIFVQ RWFGGLPAYG VDHIATVSAA RAEIAAVPGV
 EAIGAWAGGVGVP AVIADAQA AAVHRLLG

>RXN00402 TRANSLATE of: rxn00402.seq check: 8345 from: 1 to: 600

TDEKDGKPV L PYFVTPDAAY HGLKYADLGA PAFGLKVRVG LLRDTGSTLS AFNAWAAVQG
 IDTLRLRLER HNENAIKVAE FLNNHEKVEK VNFAGLKDSP WYATKEKLG L KYTGSVLTFE
 IKGGKDEAWA FIDALKLHSN LANIGDVRS L VVHPATTT HS QSDEAGLARA GVTQSTVRLS
 VGIETIDDII ADLEGGFAAI

>RXN00403 TRANSLATE of: rxn00403.seq check: 6647 from: 1 to: 1131
 MPTLAPSGQL EIQAIGDVST EAGAIITNAE IAYHRWGEYR VDKEGRSNV V LIEHALTGDS
 NAADWWADLL GPGKAINTDI YCVICTNVIG GCNGSTGPGS MHPDGNFWGN RFPATSIRDQ
 VNAEKQFLDA LGITTVA AVL GGSMGGARTL EWAAMYPETV GAAAVLAVSA RASAWQIGIQ
 SAQIKAIEND HHWHEGNYE SGCNPATGLG AARRIAHLY RGELEIDERF GTKAQKNENP
 LGPYRKPDQR FAVESYLDYQ ADKLVQRFDA GSYVLLTDAL NRHDIGRDRG GLNKALESIK
 VPVLVAGVDT DILYPYHQE HLSRNLGNLL AMAKIVSPVG HDAFLTESRQ MDRIVRNFFS
 LISPDEDNPS TYIEFYI

>RXN00420 TRANSLATE of: rxn00420.seq check: 7740 from: 1 to: 1464
 MNSSHGTSSS GASAGAHGAL PLEAQKLNGW GRTAPTAEV LTPDLDIIV DAVRQVAEQN
 DSKPDYLRG VIARGMGRSY GDPAQNAGGL VIDMQPLNKI HSIDPDSAI V DVDGGVTLDQ
 LMKAALPYGL WVPVLPGRQ VTIGGAIGPD IHGKNHHSAG SFGDHVVSME LLVADGRILH
 LEPEGTAEDP QGDLFWATVG GMGLTGIIVR ARIRMTKTET AYFIADTDRT NNLEETVAFH
 SDGSEHNYTY SSAWFDVISP EPKLGRSTIS RGS LATLAQL EELAPKLAKD PLKFNA PQLM
 KVPDIFPSWT LNKLTLSAVG VAYYAMGAPA KNQVKNLTQF YQPLDLIGEW NRGVSKGFL
 QYQFVVPTA VEPFKDIIRD MQKSGHYSAL NVFKLFGPGN RAPLSYPM PG WNVCVDFPIR
 PGLGAFLLDDL DKRVMEFGR LYLAKESRTS AENFHAMYPG MEGWLKTRNE IDPTGVFASD
 MSRRLELS

>RXN00435 TRANSLATE of: rxn00435.seq check: 2922 from: 1 to: 1173
 VGFDVARVRG LYTSLGDGWT YLNSHQIPQV PERVASGVAA AFRTHAQISE VTSQPIAVDQ
 LEAAREAVAS LAGVDPDCVV LGPTRQFLAH TLARGLGGFV RRKAGVVL SR ADADWLTAPF
 RSLDGVSFWA EPDLGTGMLP DWQYEKLVDG STRLVVLSAA HPLLGTVAPV GKIVDKVRAR
 SRAWVLVDAT TYAAYRPLRL DEWEADIVML DLGELGGPQI SALIFRDTSM FPRLDRTVPL
 ELPASSLPHG LLGGVPNLVR HLGNLDENAP SVVEAMGEMA KFHKLFEHL VESLEGLHAV
 HIVGISGDAA GQDAPFLDRV PRLTFTMEGV PADMVYRRI V DNRLITTVSP ADPLLEAMGV
 TEAGGSITIG LSPFSTYYEV DQLTRVLASL A

>RXN00437 TRANSLATE of: rxn00437.seq check: 8249 from: 1 to: 456
 MNTDPAYVAE QTGKLIDAF L TTDPLEPLLD AAKNGVCTEA MGALVTFEGI VRDHDGGARV
 TSLTYTAHPT APQVLSAVAD SIVEKHPRTR LWTARTGAL KIGDAAFLV V AASAHRADAF
 AACSDLADAV KAQVPIWKEQ TRLDGSTDWV GL

>RXN00439 TRANSLATE of: rxn00439.seq check: 3994 from: 1 to: 468
 MSELTHVRAD GSAHMDVTG KNETSRTAVA EGFVKMRGDV VKQLFSAGLP KGDALPVARI
 AGIMGAKKTP DIIPLCHPLP LGKITVDFFE LTDGVRIEAS VKTRGVTGVE MEALTAVSTA
 ALTVYD MIKA VDKMAVIDGI RVL SKTGGS GDWSVQ

>RXN00441 TRANSLATE of: rxn00441.seq check: 2659 from: 1 to: 1164
 MSRSPEQH LA EISALLPPQK STFVNLREAL GRRTFS AVTA QWDS PRFDNS QMDGFALGPS
 HLNGGTFAVG PTIPAGHDPD QWYPRGIEKD IAPIMTGARL PKNTAAIIPV EKTTPGNFDA
 PQVEIPATPQ GQFIRLQGS D ITAGDEIIPA GTELNSVHIG VLASQSIKSI EVAAKPRVLI
 ITGGSEISEQ HGPATIPDAN GPLLRSLCAR NNIEVIAGLH TNDDPERLRF ELENAIDQYQ
 PDVIITSGGI SHGKFEVFRQ ILEGTPNSWF GHVDQQPGGP QGISTFAETP VISLPGNPIS
 TLVSFTLLVA PALNRQPLRH LDARITAPVQ GLQDNREQFL RGTISYRNGP RPRHASP GHQ
 FPPAGSSCHR RLSDQDPGAD YGGGKRHR

>RXN00446 TRANSLATE of: rxn00446.seq check: 3948 from: 1 to: 864
 MGAVELREAL AEHLEVEFDQ VTVGCGSSAL CQQLVQATCA QGDEVIFPWR SFEAYPIFAQ
 VAGATPVAIP LTADQNHDL D AMAAAITDKT RLIFICNPNN PSGTTITQAO FDNFMEKVPN
 DVVVLDEAY FEFNRADDT P VATEE IHRHD NVIGLRTFSK AYGLAGLRVG YAFGNAEIIA
 AMNKVAIPFA VNSAAQAAAL ASLNSADELM ERVEETVEKR DAVVSALGAA PTQANFVWLP
 GEGAAELAAK LAEHGIVIRA FPEGARISVT NAEETDKLLR AWEAINAG

>RXN00448 TRANSLATE of: rxn00448.seq check: 8725 from: 1 to: 1020

VTTKDISRPV CILGLGLIGG SLLRDLHAAN HSVFGYNRSR SGAKSAVDEG FDVSADLEAT
 LQRAAAEDAL IVLAVPMTAI DSLLDVAVHTH APNNGFTDVV SVKTAVYDAV KARNMQHRYV
 GSHPMAGTAN SGWSASMDGL FKRAVWVTF DQLFDGTDIN STWISIWKDV VQMALAVGAE
 VVPSRVGPHD AAAARVSHLT HILAETLAIV GDNGGALSLS LAAGSYRDST RVAGTDPGLV
 RAMCESNAGP LVKALDEALA ILHEAREGLT AEQPNIEQLA DNGYRSRIRY EARSQORRAK
 ESVSPTITSS RPVLRLLHPT PNWEKQLIHA ETLGARIEVF

>RXN00450 TRANSLATE of: rxn00450.seq check: 3072 from: 1 to: 324
 VGVLPVQARI KDDERRMRHA LDIARQTPEG DVPVGAVIYA PTGEILATAT NRREADRDP
 AHAEIIALRR AARRFSDGWR LSDCTAVVTL EPCSMCAGAL VGARIGRI

>RXN00487 TRANSLATE of: rxn00487.seq check: 2450 from: 1 to: 1569
 VSLQTNHRPV LVVDFGAQYA QLIARRVREA GIYSEVIPHT ATADDVRAKN AAALVLSGGP
 SSVYAEAGAPS LDAEILDGL PVFGICYGFQ AMTHALGGTV ANTGKREYGR TDINVAGGVL
 HEGLEACHKV WMSHGDAVSE APEGFVVTAS SEGAPVAAFE NKERKMAGVQ YHPEVLHSPH
 GQAVLTRFLT EIAGLEQNWT AANIAEELIE KVREQIGEDG RAICGLSGGV DSAVAGALVQ
 RAIGDRLTCV FVDHGLLRAG EREQVEKDFV AATGAKLTV DERQAFSLKL AGVTEPEAKR
 KAIGAEFIRS FERAAGVLE EAPEGSTVDF LVQGTLYPDV VESGGSGSTA NIKSHHNVGG
 LPDDVEFKLV EPLRDLFKDE VRAVGRELGL PEEIVGRQPF PGPGLGIRII GEVTEDRLET
 LRHADLIART ELTEAGLDGV IWQCPVLLA DVRSVGVQGD GRTYGHPIVL RPVSSEDAMT
 ADWTRLPEYV LEKISTRITN EVPDVNRVVL DVTSKPPGTI EWE

>RXN00488 TRANSLATE of: rxn00488.seq check: 2147 from: 1 to: 1518
 MTTQSRVSTG GDNPNKVALV GLTFDDVLLL PDASDVVPSE VDTSTQLTRN IRLNTPILSA
 AMDTVTEARM AIGMARHGGI GVLHRNLSIQ EQAENVELVK RSESGMVTDP VTCTPDMSIQ
 EVDDLCAFR ISGLPVVDEA GKLVGICTNR DMRFESDMNR RVAEVMTPMP LVVAEEGVTK
 EQALALLSAN KVEKLPIIAK DGKLVGLITV KDFVKTEQHP NASKDASGRL LVAAGIGTGE
 ESFQAGALA DAGVDILVVD SAHAHSRGVL DMVSRVKKSF PKVDIVGGNL ATREAAQAMI
 EAGADAIKV IGPISICTTR VVAGVGAPQI TAIMEAAVPA HKAGVPIAD GGMQFSGDIA
 KALAAAGANSV MLGSMAGTA EAPGETITIN GKQYKRYRGM GSMGAMQGRG LSSEKRSYSK
 DRYFQSDVKS EDKLVPEGIE GRVPFRGPIG DIIHQVGGGL RAAMGYTGSS TIEELHNARF
 VQITSAGLKE SHPHHIQQTV EAPNYH

>RXN00508 TRANSLATE of: rxn00508.seq check: 3320 from: 1 to: 1083
 MNLLTTKIDL DAIHANTRVL KQMAGPAKLM AVVKANAYNH GVEKVAPVIA AHGADAFGVA
 TLAEAMQLRD IGISQEVLCW IWTPEQDFRA AIDRNIDLAV ISPAHAKALI ETDAEHIRVS
 IKIDSGHLRS GVDEQEWEGV FSALAAAPHI EVTGMFTHLA CADEPENPET DRQIIAFRRA
 LALARKHGLE CPVNHVCNSP AFLTRSDLHM EMVRPGLAFY GLEPVAGLEH GLKPAMTWEA
 KVSVVQIEA GQGTSYGLTW RAEDRGFVAV VPAGYADGMP RHAQGFVSVT IDGLDYPQVG
 RVCMDQFVIS LGDNPHGVEA GAKAVIFGEN GHDATDFAER LDTINYEVC RPTGRTVRAV
 V

>RXN00536 TRANSLATE of: rxn00536.seq check: 8919 from: 1 to: 1371
 MSPNDAFISA PAKIETPVGP RNEGQPAWNK QRGSSMPVNR YMPFEVEVED ISLPDRTPD
 KKITVAPQWC AVDLRDGNQA LIDPMSPERK RRMFELLVQM GFKEIEVGFV SASQTDFFV
 REIIEKGMIP DDVTIQVLVQ AREHLIRRTF EACEGAKNVI VHFYNSTSL QRVNVFRMDK
 VQVKLATDA AELIKTIAQD YPDNWRWQY SPESFTGTEV EYAKEVVDAV VEVMDPTPEN
 PMIINLPSTV EMITPNVYAD SIEWMHRNLN RDSIILSLH PHNDRGTGVG AAELGYMAGA
 DRIEGCLFGN GERTGNVCLV TLALNMLTQG VDPQLDFTDI RQIRSTVEYC NQLRVPERHP
 YGGDLVFTAF SGSHQDAVNK GLDAMAAKVQ PGASSTEVSU EQLRDTRMGG SLPAYRSKGC
 RSRLRGCPYR ELPVRQGRRC LHEDRSRSA DPSLHAG

>RXN00537 TRANSLATE of: rxn00537.seq check: 1265 from: 1 to: 2286
 MSTFVNDTVE DAIKTPELDQ PFEALGLKDD EYARIKEILG RRPTDAELTV YSVMWSEHCS
 YKSSKVHLRY FGETTTEEMA SKILAGIGEN AGVVDIGDGN AVTFRVESHN HPSFVEPHQG
 AATGVGGIVR DIMAMGARPI AVMDQLRFGA LDNPDTQRFV PGVVDGISHY GNCLGLPNIG
 GETVFDDSYA GNPLVNALCV GTLKVEDLKL AFASGTGNKV ILFGSRTGLD GIGGVSVLGS
 ASFEEGEERK LPAVQVGDPF AEKVLIECCL ELYKAGVVVG IQDLGGGGGLA CATSELAAAG
 DGGMRVNLND VPLRAENMSA AEILASESQE RMCVVTPEN VERFLEICAK WDVTCAEIGE
 VTDEKDRYV VHNGEVVIDA PPSTIDEGPV YNRPVAPEN QDELQLEGEI ARPVDVEEIK
 AAWLKLVASP ALASRAFITE QYDRYVRGNT VQAKNANAGV LRIDEETNRG VAISADASGR

YTKLEPNTGA QLALAEAYRN VVSTGARPVA VTNCLNFGSP ENAGVMWQFK EAVHGLADGS
 KLLGIPVSGG NVSFYNQTDG EPILPTPVVG VLGVLNVEQ SIGNVLPSED NDLYLLGETF
 DEFSGSIWQQ VSGAGLNLGP PVVDLLNEQR LADLFVGS DL FAASHDLSEG GLGQTLAELA
 IHQKKGMDVD LSQIHPSLFT SLFAESASRI VVATNRGEEL EKRAAELGVP VFKLGCTNDS
 AVIAVKGADV EFTVSVEELR EAWTNTLPEA FGHAVGANAV VA

>RXN00558 TRANSLATE of: rxn00558.seq check: 6587 from: 1 to: 1347
 VVKKPAGIAV GDGEQILVFK DLGLVSQVFD QPIESLRGN IAIGHTRYTT AGGNTWENAO
 PMFRMAPDGT DIALGHNGNL INYIELLDKA TELGLVDPK KPSD TDVLTG LLASGVHDGN
 NLFDSAKELL PSVKGAYCLT FTDGHTLYAA RDPFGIRPLS IGRLERGWV ASETAALDIV
 GASHVREVEP GELIAIDESG LKSARFAETT RKGCVFEYVY LARPDSVIK RNVNEARLEI
 GRKLAAEAPA VGLDVITPE SGTAAVGFQ QASGIPFGQG MVKNAYVGRT FIQPSD TLRQ
 LGIRLKLNLPL REVIAGKRLV VVDDSIVRGN TQRAVIRMLR EAGAAEVHVR IASPPVKWPC
 FYGIDFATPG ELIANAVTSD NEAEMVEAVR SAIGADTLGY VSIDSMVAAT EQPANELCIA
 CFDGKYPMGL PQGNSNADLV RKMQATASS

>RXN00618 TRANSLATE of: rxn00618.seq check: 4181 from: 1 to: 1107
 MQMLDRVHRR RREGKDTLMF CAGQPSTGAP EAVIEEAEIA LRSGPLGYTE VIGDREFRER
 IADWHSATYD VDTNPDNVIV TTGSSGGFVA SFIATLDHGD YVAMPTPGYP AYRNILESLG
 AKVLNLRCTA ETRFQPTAQM LEELPHKPKA VIVTSPGNPT GTIIDPEELE RIAKWCDND
 AVLISDEDYH GMSFGRPLAT AHQFSKNAIV VGTLSKYFSM TGWRVGVWIIIV PDELVTPIEN
 LQASLSLCPA AIGQAAGRAA FTLEAGAELD AHVEAYREAR EVFVDKLPEI GLGT FADPDG
 GLYLWVDVSA YTDDSEEWAL RLLDEAGVAV APGVDFDPEE GHKWIRLSLC ASKEDTIEGV
 RKIGEFIKK

>RXN00626 TRANSLATE of: rxn00626.seq check: 4739 from: 1 to: 1263
 MRILVIGSGA REHALLRGLS TDPATTELHV APGNAGLGI ATVHPGIKAD DPEAVTALAK
 ELNSDLVVIG PEIPLVAGVA DALRAAGIAV FGPKNDAARI EGSKAFKDV MAAQGVRTAH
 AETITPGASS EDIDAAIDRF GPTWVVKDDG LSAGKGVVVT PDRAAARAHV DAYLEGGNPV
 LLESFLDGPV VSLFCLVDGE TVVPLLPQAD HKRAYDNDEG PNTGGMGAYA PLPWLPELGDV
 QRIVDEVCPV VAREMVARGC AYSGLLYAGI AWGAEGPAVV EFNCRFGDPE TQAVLALLKT
 PLAVLLNAVA TGTLAEQPAL EWEDAYALTV VLASYNYPEA PRTGDVIRNA DADNVLHAGT
 ALNAEGELVS AGGRVLNVIG VGETLEAARD NAYTTIKDIE LEGSHYRSDI ALAALEGRIS
 I

>RXN00636 TRANSLATE of: rxn00636.seq check: 8124 from: 1 to: 1029
 MMIDTFAVLI DRERLTANIS RMAAHAGAHE IALRPHVKTH KIIEIAQMQV DAGARGITCA
 TIGEAEIFAG AGFTDIFIAY PLYLTDHAVQ RLNAIPGEIS IGVDSEVMAQ ATAGLREDIK
 ALIEVDSGHR RSGVTATASE LSQIREALGS RYAGVFTFPG HSYGPGNGEQ AADELQALN
 NSVQRLAGGL TSGGSSPSAQ FTDAIDEMRP GVVVFNDSSQ ITSGACTEKQ VAMTVLSTVV
 SRNVSDRRII LDAGSKILST DKPAWIDGNG FVLGNPEARI SALSEHHATI FWPDKVLLPV
 IGEQLNIVPN HACNVINLVD EVYVREADGT FRTWKVVARG RNN

>RXN00667 TRANSLATE of: rxn00667.seq check: 6088 from: 1 to: 1014
 MIALKSMNR VVQPKMKAP LPIRDGLNPS RVRLPLDAAP IRAIDFVEYL ISTQRHRNPA
 DNAEALQARF DADLVVNHYG EPYAPDTMVQ PDDDIWFYRM PAAERPIYK IHVIHEDDDI
 LVIDKPPYLA TMPRGHRITE TALVKMRVLT GNNDLTPAHR LDRLTSGVLV MVKKPELRGA
 YQTLFARREA SKTYEIAIAEF VPGLLDDGPA IWESRIEKER GIVQAFVVEG PVNARTELVS
 VTPVEDAEQS ILEEMHGPLP RQARYVLAPS TGKTHQLRIH MRDFAAPILG DPLYPVLHAV
 DDEDTTPMH LIARTLTFVD PQTNEERTFV SNRPTGSL

>RXN00708 TRANSLATE of: rxn00708.seq check: 9995 from: 1 to: 807
 MTLSPPIGF GTVHLDGAPG VEAIAATAIDA GYRLIDTAYN YENEGTVGKA VRESGVPREE
 LIVTSKLPGF FHARDLGRVR IEESLYRLNL DYIDLLLIHW PNPSKDLYVE AWETLIEVRD
 AGLVKHIGVS NFLPNHIDRL RRETGELPAV NQIELHPYFP QVEQVDFHDE LGIITEAWSP
 LSNRGLVEE PLLKEIGERY GVGSGEIALA WHHARGIVPI PRSTNPARQR SNLEAVKISL
 IDEDVQAITA LARKNGRIKD QDPAVYEEF

>RXN00770 TRANSLATE of: rxn00770.seq check: 6183 from: 1 to: 1170
 LLSPYAWGLS RALLDSYVPN KFQTPAGEAK YTMSDHQDTT AEGVSYAAAG VDIEAGDRAV
 ELFAPMAKRA TRPEVLGNLG GFAGLFELGK YKKPILAAGS DGVGTLKLVIA QMMDKHDTIG

IDLVAMCVDD LVVGTGAEPFL LQDYIAIGKV VPEHVAEIVS GIAEGCVQAG CALLGGETAE
 HPGVMEPDHY DVSATAVGVV EADELLGPDR VRAGDVLIGM ASSGLHSNGY SLARHVLLEK
 AGLALDGHIE ELGRTLGEEL LEPTRIYAKD CLALIAECEV HTFCHVTGGG LAGNLERVVP
 EGLVAEMSRA TWTPGQIFRT ISSVGKVSRE EMEKTFNMGV GMVAVVAEKD RDRALAMLT
 RHIDCWEIGT VRNGEEGEPR VILNGEHPGY

>RXN00954 TRANSLATE of: rxn00954.seq check: 8841 from: 1 to: 621
 AVKWFASNF TFLFAPAYNP AIAHVQPVQR ALKFPTIFNT LGPLLSPARP ERQIMGVANA
 NHGQLIAEVF RELGRTRALV VHAGTDEIA VHGTTLVWEL KEDGTIEHYT IEPEDLGLGR
 YTLEDLVGGL GTENAEAMRA TFAGTGPDHA RDALAASAGA MFYLNQDVDS LKDGAKQALS
 LLADGTTQAW LAKHEEIDYS EKESND

>RXN00956 TRANSLATE of: rxn00956.seq check: 8058 from: 1 to: 1137
 MTEKENLGGG TLLPAYFGEF GGQFVAESLL PALDQLEKAF VDATNSPEFR EELGGYLRDY
 LGRPTPLTEC SNLPLAGEGK GFARIFLKRE DLVHGGAHKT NQVIGQVLLA KRMGKTRIIA
 ETGAGQHGT TALACALMGL ECVVYMGAKD VARQQPNVYR MQLHGAKVIP VESGSGTLKD
 AVNEALRDWT ATFHESHYLL GTPAGPHFPF TIVREFHKVI SEEAKAQMLE RTGKLPDVVV
 ACVGGGSNAI GMFADFIDDE GVELVGAEPA GEGLDGSKHG ATITNGQIGI LHGTRSYLMR
 NSDGQVEESY SISAGLDYFG VGPQHAHLHA TGRATYVGIT DAEALQAFQY LARYEGIIPA
 LESSHAFAYA LKRAKTAEV

>RXN00957 TRANSLATE of: rxn00957.seq check: 8921 from: 1 to: 1554
 MSTNPHVFSL DVRYHEDASA LFAHLGGTTA DDAALLESAD ITTKNGISSL AVLKSSVRIT
 CTGNTVVTQP LTDSGRAVVA RLTQQLGQYN TAENTFSFPA SDAVDERERL TAPSTIEVLR
 KLQFESGYSD ASLPLLMMGG AFDFLETFT LPAVEESVNT YPDYQFVLAE IVLDINHQQDQ
 TAKLAGVSNA PGELEAELNK LSLLIDAALP ATEHAYQTP HDGDTLRVVA DIPDAQFRTQ
 INELKENIYN GDIYQVVPAR TFTAPCPDAF AAYLQLRATN PSPYMFYIRG LNEGRSYELF
 GASPEENLKF TAANRELQY PIAGTRPRGL NPDGSINDEL DIRNELDMRT DAKETIAEHTM
 LVDLARNDLA RVSVPASRRV ADLLQVDYRS RVMHLVSRVT ATLDPELDAL DAYRACNMNG
 TLTGAPKLRA MELLRGVEKR RRGSYGGAVG YLRNGMDMDN CIVIRSAFVQ DGVAAVQAGA
 GVVRDSNPQS EADETLHKAY AVLNAIALAA GSTLEVIR

>RXN00969 TRANSLATE of: rxn00969.seq check: 5693 from: 1 to: 1335
 MTSASAPSFN PGKPGSAVG IALLGFGTVG TEVMRLMTEY GDELAHRIGG PLEVRGIAVS
 DISKPREGVA PELLTEDAFA LIEREDVDIV VEVIGGIEYP REVVLAALKA GKS SVTANKA
 LVAAHSAELA DAAEAANVDL YFEAAVACAI PVVGPLRRSL AGDQIQSVMG IVNGTTNFIL
 DAMDSTGADY ADSLAEATRL GYAEADPTAN VEGHDAASKA AILACIAFHT RVTADDVYCE
 GIRNINAADI EAAQQAGHTI KLLAICEKFT NKEGKSAISA RVHPTLLPVS HPLASVNKSF
 NAIFVEAEAA GRIMFYNGA GGAPTASAVL GDVVGAARNK VHGGRAPGES TYANLPIADF
 GETTTRYHLD MDVEDRVGVL AELASLFSEQ GISLRTIRQE ERDDDARLIV VTHSAESDL
 SRTVELLKAK PVVKAINSVI RLERD

>RXN01026 TRANSLATE of: rxn01026.seq check: 8609 from: 1 to: 1659
 MTSPVENSTS TEKLTAEKV WRDHVVSKE NGEPDLLYID LQLLHEVTSP QAFDGLRMTG
 RKLRLPELHL ATEDHNPTE GIKTGSLEI NDKISRLQVS TLRDNCEEFV VRLHPMGDVR
 QGIVHTVGPQ LGATQPGMTI VCGDSHTSTH GAFGSMAGFI GTSEVEHVMA TQTLPLKPFK
 TMAIEVTGEL QPGVSSKDLI LAIIAKIGTG GGQGYVLEYR GEAIRKMSMD ARMTMCNMSI
 EAGARAGMIA PDQTTFDYVE GREMAPKGAD WDEAVAYWKT LPTDEGATFD KVVEIDGSAL
 TPFITWGTNP GQGLPLGESV PSPEDFTNDN DKA AEKALQ YMDLVPGTPL RDIKIDTVFL
 GSCTNARIED LQIAADILKG HKIADGMRMM VVPSSTWIKQ EAEALGLDKI FTDAGAEWRT
 AGCSMCLGMN PDQLKPGERS AFTSNRNFEG RQGPGRTHL VSPAVAAATE SADPVLTCRY
 LRKARKQWKN LPPTPALAFH CSDPTWTPTR SSQPSTSSAS PGPASKTDCF PTGAKTTPTL
 SSTPTPTRTA PFS

>RXN01027 TRANSLATE of: rxn01027.seq check: 2562 from: 1 to: 1008
 MANKNNKPHE VDKDQDSAML INGRLLQIPA RPTTEFTRPT LAAGAVLWRG DITNPDSEIV
 AVIHRPHYDD WSLAKGKVDG GESIPTTAAR EILEETGYDI RLKGLIGKVT YPVLDRTKVV
 YYWTAQVLGG EFVPNDEVDE IRWLSVDEAC ELLSYQVDTE VLAKAAKRFR TPSTTRVLYV
 RHAAHGRQT WGGDDNKRL DKKGRRQAEM LVPMLLPFKP TAIYSAVPDR CQATALPLAD
 ELGLDVSVNR LFGDDAWETD PEACKKRFTD VVAQGGVPMI VGQGDIIPEM IKWFSENGTL
 PIDEKIKAKK GSVVLSFHD GVFTGADYLA SSLPVK

>RXN01079 TRANSLATE of: rxn01079.seq check: 5671 from: 1 to: 2103
MDFHALNALL NLYDDNGKIQ FEKDREANQ YFLQHVNT VFFHNLQEKI DYLVENKYYD
PIVLDKYDFQ FIKDLFKRAY GFKFRFQSFL GAYKYYTSYT LKTFDGRRYL ERFEDRVCMV
ALTLDAGDRA LAENLVDEIM SGRFQPATPT FLNSGKAQRG EPVSCFLLRI EDNMESIGRS
INSALQLSKR GGGVALLLSN LREAGAPIKK IENQSSGVIP VMKLLEDAFS YANQLGARQG
AGAVYLNAAH PDILSFLDTK RENADEKIRI KTLISLGVVIP DITFELAKRN DDMYLFSPYD
VERIYGKPPFA DVSITEHYDE MVDDDRIRKT KINARQFFQT LAEIQFESGY PYIMYEDTVN
ASNPIEGRIT HSNLCSEILQ VSTPSEFNDD LTYAEVGEDI SCNLGSLNVA MAMDAPNFEK
TIETEIRGLT AVPEQTSIDS VPSIRKNEA AHAIGLGQMN LHGYFGREHM HYGSEEALDF
TNAYFAAVLY QCLRASNQIA TERGERFKNF ENSKYATGEY FDDFDANDFA PKSDKVKELF
AKSNIHTPTV EDWAALKADV MEHGLFNRNL QAVPPTGSIS YINNSTSSIH PIASKIEIRK
EGKIGRVYYP APHMDNDNLE YFEDAYEIGY EKIIDTYAVA TKYVDQGLSL TLFFKDTATT
RDINRAQIYA WRKGIKTLYY IRLRQVALEG TEVDGCVSCM L

>RXN01095 TRANSLATE of: rxn01095.seq check: 7184 from: 1 to: 783
MVATENRMLM EIAAEISARE ATLGFEVKT KRSRAGLTAA FDIASVFFSS GCNVVAVFDR
FASNWDHSD HVDYAAQVAG FGASMLAYTV RRGQFDTAVR DIRDIKSEVD IPILLHDPPI
DPYQIHEARV MGIDALQFPV WAMEQARLES LVDRTESLGM TAIVSVRNHE EAHRAVDAGA
TVVAIDITGY TGSLLTPEAF SGITQFMPKE VARIVLGGCS SPKELMRFA HSADAIFVPH
ADLATTKSLV TAGMHPACPS R

>RXN01104 TRANSLATE of: rxn01104.seq check: 5920 from: 1 to: 606
MTVAPRIGTA TRTTSESDIT VEINLDGTGK VDIDTGLPFF DHMLTAFGVH GSFDLKVHAK
GDIEIDAHHT VEDTAIVLGQ ALLDAIGDKK GIRRFASCQL PMDEALVESV VDISGRPYFV
ISGEPDHMIT SVIGGHYATV INEHFFETLA LNSRITLHVI CHYGRDPHHI TEAEYKAVAR
ALRGAVEMDP RQTGIPSTKG AL

>RXN01115 TRANSLATE of: rxn01115.seq check: 5062 from: 1 to: 753
MAILHSVSYG TSDNTLVFIG SLGSTTDMWL PQLDALHKDF RVIAVDHRGH GLSELIEGTP
TVADLAQDVL DTLDDLGVGN FGVIGLSLGG AVAQYLAATS DRVTKAAFMC TAAKFGEPPG
WLDRAAACRE NGTGSLSSEAV IQRWFSPTWL ENNPASREHF EAMVAGTPSE GYALCCEALA
TWDFTDRLGE ITVPVLTIAG ADDPSTPPAT VQIIADGVGG ESRAEVLSPA AHVPTVERPN
EVNELLAQHF A

>RXN01116 TRANSLATE of: rxn01116.seq check: 6039 from: 1 to: 612
MAARVAQELE DGQYVNLGIG MPTLIPGYLP EGLEVILHSE NGVLGVGPYP TEEELDPELI
NAGKETITVA PGASYFSSD SFAMIRSKSV DVAVLGVMEV SQYGDLANWM IPGKLVKGMG
GAMDLVHGAS KIIAMTDHIT KKGAPKILKE CRLPLTGAKC VDMIVTTHAV FSVDPPEGLT
LIECADGVTV EELREITEAD FKVA

>RXN01127 TRANSLATE of: rxn01127.seq check: 8381 from: 1 to: 1020
MKLAVIGGDG IGPEVTAEAL KVLNAVRDDI ETDDYDLGAR RYLKNGELLT DEDLASLREH
DAILLGAIGA PGSVPPGILE RGLLLKMRFA LDHHVNLRPS KLYDGVESPL RNPBKIDFV
VREGTEGAYT GNGGAIRVGT PHEIANETSV NTRYGAERVI RYAFELAQSR RKKLTLVHKT
NVLVHGGGLW QRTVDEVAKE YPEVAVDYNH IDAATIYLVLT DPSRFDVIVT DNLFGDILTD
EAGAVSGGIG LAASGNIDAT GTNPSMFEPV HGSAPDIAGQ GIADPTAAIL SAAMLLRHLG
DEDNAVRIET AIAADVAGRD NSQPISTTEV GDRIVKALQS

>RXN01162 TRANSLATE of: rxn01162.seq check: 4305 from: 1 to: 1326
MYIVGICLQL VVMSQPMSAP DSAPGTERGH ERTHEAVVGD SQDPAQATAP RAPAESITLI
GIGTDGFEGE GLKAQQALQR ASVVIGSWRQ LNLVPDAIKA ERRPWPGNTK HPDLDFLKE
FLGRHVAVLA SGDPLFYGVG TAMVHVLGMD RLTVIPGPSS ASLACARLGW TVNRTRVYL
GQEPITLIP IIESGAQFLV LGKDEFSTAQ VATLLNELGL GETPLTVLSD LGSTDEEITQ
GTASHPPAAV SVLNVIAGVA RTAMPKPHFE GDVSNEDLRA LTVAALEPTQ GQMLWTFGDI
GAALACDWLR AAGNKAHAIS FASMVEQSQR NARKLGVSTL SVKETLSPKT LKDIRYVQGP
ESASPHAIFM NKGLGIDLVP ETAWMMLRPG GKLIQAQSTE DNIAKLHTLQ EQHGIIKHI
RIDDTDVHQW RVTKPVTPEA VN

>RXN01209 TRANSLATE of: rxn01209.seq check: 6515 from: 1 to: 1428
MCERPEKYVT DFSLYLVTDV VLGGGPKKVA GIVDSAISGG VSVVQLRDN SGVEDVRAAA

KELKELCDAR GVALVVNDYL DIAVELGLHL HIGQGDTPYT QARELLPAHL ELGLSIENLD
 QLHAVIAQCA ETGVALPDVI GIGPVASTAT KPDAAPALGV EGIAEIAAVA QDHGIASVAI
 GGVGLRNAAE LAATPIDGLC VVSEIMTAAN PAAAATRLRT AFQPTFSPET QTELSQTELQ
 GAFVNSPSAP RVLISIAGTDP TGGAGIQADL KSIAAGGGYG MCVVTSVLAQ NTHGVNTIHT
 PPLTFLEEQL EAVFSDVTV DAIKLGMLGSA DTVDLVASWL GSHEHGPVVL DPVMIATSGD
 RLLDASAEES LRRLAVHVDV VTPNIPELAV LCDSAPAITM DEAIQAQGF ARTHDTIVIV
 KGGHLTGALA DNAVVRPDGS VFQVENLRVN TTNSHGTGCS LSASLATKIA AGESVE

>RXN01239 TRANSLATE of: rxn01239.seq check: 4668 from: 1 to: 2433
 MARPISATYR LQMRGPQADS AGRSFGFAQA KAQLPYLKKL GISHLYLSPI FTAMPDSNHG
 YDVIDPTTIN EELGGMEGLR DLAAATHELK MGIIIDIVPN HLGVAVPHLN PWWWDVLKNG
 KDSAFEFYFD IDWHEDNMSG GKLGMPIGGA EGDEDKLEFA ELDGEKVLKY FDHLFPIAPG
 TEEGTPQEVY KRQHYRLQFW RDGVINFRRF FSVNTLAGIR QEDPLVFEHT HRLRLRELVAE
 DLIDGVRVDH PDGLSDPFY LHRLRDLIGP DRWLIIEKIL SVDEPLDPRL AVDGTGTYDA
 LRELDGVFIS RESEDKFSML ALTHSGSTWD ERALKSTEE LKRVVAQQL AAEILRLARA
 MRRDNFSTAG TNVTEDKLSE TIELVAAMP VYRADIYLS RTTATVIAEM SKRFPSRRDA
 LDLIAAALLG NGEAKIRFAQ VCGAVMAKGV EDTTFYRASR LVALQEVGGA PGRFGVSAAE
 FHLLQEERSL LWPRTMTTLS THDTKRGEDT RARIISLSEV PDMYSELVNR VFAVLPAAPDG
 ATGSFLLQNL LGVWPADGVI TDALRDRFRE YALKAIREAS TKTTWVDPNE SFEAAVCDWV
 EALFDGPSTS LITEFVSHIN RGSVQISLGR KLLQMVGAGI PDTYQGTEFL EDSLVDPNR
 RFVDYTAREQ VLERLQWAW TQVNSVEDLV DNADIAKMAV VHKSLELRAE FRASFVGGDH
 QAVFGEGRAE SHIMGIARGT DRNHLNIIAL ATRRPLIED RGGWYDTTVP LPGGQWEDRL
 TGQRFSGVVP ATDLFSLHPV SLLVLVPDSE F

>RXN01240 TRANSLATE of: rxn01240.seq check: 5900 from: 1 to: 1023
 MSDNTLSQFG SYHEFRRAH PMADVEFLLA IEELLTDGGV TFDRVTTRIK EWSSLKAKAR
 KRRNDGSLIY PDPRKDIHDM IGVRITTYHS TEIPVALKVL QDSFIVHKS DKAETRISG
 GFGYGSHELLI LEVDDTSDDL QDYKGLVFEV QVRTVLQHAW AEFEHDIRYK RADVSNPEDF
 SAEVDRMFTL AAGLIELADQ QFDQIAALKE TSRVADESVE LTAETLPGVL AMLIGNRFRP
 PRSTNYRFE DILVANSITS VVQLRELLNP TDIEVLLKVM NYRFHPPGQIR IIDLLLLKRF
 GQSHIDATVA TDSQPLNAKR HRQLKRLKLEL MTQAHLVEPP N

>RXN01304 TRANSLATE of: rxn01304.seq check: 600 from: 1 to: 486
 MPAQNKNLPG SVIVVSDRIK SGERIDKAGP VAVDLLQESG VEISTFTVVE EGFEPVHQEL
 VKALARRDRV IITIGGTGVG PRNRTPEATE PHIDTLLPGL MTQILFSGLS NTAQAGLSRG
 LVGLSARDST AALIVNAPSS SGGVRDALGV VCPLFGSIFE RL

>RXN01321 TRANSLATE of: rxn01321.seq check: 6043 from: 1 to: 921
 MQRMPSSPE VRNRPSAAPE ERQFVLTEGC PDSTGIVAKL SSFLAERGGW ITEAGYFTDP
 DSNWFFTRQA IRAESIDTTI EQLREEFAPL AEEFGPRAKW SFTDTAQVKK AVLLVSKEGH
 CLHDLLGRVA ENDYPMEVVA VVGHNENLRY IAENHNVPFF HVPFPKDAVG KRKAQDQVAE
 IVNGYDPDAI VLARFMQILP PDLCEMWAGR VLNIHHSFLP SFMGARPYHQ AYSRGVKLIG
 ATCHYATGDL DDGPIIEQDV IRVTHKDTPT EMQRLGRDAE KQVLARGLRF HLEDRLVYG
 NRTVVFD

>RXN01413 TRANSLATE of: rxn01413.seq check: 5704 from: 1 to: 600
 LTHLFLELDE RLVLGVQQDG YQWTEHLFRL PLQHLRNSPN DLQGLKIRWC ELYSTTGKDQ
 GVLELLPQATV VTPNNFEAST LSGLEKLETV EDLKEAARLI YEQGPQYVVV KGGMDFPGEN
 AVDLVFDGSS YHVFSEPKIG EERVSGAVCT FAAVITAELA KGAEVVDPA TAKRVVTRAV
 QDAVASNAPF TSVWLAEDNK

>RXN01420 TRANSLATE of: rxn01420.seq check: 1274 from: 1 to: 942
 VTLGGLNVPS WSLGAEMLFY LTFPLFIPLV RKVKGVGNWW AFGITFAVSL ALITVIHFYA
 DGPKGIENFF VPRLWDTNVS PVAEVHADPV WFMQEEIPVL ESYWLSYYFP LTRLIEFYLG
 VFGAKLVAEG MFKNTNITIP LIALAVSFVA TWFVPLAFKM SVIMSLPMAF VVATLAVRDI
 EGKSGEIASP RAVLLGNISF AFYMVQFPVM VFVQRYFIAG KEYGFLGWAF YAVVCFIVSV
 ILAWVLFTFV DDPLMKATAR KKGSRRLKQS NILVRDLKVL FGKSPEKPLK VETRAENLTE
 NSEAPAKVAT GIKS

>RXN01488 TRANSLATE of: rxn01488.seq check: 8876 from: 1 to: 948
 MSKKAILDID TGIDDALALA YALGSPELEL IGVTTTTYGNV LLETGAVNDL ALLDLFGAPE

VPVYLGEPAH QTKDGFEEVLE ISAFIHGQNG IGEVELPASE SKALPGAVDF LIDSVNTHGD
 DLVIIATGPM TNLAAIAKD PSFASKAHVV IMGGALTVPG NVSTWAEANI NQDPDAANDL
 FRSGADVMTI GLDVTLQTLT TKKHTAQWRE LGTPAAIALA DMTDYIKAY ETTAPHLGGC
 GLHDPLAVGV AVDPSLVTLT PINLKVDIEG ETRGRTIGDE VRLNDPVRTS RAAVAVDVDR
 FLSEFMTRIG RVAAQQ

>RXN01560 TRANSLATE of: rxn01560.seq check: 2973 from: 1 to: 330
 VGVSYIIAGD EQLDMAEAVR KIGETFKTEE IILGGGGTLN WSMLRDGLCD EVSIVMMPIA
 DGEKHTHSLF EADEKYSAPL PIGFSLASVE PLEDGSVWMR YGVNGPVDAN

>RXN01617 TRANSLATE of: rxn01617.seq check: 7053 from: 1 to: 672
 LILKTTGITV LSRFDAQVIA NQIEAATAAH DLDVVKIGML GTPATIDTVA TALEENSFKH
 VVLDPVCLICK GQEPGAALDT DTALRAKVL P QATVVTNNF EATTLSGLDK LETIDDLKEA
 ARLIHEQGPQ YVVVKGGIDF PGDNAVDVLF DGTDYHVFSE PKIGDERVSG AGCTFAAVIT
 AELAKGNSAV DAVTTAKRVV TRAVKDAVAS NAPFTSVWLA EDNK

>RXN01657 TRANSLATE of: rxn01657.seq check: 7845 from: 1 to: 600
 VIVGVLALQG GVEEHLTALE ALGATTRKVR VPKDLGLGEG IVIPGGESTV LDKLARTFDV
 VEPLANLIRD GLPVFATCAG LIYLAKHLDN PARGQOTLAV VDVVVRNNAF GAQRESFDTT
 VDVSFDGATF PGVQASFIRA PIVTAFGPTV EAIAALNGGE VVGVRQGNII ALSFHPEETG
 DYRIHQAWLD LVRKHAELAI

>RXN01690 TRANSLATE of: rxn01690.seq check: 7996 from: 1 to: 1101
 MTSLEFTVTR TENPTSPDRL KEILAAPKFG KFFTDHMTI DWNESEGWHN AQLVPYAPIP
 MDPATTVFHY GQAFEGIKA YRHSDETIKT FRPDENAERM QRSARMAMP QLPTEDFIKA
 LELLVDADQD WVPEYGGAS LYLRFPMIST EIGLGVSPAD AYKFLVIASP VGAYFTGGIK
 PVS VWLSEYD VRAAPGGTGD AKFAGNYAAS LLAQSQAEEK GCDQVWVWLD IEHKYIEEMG
 GMNLGFIYRN GDQVKLVTP E LSGSLLPGIT RKSLLQVARD LGYEVEERKI TTTEWEEDAK
 SGAMTEAFAC GTAAVITPVG TVKSAHGTFE VNNNEVGEIT MKLRETTLTI QQGNVEDQNG
 WLYPLVG

>RXN01698 TRANSLATE of: rxn01698.seq check: 9592 from: 1 to: 1230
 MLGMLRWTTA GESHGQALIA TVEHMPAGVP VTKDEVSYQL ARRLGYGRG ARMKFEQDAL
 TFLTGIHRLG TLGSPISIMI GNTWDKWTI IMSSDALDME DPNVAAMSS GRGAKLTRPR
 PGHADIYAGML KYGFDDARNV LERSSARETA ARVAAATVAR SFLRETGLVE VLSHVISIGA
 SEPYTGAEPT FADIQAIDDS PVRAFCKDAE ESMIAEIEAA KKAGDTLGGI VEVIVEGLPI
 GLGSHISGED RLDAQIAAAL MGIQAIKVE IGDGFEEARR RGSEAHDEVF LDDNGVYRNT
 NRAGGLEGGM TNGETLRVRA GMKPISTVPR ALKTIDMENG KAATGIHQRS DVCAPPAAGV
 VAEAMVTLVL ARAVLQKFGG DSLSETKSN DTYLKNIEER MKFEGLEDGA

>RXN01712 TRANSLATE of: rxn01712.seq check: 1222 from: 1 to: 696
 MVDILELIGP LPFVSTPELR AIVVTAINGS TTINGTSGQL GNSTDTELL ALRRWSDVVL
 VGSSTVKAEN YGGVEVSPEI QKQRELQGE AIPPIAVMSG SLNFDVDTRF FLEAEVPII
 ITDSDQAKQ QRLVDAGA QV IEVETLTAEV GVEKLRLSLGY ARIDCEGGAT LYQMLAADL
 VD VWHHTIDP TLGSGVERPT VKGGDDAPRR FALEHVFVDD DSTLFLRYKR AK

>RXN01810 TRANSLATE of: rxn01810.seq check: 7446 from: 1 to: 1077
 MNNAFRRTL SVVLAASLAL TACASWDSPT ASSNGDLIE IQASSTSTDP RTFTGLSIVE
 DIGDVVPVTD NASPALPVSL TDADGNDVVV ENVSRIPLD LYGTYSKTIA GLGLVDNIVG
 RTVSSTEPAL ADIEVVTGG HTLNAEAILN LHPTLVIIH SIGPREVIDQ IRAAGVATVI
 MSPQRSIASI GDDIRDIASV VGLPEEGEKL AERSVAEVEE ASTVVDLTP EDPLKMFVLY
 ARGTTGGVFFI LGDAYGGRDL IEGLGGVDMA AEKGIMDLAP ANAEALAE LN PDVFVMMSEG
 LVSTGGIDGL MERPGIAQTT AGQNQRVLAL PDGQSLAFGA QTGELLRLAS RELYVQGG

>RXN01892 TRANSLATE of: rxn01892.seq check: 2496 from: 1 to: 729
 VTTSSQPRRT GYKRVMLKLG GEMFGGKVG VDPDVVDNVA RQIAEVAKTG AEIADVIGGG
 NFFRGAEQQ RGMDRARS DY MGLGTVMNC LALQDFLGQH GVECRVQTAI NMAQVAEPYL
 PLRAERHLEK GRVIFGAGM GMPYFSTDTT AAQRALEIGC DVLLMAKAVD GVSDDPRTN
 PDAELFTEIT PKEVIEKGLK VADATAFSLC MDNKMPILVF NLLTEGNIAR AISGERIGTL
 VES

>RXN01920 TRANSLATE of: rxn01920.seq check: 452 from: 1 to: 1002
 MAADSDLSVH DAYLKEHVAP VKAINWNSIP DSKDLEVWDR LTGNFWLPEK VPVSNDIKSW
 GTLNEVEKAA TMRVFTGLTL LDTIQGTGVA ISLLPDADSL HEEAVLTNIA FMESVHAKSY
 SNIFMTLAST AEINDAFRWS EENENLQKKA KIILSYEGD DPLKRKIASV ILESFLFYSG
 FYLPMYWSSH SKLANTADVI RLIIRDEAVH GYYIGYKYQK AVAKETPERQ EELKEYTFDL
 LYDLYDNETQ YSEDLYDDLG WTEDVKRFLR YNANKALNNL GYEGFLPADE TKVSPNILSA
 LSPNADENHD FFSGSGSSYV IGKAENTEDD DWDF

>RXN01929 TRANSLATE of: rxn01929.seq check: 5174 from: 1 to: 813
 MPMSGIDAKK ITRHFREK VNGQKVSILT SYDALSARIF DEAGVDMMLV GDSAANVVLG
 RDTTSLITLD EMIVLAKAVT IATKRALVVV DLPFGTYEVS PNQAVESAIR VMRETGAAAV
 KIEGGVEIAQ TIRRIVDAGI PVVGHIGYTP QSEHSLGGHV VQGRGASSGK LIADARALEQ
 AGAFVAVLEM VPAAEAAREVT EDLSITTIGI GAGNGTDGQV LVWQDAFGLN RGKKPRFVRE
 YATLGDSLHD AAQAYIADIH AGTFPGEAES F

>RXN01940 TRANSLATE of: rxn01940.seq check: 4990 from: 1 to: 936
 MTTKIILDCD PGHDDAVAML LAAGSPEIEL LGITTVGGNQ TLDKVTHTNTQ VVATIADINA
 PIYRGVTRPL VRPVEVAEDI HGDTGMEIHK YELPEPTKQV EDTHAVDFII DTIMNNEPGS
 VALVPTGPLT NIALAVRKEP RIAERVKEVV LMGGGYHVGN WTAVAEFNIK IDPEAAHIVF
 NEKWPLTMVG LDLTHQALAT PEIEAKFNEL GTDVADEFVVA LFDADRKNYQ DAQGFDPNPV
 HDPCAVAYLV DPTVFTTRKA PLDVELYGAL TTGMTVADFR APAPADCTTQ VAVDLDFDKF
 WNMVIDAVKR IG

>RXN02008 TRANSLATE of: rxn02008.seq check: 2069 from: 1 to: 1134
 VYAAIGVVHS LFNALPGRFK DYISAPRFGV YQSLHTTVMG PGGKPLEVQA RTHDMHYNAE
 FGIAAHWRYK ETKGSHSGEQ AEVDQMAWMM QLLDWQKEAA DPNEFLDSL RYDLTSKQIFV
 FTPKGDVVNL PVNSTPVDFE YAVHTEVGHR CIGAKINGKL VALETCLKSG DRVEVFTSKD
 QNAGPSRGWQ EFVVSAPRAK KIRQWFAKER REEYLEAGRD ALAAVIQRGG LPMHRLFTAS
 SMKTVALETH YPDVDALYTA IGSGSVSAQH VVNRLMAIFG DEEDAEDALV ARTPFSELVN
 SRATTESSTG ILVEGSPDVM AKLAKCCMPV PGDEIFGFVT RGGGVSVHRT DCTNVEKLKE
 EPERIVSVSW ASEQQGSV

>RXN02027 TRANSLATE of: rxn02027.seq check: 4731 from: 1 to: 501
 MSQTKQELRT KLREARTNMD EASRTRENA IIANVSYYIR SKQPKRIIAY VPVRTEPGGR
 LLLDALHAET SALILPVSLE DRRLDWALYE GPTSLVPGAF GIQEPGGTRL GPEALNFCDL
 VIAPALACTP SGIRLGKGGG FYDRALATGV KADVITLLFN GEIRDDI

>RXN02085 TRANSLATE of: rxn02085.seq check: 9107 from: 1 to: 2235
 MTSNFSSTVA GLPRIGAKRE LKFALEGYWN GSIEGRELAQ TARQLVNTAS DSLSGLDSVP
 FAGRSYYDAM LDAAAILGVL PERFDIADH ENDGLPLWID RYFGAARGTE TLPAQAMTKW
 FDTNYHYLVP ELSADTRFVL DASALIEDLR CQQVRGVNAR PVLVGPLTFL SLARTTDGSN
 PLDHLPALFE VYERLIKSF DTEWVQIDEP LVTDVAVEVL EQVRAGYTTL AKRDGVFVNT
 YFGSGDQALN TLAGIGLGAI GVDLVTHGVT ELAAWKGEEL LVAGIVDGRN IWRTDLCAAL
 ASLKRLAARG PIAVSTSCSL LHVPYTLAE NIEPEVRDWL AFGSEKITEV KLLADALAGN
 IDAAAFDAAS AAIASRRSTP RTAPITQELP GRSRGSFDTR VTLQEKSL ELPLTTTIGS
 FPQTPSIRSA RARLRKESIT LEQYEEAMRE EIDLVIKQE ELGLDVLVHG EPERNDMVQY
 FSELDDGFLS TANGWVQSYG SRCVRPPVLF GNVSRPAPMT VKWFQYASL TQKHVKGMLT
 GPVTILAWSF VRDDQPLATT ADQVALALRD EINDLIEAGA KIIQVDEPAI RELLPLRDVD
 KPAYLQWSVD SFRLATAGAP DDVQIHTHMC YSEFNEVISS VIALDADVTT IEAARSMDQV
 LAALKSSGFE LGVGPVWDI HSPRVPSAQK VDGLLEAALQ SVDPRQLWVN PDCGLKTRGW
 PEVEASLKV L VESAKQAREK IGATI

>RXN02153 TRANSLATE of: rxn02153.seq check: 56 from: 1 to: 780
 MIMHNVYGV TTIKVAIAGA SGYAGGEILR LLLGHAPAYAS GELEIGALTA ASTAGSTLGE
 LMPHIPQLAD RVIQDTTAE LAGHDVVFLG LPHGFSAEIA LQLGPDVTVI DCAADFRLQN
 AADWEKFYGS EHQTWPYGI PEMPGHREAL RGAKRVAVPG CFPTGATLAL LPAVQAGLIE
 PDVSVVSITG VSGAGKKASV ALLGSETMGS LKAYNTSGKH RHTPEIAQNL GEVSDKPVKV
 SFTPLAPLP REFSPLQPHL

>RXN02154 TRANSLATE of: rxn02154.seq check: 6613 from: 1 to: 291
 LKEGVTAEQ RAVYEEFYAQ ETFVHVLPEG AQPQTQAVLG SNMCHVQVEI DEEAGKVLVT

SAIDNLTGKT AGAAVQCMNL SVGFDEAAGL PQVGVAP

>RXN02162 TRANSLATE of: rxn02162.seq check: 5865 from: 1 to: 1431
 MEQHGHTNEGA LWGGRFSGGP SEAMFALSVS THFDWVLAPY DVLASKAHAK VLHQADLLSD
 EDLATMLAGL DQLGKDADG TFGPLPSDED VHGMERGV DRVGPEVGGR LRAGRSRNDQ
 VATLFRMWVR DAVRDIALGT TELVDALSAQ AKAHAGAIMP GKTHFQAAQP VLLAHQLLAH
 AQPLLRDIDR IRDLKRLAV SPYSGALAG SSLKLNPEAI AEELGFDSAA DNSIDATSSR
 DFASETAFLV AQLAVDMSRL AEEIIAWCTP EFGYITLSDS WSTGSSIMPQ KKNPDVAELT
 RGKSGRLIGN LTGLLATLKA QPLAYNRDLQ EDKEPIVDSV AQLNLLLPAM TGLVSTLTFFN
 TERMRELAPA GFTLATDLAE WMVRQGVPPR EAHEASGACV RIAESRGVDL IDLTDEELSG
 VDARLTPEVR EVLTIDGAVA SRATRGGTAG VRVAEQRARV DAASTAHAEW ARAGVRR

>RXN02198 TRANSLATE of: rxn02198.seq check: 9108 from: 1 to: 2499
 MSTSVTSPAH NNAHSSEFLD ALANHVLIGD GAMGTQLQGF DLDVEKDFLD LEGCNEILND
 TRPDVLRQIH RAYFEAGADL VETNTFGCNL PNLADYDIAD RCRELAYKGT AVAREVADEM
 GPGRNGMRRF VVGSLGPGTK LPSLGHPYA DLRGHYKEAA LGIIDGGGDA FLIETAQDLL
 QVKAHVHGVQ DAMAELDTFL PIICHVTVET TGTMLMGSEI GAALTALQPL GIDMIGLNCA
 TGPDEMSEHL RYLSKHADIP VSVMPNAGLP VLKNGAEYP LEAEDLAQAL AGFVSEYGLS
 MVGCCGCTTP EHIRAVRDV VGVPEQETST LTKIPAGPVE QASREVEKED SVASLYTSVP
 LSQETGISMI GERTNSNGSK AFREAMLSGD WEKCVDIKQ QTRDGAHMLD LCVDYVGRDG
 TADMATLAAL LATSSTLPIM IDSTEPEVIR TGLEHLGGRS IVNSVNFEDG DGPESTRYQRI
 MKLVKQHGAA VVALTIDEEG QARTAEHKVR IAKRLIDDIIT GSYGLDIKDI VVDCLTFPIS
 TGQEETRRDG IETIEAIREL KKLYPEIHTT LGLSNISFGL NPAARQVLNS VFLNECIEAG
 LDSAIAHSSK ILPMNRIDDR QREVALDMVY DRRTEDYDPL QEFMQLFEGV SAADAKDARA
 EQLAAMPLFE RLAQRIIDGD KNGLEDDLEA GMKEKSPIAI INEDLLNGMK TVGELFGSGQ
 MQLPFVLQSA ETMKTAVAYL EPFMEEEAEA TGSAQAEGKG KIVVATVKGD VHDIGKNLVD
 IILSNNGYDV VNLGIKQPLS AMLEAAEEHK ADVIGMSGLL VKSTVVMKQT ISD

>RXN02234 TRANSLATE of: rxn02234.seq check: 4131 from: 1 to: 3339
 MPKRSDINH LVIGSGPIVI GOACEFDYSG TQACRVLKEE GLRVTLINSN PATIMTDPEM
 ADHTYVEPIE PEYIDKIFAK EIEQGHPIA VLATLGGQTA LNAAIQDLRL GILEKYGVEL
 IGADIDAIER GEDRQKFEDI VTTIGGESAR SRVCHNMEEV HETVAELGLP VVVRPSFTMG
 GLGSGLAYNT EDLERIAGGG LAASPEANVL IEESILGWKE FELELMRDTA DNVVVICSIE
 NVDALGVHTG DSVTVAPALT LTDREFQKMR DQGIAIIREV GVDTGCCNIQ FAINPVDGRI
 ITIEMNPRVS RSSALASKAT GFPIAKMAAK LAIGYTLDEI TNDITGETPA AFEPTIDYVV
 VKAPRFAFEK FVGADDTLTT TMKSVGEVMS LGRNYIAALN KALRSLETKQ QGFWTKPDEF
 FAGERATDKA AVLEDLKRPT EGRLYDVELA MRLGASVEEL YEASSIDPWF LAELEALVQF
 RQKLVDAPFL NEDLLREAKE MGLSDLQIAA LRPEFAGEDG VRTLRLSLGI RPVFKTVDTCT
 AAEEFEAKTPY HYSAYELDPA AESEVAPQTE REKVLILGSG PNRIGQGIEF DYSCVHAAL
 LSRVGYETVM VNCNPETVST DYDTADRLYF EPLTFEDVME VYHAEASGT VAGVIVQLGG
 QTPLGLADRL KKAGVPVIGT SPEAIDMAED RGEFGALLNR EQLPAPAFGT ATSFEEARTV
 ADEISYPVLV RPSYVLGGRG MEIVYDEASL EDYINRATEL SSDHPVLVDR FLDNAIEIDV
 DALCDGDEVY LAGVMEHIEE AGIHSGDSAC ALPPMTLGAQ DIEKVREATK KLALGIGVQG
 LMNVQYALKD DILYVIEANP RASRTVPFVS KATGVNLAKA ASRIAVGATI KDLQDEGMIP
 TEYDGGSLPL DAPIAVKEAV LPPNRFRRPD GKTLDTLLSP EMKSTGEVMG LANNFGAAYA
 KAEAGAFGAL PTEGTVFVTV ANRDKRTLIL PIQRLALMGY KILATEGTAG MLRRNGIECE
 VVLKASDIRE GVEGKSIVDR IREGEVDLIL NTPAGSAGAR HDGYDIRAAA VTVGVPLITT
 VQGVTAAVQG IEALREGVVS VRALQELDHA VKA

>RXN02246 TRANSLATE of: rxn02246.seq check: 1512 from: 1 to: 984
 MDVAHALDLA HHVSDQVRGT TSPNPPVGAV ILDADGEVVG VGATAPPGGP HAEVVALAAA
 GVRANGGTAV VTLEPCNHYG RTGPCSKALL DAGIAHVFFA NADPFPSAAG GGAFLAEAGV
 DTHFLDERIR ALEPWLAVTR LGRPHVTLKF ASTVDGFAGA TDGTSQWITG PDARAFVHED
 RSKRDAIIVG TGTALTDNPS LTARTDTGLY ENQPRRVVIG SREVPADSNL ARLGYEQYAG
 IPEALSALWD KGCARDILIEG GPTLAGAALR LGIVDQVQAY VAPALLGAGR SVINWPQETT
 MDQIMRFDTT SVRQLGSDVL IEMMRKEH

>RXN02248 TRANSLATE of: rxn02248.seq check: 4306 from: 1 to: 1266
 VSEHEQAHSQ LDSVEEAIAD IAAGKAVVVV DDEDRENEGD IIFAAELATP ELVAFMVRYS
 SGYICAPLTA KDADRLDLPP MTAHNQDARG TAYTVTV DAN TGTTGISATD RAHTLRLLAD
 PEADRTDFTR PGHVPLRLAR EGGVLVRAGH TEAAVDLARA AGLRPAGVIC EVVSEEDPTG

MARVPELRRF CDEHDLKLIS IEQLIEWRRK NEILVERQVE TVLPTDFGTF KAVGYRSIID
 GTELVAVIAG DVASDGGENV LVRVHSECLT GDVFGSRRCD CGQQ LHESLR LIQEAGRGVV
 VYMRGHEGRG IGLLAKLRAY QLQDEGADTV DANLALGLPA DAREFGTSAQ ILYDLGVRSL
 NLISNNPAKK VGLEGHGISI ASRTPIPVAV HEDNVRYLKT KRDRMGHDLP DVALWEQEHF
 EN

>RXN02249 TRANSLATE of: rxn02249.seq check: 5182 from: 1 to: 477
 MAKEGLPAVE LPDASGLKVA VVTARWNAEI CDRLHKHAVD AGRAAGATVS EYRVIGALEL
 PVVVQELART HDAVVALGCV VRGGTPHFDY VCDVTEGLT RIALDTSTPI GNGVLTNTTE
 EQAVERSNGE GSVEDKGAEA MVAALDTALV LSQIRATEG

>RXN02263 TRANSLATE of: rxn02263.seq check: 627 from: 1 to: 378
 MKIAVIGLGS TGSMALWHLN NIPGVEAIGF EQFGISHGYG AFTGESRLFR MAYHEGSTYV
 PLLKRARALW SSLSEISGRE LFHNFGVLST GKEDEAPFQR LVESVERYEL PHERLTAAQM
 RSVTQV

>RXN02272 TRANSLATE of: rxn02272.seq check: 3652 from: 1 to: 1245
 VRITNAQVKN YAEVLDTITIE GEKISSITPS SIRSEEDHRA DDYDAAGRLV APQFAEAIH
 LDYANTAGIP RENSSGTLFE AIEIWADRKT QGFHIKEDIK AKALQAARRA AEHGVGFIRT
 HVDVTDPTFA GFEAIAELRD EVREWCIDIQI VAFPPQNGIYA YEGGQKLISD AMSAGADVVG
 GIPHLEPTRD DGVESVKWLF DLAEKHSAPI DIHTDEIDDP HSRFVEVLAA EAAKRDMAQ
 TVVSHSVAMA YYSPGYMARL LPKLAASKVR FAVCPNENLH LQGLGFQGPV PRGVAPVKQL
 TEWGIPVSFC QDSLNDPFYP MGDGDLRLIL DSGLHVSHML TASHLKNALS FITTNPAGNL
 GLDNYDIAEN SPANLLVLDA SSEKEAVQRK ASVLLSIHRG KKVLSREPEQ VDWNI

>RXN02281 TRANSLATE of: rxn02281.seq check: 6251 from: 1 to: 1431
 VQKDSVVRME ATTIDDAIAK LIDIYDTSTK LAKETLNNED YAAYADVVP KLTVDVLEWK
 PIDRTEPFY VDRAGRYSAT LSKPRVIERY LREQLERLTS NYPCKIYVSE SDIRIPPEYI
 RGAPSATEAR RAGDVADIIP RPTLDEVHDA IIDGDWHAFN GPPLPLFHFG PQRFDIACAR
 IEHYTGINVE HVQKYILFTN YAMHTTEFVH FAMELTSED SRYVGLSLPN GQVIDRETAT
 SLGTETLDLT SRFQMPRYDL ITEAGDGITI INIGVGPSNA KTITDCLAVL RPEAWVMIGH
 CAGMDARMRI GDLILGNAYQ REDHILNTRI PLGNPIPAIP EIQALEASEV DEIYGSDNSL
 MRTGTVLSTD DRNWEWHTPE NLWNWLKGST AAAMDMESS LATNGYRFRI PYGTLLSVSD
 LPLHAVPKLS AQAQAFYFNS KEAHVMCAVR AMEYLAVDPE RLRTKLRLRT LGEVPFR

>RXN02345 TRANSLATE of: rxn02345.seq check: 1896 from: 1 to: 1197
 VTSTGNQAHV PGMPIVAVIG DGQLARMMQT SAIELGQSLR VLAGAPDSSA AQVAADVVLG
 DYTNIIDLRV AIEGADVMTF DHEHVPNEHL HQLIAEGVNV QPRPEALVNA QDKLVMRKRL
 RELGAPVPPF AAIESVEDAV GFFEAVDQOV CLKARRGGYD GKGWVFPADV AELQSLVAEL
 LDGGTPLMAE KKVALNRELS AMVARTPSGE TKAWPVVESV QKNGVCAEAI APAPELSAEL
 QESTRGLAQK IATELGVTGV LAVELFETLD QNGQPEIFVN ELAMRSHNTG HWTQDGCVTS
 QFEQHLRAVL DYPLGATDTL ADYTVMANVL GADTDPEMPM ATRMVEVGRK YPDAKIHLYG
 KGRHPGRKIG HVNMVGSDEL KTRAEALACA YFLVNARWD

>RXN02350 TRANSLATE of: rxn02350.seq check: 8700 from: 1 to: 495
 VGPLVGLIMG SDSWDVTAP AAEVLAEFGI PFEVGVVSAH RTPEKMLNYA KTAHERGIKT
 IIACAGGAAH LPGMVAAATP LPVIGVPRAL KDLDGLDSSL SIVQMPGGVP VATVSIGGAK
 NAGLLAVRIL GAGDPSLVTK MADYQENMAK EVEAKDEALK KRLLG

>RXN02355 TRANSLATE of: rxn02355.seq check: 2794 from: 1 to: 732
 MSSISRKTGA SLAATTLAA IALAGCSSDS SSDSTDSTAS EGADSRGPIT FAMGKNDTDK
 VIPIIDRWNE AHPDEQVTIN ELAGEADAQR ETLVQSLQAG NSDYDVMALD VIWTADFAAN
 QWLAPLEGDL EVDTSGLLQS TVDSATYNGT LYALPQNTNG QLLFRNTEII PEAPANWADL
 VESCTLAEEA GVDCLTTQLK QYEGLSVNTI GFIEGWGGSV LDDDGKRHRH QHDGKAGLQA
 LVDG

>RXN02382 TRANSLATE of: rxn02382.seq check: 5059 from: 1 to: 1296
 MSSTLTDDQ IRDNERTVL AKATAAKNIV PDIAVLGTGP KNAILRAAAD ELVARSAEII
 EANASDIEAG RANGMEESMI DRLALDESRI EGIAGGLRQV AGLTDPVGEV LRGHVMENGI
 QMKQVRVPLG VMGMVYEAP NVTVDAFGLA LKSGNVALLR GSSTAVHSNT KLVEILQDVL
 ERFELPRETV QLLPCQTRGS VQDLITARGV VDVVIPRGA GLINAVVTGA TVPTIETGTG

NCHFYIDAEA KLDQAIAMVI NGKTRRC SVC NATETALLDA ALSDSCLKAV VQALQEAGVT
 IHGRVAELEA FGATDVVEAT ETDWDSEYLS FDIHAVVVDG VDGALAHIAK YSTKHTEAIA
 TQNIETAQRF ADRVDAAAVM INASTAYTDG EQYMGAEIG ISTQKLHARG PMALPELTST
 KWILQGTGQI RP

>RXN02384 TRANSLATE of: rxn02384.seq check: 8362 from: 1 to: 708
 VTRRLILLRH GQTEYNATSR MQGQLDTELS DLGFQQAASA ASVLVQKNIT HVFSSDLSRA
 FNTASAVAAL IDAEVRVDKR LRETHLGEWQ AKTHTEVDSE YPGARAQWRH DPQWAPPGGE
 SRVDVARRAR QVVDELMVSL DDWDEGTVLI VAHGGTINAL TSNLLDLAYD QYPMFSGLGN
 TCWAQLTARP RYYAGSENPE DDLKISSAVS NSPHFEGNNV ENAQWYLDGW NMGVTO

>RXN02503 TRANSLATE of: rxn02503.seq check: 7437 from: 1 to: 399
 MTLKIGTRGS KLATTQAGTI RDQLKHYGRD AELHIVTTPG DVNMSPVERI GVGVTQALR
 DVLHSGECDV AVHSMKDLPT ATDPRFHLVV PTRADSREAL IARDGLTLAE LPERRKGGNF
 RSSTHLP AQG NPP

>RXN02504 TRANSLATE of: rxn02504.seq check: 8 from: 1 to: 558
 VGTSAPRRIS QLKAIAPDLE ILPLRGNI DT GMGKVTSGEL DAVMLAYAGL TRVGMQDRAT
 EVFDADIIMP APAQGALAI E CRADDTETVR ALNMLMHADT FVSVAERTV LNRLEAGCTA
 PVAAHATLDG YSGDTMTLTA GUYALDGS DQ LVFSAEGDGA RPEELGELVA QQLIDAGAN
 LLGDRS

>RXN02648 TRANSLATE of: rxn02648.seq check: 6219 from: 1 to: 1203
 MSQNRIRTH VGSLPRTP EL LDANIKRSNG EIGEEFFQI LQSSVDDVIK RQVDLGIDIL
 NEGEYGHVTS GAVDFGAWWN YSFTRLGGLT MTDTDRWASQ EAVRSTPGNI ELTSFSDRRD
 RALFSEAYED PVSGIFTGRA SVGNPEFTGP ITYIQEETQ TDVDLLKKGM NAAGATDGFV
 AALSPGSAAR LTNKFYDTDE EVVAACADAL SQEYKIITDA GLTVQLDAPD LAEAWDQINP
 EPSVKDYLDW IGTRIDAINS AVKGLPKEQT RLHICWGSWH GPHVTDIPFG DIIGEILRAE
 VGGFSFEGAS PRHAHEWRVW EENKLPEGSV IYPGVVSHSI NAVEHPRLVA DRIVQFAKLV
 GPENVIASD CGLGGRLLHSQ IAWAKLESLV EGARIASKEL F

>RXN02754 TRANSLATE of: rxn02754.seq check: 5967 from: 1 to: 1338
 VNTNPSEFSS NRSTALLTDK YELTMLQAAL ADGSAERPST FEVFSRRLPN ERRYGVVAGT
 ARVLKAIRDF VFTEEQLADL DFLDDRTLEY LRNYRFTGQV DGYREGEIYF PQSPLLTVRG
 TFAECVILET VILSIMNADS AVASAAARMV TAADGRPIIE MGSRRTHEYS AVTASRAAYL
 AGFSTTSNLE AAYRYGIPAS GTSAAHAWTLL HINDDGT PNE AAAFKAQVES LGVDTTLLVD
 TYDITQGVAT AIEVAGPDLG GVRIDSGDLG VLARKVRKQL DDLNAHNTKI VVSSDLDEFA
 IAGLRGEPVD VFGVGTSVVT GSGAPTAGLV YKIGEVAGHP VAKRSRNKES YGGGKKAVRT
 HRKSGTAIEE IVYPFNAEAP DTGKLDLTL SL TIPLMRDGEI VPGLPTLEDS RAYLAKQLVS
 LPWEGLLALS DEPVLHTRFV GFPPAA

>RXN02758 TRANSLATE of: rxn02758.seq check: 5860 from: 1 to: 1299
 VTELIQNESQEI AELEAGQQVALREGYLP AVITVSGKDRPGVTAAFFRVLSANQVQVLDV
 EQSMFRGFLNLAA FVGIAPERVETVTTGLTDTLKVHGQSVVVELQETVQSSRPRSSHVVV
 VLGDVPDALDISRIGQTLADYDANIDTIRGISDYPVTGLELKVTPDVSPGGGEAMRKAL
 AALTSELNVDIAIERSGLLRSKRLVCFDCDSTLITGEVIEMLAAHAGKEAEVA AVTERA
 MRGELDFEESLRERVKALAGLDASVIDEVA AAIELTPGARTTIRTLNRMGYQTAVVSGGF
 IQVLEGLAEELDYVRANTLEIVDGKLTGNVTGKIVDRAAKAEFLREFAADSGLKMYQT
 VAVGDGANDIDMLS AAGLGVA FNAPALKEIADTSVNHPFLDEV LHIMGISRDEIDLADQ
 EDGTFHRVPLTNA

>RXN02772 TRANSLATE of: rxn02772.seq check: 845 from: 1 to: 1035
 MSLERNQKS SMGVRMSAR LARSLTGNRV RTNPVLDPLL SIHRQFHPRA DVQVLERAYD
 TAERLHDGVI RKSGDPYITH PLAVATIAAE IGMDDTTTLVA ALLHDTVEDT DYSLDDLTRD
 FGEEVARLVD GVTKLKVAL GAAAEAE TIR KMIVAMSQDP RVLVIKVADR LHNMRMTMRL
 PPEKQAKKAR QTLEVIAPLA HRLGMASVKW ELEDLSFAIL YPKKYEEIVR LVADRAPS RD
 RYLKEIIDQV TGGLRENNIA AEVLGRPKHY WSIYQKMIVR GRDFDDIFDL VGIRILVDNV
 NNCVRRHR CR ALPVQCSAWP IQRLYFSPAL RCLPIPAHHR DGTWR

>RXN02802 TRANSLATE of: rxn02802.seq check: 8099 from: 1 to: 1071
 VKNLDIARYR RQIMLGEIGQ QKQQSLF DAK VSVIGAGGLG SPALLYLAGA GVGHIHIIDD

DLVDLSNLHR QVIHTTAGVG TPKAESAREA MLALNPSVKV TVSVRRLDWS NALSELADSD
 VILDGSDNFD TRHLASWAAA KLGIPHVWAS ILGFDAQLSV FHAGHGPIYE DLFPPTPPPG
 SVSPCSQAGV LGPVVGVMGS AMAMEALKII TGVGTPLIGK LGYSSLDGT WEYIPVVGSP
 EVLERVLGSA GVSIGSGGFG EVLDVPRVSA LVDGVSLIDV REPSEFSAYS IPGAHNTPLS
 AIREGAIPPS VSAGKEVIVY CAAGVRSQA IAILESAGYT GMSSLDGGIE GWLDSLG

>RXN02909 TRANSLATE of: rxn02909.seq check: 3255 from: 1 to: 486
 MNRARIATIG VLPLALLAS CGSDTVEMTD STWLVTNIYT DPDESNSISN LVISQPSLDF
 GNSSLSGFTG CVPFTGRAEF FQNGEQSSVL DADYVTLSSL DFDKLPDDCQ GQELKVHNEL
 VDLLPGSFEEI SRTSGSEILL TSDVDELDRP AIRLVSWIAP TS

>RXN02912 TRANSLATE of: rxn02912.seq check: 8900 from: 1 to: 753
 VTSPELQNIL NNYWSGRAEA YHLNQTQSER AQFERPIWEK VWSKALPIVS EEAVKVLDLG
 CGAGYVTHLL SDCGYETIGV DGSEEMINQA TQENGLRRST GRATAIFQVG DAHDPEFREG
 SFDAITSRVY LWTLLDPQAA INRWVSLKP GGVIACVDAA WYPKGIDAGT EVDSVDGPSA
 FVETYPPELL RNLPMSTTST GHNFAELFHN AGLKEVTLTP IEGLAELDQR FGLSPGHST
 PQFLFRGIKS S

>RXN02918 TRANSLATE of: rxn02918.seq check: 9454 from: 1 to: 441
 MSEILETYWA PHFGKTEEAT ALVSYLAQAS GDPIEVHTLF GDLGLDGLSG NYTDTEIDGY
 GDAFLLVAAL SVLMAENKAT GGVNLGELGG ADKSIRLHVE SKENTQINTA LKYFALSPED
 HAAADRDEED DLSELANLSE ELRGQLD

>RXN02965 TRANSLATE of: rxn02965.seq check: 5418 from: 1 to: 591
 MEKFTTYTGV GVPLQRSNVD TDQIIPAVYL KRVTRTGFED GLFSNWRQND PNFVLNTDTY
 KNGSVLVAGP DFGTGSSREH AVWALMDYGF RAVFSSRFAD IFRGNSGKAG MLTGIMEQSD
 IELLWKLMEQ TPGLLTVNL EKQIVTAGDV VISFEVDPYI RWRLMEGLDD AGLTLRKLDE
 IEDYEAKRPA FKPRNA

>RXN02970 TRANSLATE of: rxn02970.seq check: 6259 from: 1 to: 1368
 LALKGYTNFD GEFIEFGSVQ AKEEEKRAFD NDRAHVFWHSW SAQDKISPKV WAAAEGSTLY
 DFDGNAFIDM GSQLVSANLG HNNPRLVEAI QRQAARLTNI NPAFGNDVRS DVAAKIVSMA
 RGEFHVFFFT NGGADAIEHS IRMARLHTGR NKILSAYRSY HGATGSAMML TGEHRRLGNP
 TTDPDIYHFW APFLHSSFF ATTQEEECER ALKHLEDVIA FEGAGMIAAI VLEPVVGSSG
 IILPPAGYLN GVRELCNKHG ILFIADVMV GFGRTGKLFA YEHAGDDFQP DMITFAKGVN
 AGYAPLGGIV MTQSIRDFTG SEAYSGGLTY SGHPLAVAPA KAALEIYAEG EIIPRVARLG
 AELIEPRLRE LAEENVAIAD VRGIGFFWAV EFNADATAMA AGAAEFKERG VWPMISGNRF
 HIAPPLTTTD DELVALLDAV EAAAQAVELT FAGALF

>RXN03003 TRANSLATE of: rxn03003.seq check: 6068 from: 1 to: 675
 MTSRTPLVSV LPDFPWDSLA SAKAKAASHP DGIVNLSVGT PVDPVAPSIQ IALAEAAGFS
 GYPQTIGTPE LRRAIRGALE RRYNMTKLVD ASLLPVVGTK EAIALLPFAL GISGTVVIPE
 IAYPTYEVAV VAAGCTVLRS DSLFKLGPQI PSMMFINSPS NPTGKVLGIP HLRKVVKWQAQ
 ENNVILAADE CYLGLGWDE NPPISILDPR VCDGDHTNLI AIHSL

>RXN03004 TRANSLATE of: rxn03004.seq check: 4340 from: 1 to: 480
 VLLSDRDIRK SIDAGDLGIE PFDAELIQPS SVDVRMDRYF RVFNNSKYTH IDPKLNQDEL
 TSLVEVEDGE GFVLHPGEFV LASTLEKFTL PAHLAGRLEG KSSLGRLGLL THSTAGFIDP
 GFSGYITLLEL SNVANLPITL WPGMKVGQLA LFQMSSPAET

>RXN03007 TRANSLATE of: rxn03007.seq check: 3470 from: 1 to: 369
 MTSPTLKV L NAYLDNPTPT LEEAIEVFTP LTVGEYDDVH IAALLATIRT RGEQFADIAG
 AAKAFLAAAR PFPITGAGLL DSAGTGGDGA NTINITTGAS LIAASGGVKL VKHGNRSVSS
 KSG

>RXN03058 TRANSLATE of: rxn03058.seq check: 2459 from: 1 to: 483
 VSKLKGSRSL LDVSGDHSF ADLAGRQVAH VDVVDPLINT TFEFQPTQS YDAITFIASL
 HHMNAEEGLN KAVRILNPGG KLLIVGLAKN KTASDWIISG LQAFLSRPIS LINREQQIYP
 FPTKEPSESL HEIRQLTKQL LPHRRIRRG I HFRYLLEWTK P

>RXN03063 TRANSLATE of: rxn03063.seq check: 3919 from: 1 to: 1032
VEDLSYRIPQ SRTVAEQVPG PKSKALDERR QAAVARALAP GLPGYVVDAD GGILADADGN
RFIDLASGIA VTTVGGSNAA VAKAVGAAAA RFTHTCFMVS PYETYVAMAE RLNALTPGDH
DKKSALFNSG AEAVENAVKV ARAYTGKGAV VVFDNAYHGR TNLTAMAMTAK NRPYKSGFGP
LAADVYRAPM SYPLRDGLSG PEAAERAISV IESQVGAENL ACVVIEPIQG EGGFIVPAPG
FLAAISTWCR ENDVVFIAD EIQSGFLRTGD WFASDAEGVI PDVITTAKGI AGGMPLSAVT
GRAEIMDAPG PGALGGTYGG NPVACAAALA AIEVMEQADL KTRA

>RXN03074 TRANSLATE of: rxn03074.seq check: 6105 from: 1 to: 498
MTQSAPEFIA TADLVDIIGD NAQSCDTQFQ NLGGATEFHG IITTVKCFQD NALLKSILSE
DNPGGVLVLD GDASVHTALV GDIIAGLGKD HGWSGVIVNG AIRDSAVIGT MTFGCKALGT
NPRKSTKTGS GERDVVVSIG GIDFIPGHYV YADSDGIIVT EAPIKQ

>RXN03105 TRANSLATE of: rxn03105.seq check: 7399 from: 1 to: 435
LILPVQEGIS YFPTPLHLNH IGGSRLSAHV EDEDLRLDRD AVSEFGRKTH ELFPQVNPEP
NRFSVHYDTY TADKSPIIDA VDNVIVLTGG SGHAFKLSPA YGELAAQRAV GNTSPLYSED
FRIASHEPIK ERCTYRKLTF LSARF

>RXN03114 TRANSLATE of: rxn03114.seq check: 9278 from: 1 to: 552
TPGHFVALAR EIAGAVRREL TVGLDAGDGP ILRQSFVGVF LLVDASFHIIH INGVSTGQSV
APDDVVEVVR GLADASELSV ESVAELCTPV APVSLSEAQG NPAPIGWLEH DGVSLSGAGI
PGGRVEARLA RFIAVIEAET TITPWNLSII HDLYEGVAEQ VVKVLAPMGL VFDANSPLLE
SPAL

>RXN03137 TRANSLATE of: rxn03137.seq check: 1609 from: 1 to: 102
LELNKAAYMF EYSFDDITVS GYDPHPLIRG KVAV

>RXN03171 TRANSLATE of: rxn03171.seq check: 5756 from: 1 to: 513
MDITIVNHPL VASRLTLLRD ERSDNAAFRA AANDLGAMLI YEASRDLEVE HFDTKTPVAM
AEGTRLKQPP IIVPIIRAGL GMIDPALSMI PDAQVGFIGL ARDEETHEPV PYLEALPQDL
SNQPVFLVDP MLATGGSL LH AIRLLADRG A TDITAICMVS AQPQVDALAE S

>RXN03176 TRANSLATE of: rxn03176.seq check: 4586 from: 1 to: 861
ELADYIPELK SADPNPLAVA LCTVNGHIYS AGDDDIEFTM QSISKPFAYA LALQECGFDE
VSASVALEPS GEAFNELSLD GENRPMNPMI NAGAIINQL INGSdstVED RVEKIRHYFS
ELAGRELtid RVLAESLAG ADRNLSIAHM LRNYGVIEDE AHDAVLSYTL QCAIKVTTRD
LAVMTATLAA GGTHPITGKK LLDARVCRLT LSVMASAGMY DEAGQWLSTV GIPAKSGVAG
GLIGILPGQL GIATFSPRLN PKGNSVRGVK IFKQLSDDMG LHLMSTE

>RXS00116 TRANSLATE of: RXS00116.seq check: 3330 from: 1 to: 1161
MSNDFVVSRLRPFGETIFATMTQRAVEAGAINLGQGFPEDEGPRRMLEIASEQILGGNNQYSAGRGDAS
LRAAVARDHLERFDLEYNPDSEVLITVGATEAITATVGLVEPGDEVIVLEPYDAYAAIALAGATRV
AVPLQEVENSVDVDVKLHAAVTKKTRMI IVNSPHNPTGSVFSKKALKQLAGVARAYDLLVLSDEVYEH
LVFDDQKHVSVAKLPGMWDRTVTVSSAAKTENVTGWKTGWALAPEPLLEAVLKAKQFMSYVGATPFQPA
VAHAIEHEQKWVSKMSKGLELKRDLRTALDKAGLKTHDSMGTYFIVADIGDRDGAEFCELIKVGVA
AIPVQAFVDHPKKWSSKVRFAFCKKEETLREAAERLKGIKKL

>RXS00147 TRANSLATE of: RXS00147.seq check: 7603 from: 1 to: 1179
VSKDTTTYQGVTEIGSVPAYLVLDGRFTFTGFGGAIGTTLGEAVFTTAMTGYQETMTDPSYHRQIVVA
TAPQIGNTGWNDEDNESRDGKIWVAGLVIRDLAARVSNWRATTSLQOEMAGQGIVGIGGIDTRALVRHL
RNEGSIAAGIFSGADAQRPEELVEIVKNQAMPATGANLSVEVSADETYVIEAEGEERHTVVAYDLGIKQ
NTPRRFSARGVRTVIVPAETPFEDIKQYNPSGVFISNGPGDPAAADVMVDIVREVLEADIPFGICFGN
QILGRAFGMETYKLFKFGHRGINVPVKNHITGKIDITAQNHGFAKGEAGQEFETDFGTAVTHTCLNDG
VVEGIALKSGRAYSVQYHPEAAAGPNDASPLFDQFVELMDADAQKKA

>RXS00349 TRANSLATE of: RXS00349.seq check: 102 from: 1 to: 1467
MLSFATLRGRISTVDAAKAAPPSPLAPIDLTDSQVAGVMNLAARIGDILLSSGTSNSDTKVQVRAVT
SAYGLYYTHVDITLNTITIFTNIGVERKMPVNVFHVVGKLDTNFSKLSEVDRLIRSIQAGATPPEVAEK
ILDELEQSPASYGFPVALLGWAMMGAVAVLLGGGWQVSLIAFITAFITIIATTSFLGKKGLPTFFQNVV
GGFIATLPASIAYSALALQFGLKIPSQIIASGIVVLLAGLTLVQSLQDGITGAPVTASARFFETLLFTG

GIVAGVGLGIQLSEILHVMLPAMESAAAPNYSSTFARI IAGGVTAFAVGCYAEWSSVIIAGLTALMG
SAFYLLFVVYLGVPVSAIAATAVGFTGGLLARRFLIPPLIVAIAGITPMLPGLAIYRCMYATLNDQTL
MGFTNIAVALATASSLAAGVVLGEWIARRLRPPRFNPNYRAFTKANEFQEEAEQNQRQRKRPKTNQ
RFGNKR

>RXS00389 TRANSLATE of: RXS00389.seq check: 9029 from: 1 to: 1560
MITATALHGCSLIDGEWVAGKNGEITGFDPRTNASLNPSYSLANSAQLRAATTSAKRAFESYRLTTPPEV
RADFLDSIADNIDALSGEIVQRASLETGLGTTTLTGEVARTSNQLRLFAETVRSQGQFHRVRIERGPRID
LRQRQVPLGPVAVFGASNFPVAFSTAGGDTASALAAGCPVVFKAHNAHPGTAEVLGQAVRGAVEKHEFD
AGVFNLVYGRGVEIGQELAADPNITAIGFTGSRQGGALSLQTAFSRPVPVPVFAEMSATNPVVFPGAL
ADLDASSSLAEFTASVTGSSGQLCTKPGLVFI PRGVVGDFAFVALVAAKFKETTGQTMLTQGIQAQWQR
GVDNLAAQPSVKILAQGT PGDGENAPGPVVFESDVQALLNNVVLQEEIFGAASLVVRYDSPDQLHQVAN
SLEGQLTATI HASQDDFQEVSKLIPLLEDLAGRVLYGGWPTGVEVGHTVIHGGPYPATSNQSTSVGTL
AIERFMRPVSYQTFPAELLDPDVSEANKWAVPREIDR

>RXS00391 TRANSLATE of: RXS00391.seq check: 5340 from: 1 to: 720
LLRDSQRVGLAIDPSIALVMATSGSTGTPKGAQLTPLNLVSSADATHQFLGGEGQWLLAMPAHHIAGMQ
VLLRSLIAGVEPLAIDLSTGFHIDAFAGAAELKNTGDRVYTSLTQMQLLKAMDSLQIEALKLFDVIL
VGGAALSKQARISAEQLDINIVTTYGSSETSGGCVDGKPIPGAKVRISDERIELGGPMIAQGYRNAPE
HPDFANEGWFTTSDSGELHDGILTVTGRVDTRH

>RXS00393 TRANSLATE of: RXS00393.seq check: 4530 from: 1 to: 894
MSHTEPQPNSVTLSDWIQGARPRTWANAFAPVIAGSGVAAFHDGFVWWKALLALVVAWALIIGVNYAND
YSDGIRGTDEDRTGPLRLTGSGLAEPKKVKAASFISFGIAGVAGTALSLLSAWWLILIGILCVLGAWFY
TGGKNPYGYRGLGEIAVFIFFGLVAVMGTQFTQTGTSVSWAGLAAVGVGMSAGVNLANNIRDIPTDSK
TGKITLAVRLGDAGARKLFLALISTPFIMSICLAFVAPALIAIIVFPLALKAAAGPIRNNATGKDILPV
IGSTGRAMALWAVLTGLALAFS

>RXS00405 TRANSLATE of: RXS00405.seq check: 4870 from: 1 to: 513
MPKYDNSNADQWGFETRSHAGQSVDAQTSARNLPIYQSTAFVFDSEAHAKQRFALDLPVYSRLTNP
TVEALENRIASLEGGVHAVAFSSQAATTNAILNLAGAGDHIVTSRPLYGGTETLFLITLNLRLGIDVSF
VENPDDPESWQAAVQPNTKAFFGETFANPQADV

>RXS00419 TRANSLATE of: RXS00419.seq check: 8218 from: 1 to: 759
MLNAVGAQNILLGGTSEIGISIVSRFLKQGPGSHVTLAARKDSPRVDAVAEIKAGAASVAVVDFDA
LDTESHPAAIDAAFENGDDVDAIVAFAFGILGDNEAQWRDQALAVEATTVNYTAGVSVGVLLGQKFEQQGH
GTIVALSSVAGQVRRSNFVYGSAGAGFDGFTYQLGEALRGSGANVLVVRPGQVVRTKMSADGGEAPLTV
NREDVADAVYDAVVNKKDIIIFVHPLFQYVSFAFQFIPRAIFRKLPF

>RXS00446 TRANSLATE of: RXS00446.seq check: 3948 from: 1 to: 864
MGAVELREALAEHLEVEFDQVTVGCGSSALCQQLVQATCAQGDEVIFPWSFEAYPIFAQVAGATPVAI
PLTADQNHDLDAMAAAITDKTRLIFICNPNNSGTTITQAQFDNFMEKVPNDVVVGLDEAYFEFNRAAD
TPVATEEIIHRHDNVI GLRTFSKAYGLAGLRVGYAFGNAEIIAAMNKVAIPFAVNSAAQAAALASLNSAD
ELMERVEETVEKRDVAVSALGAAPTQANFVWLPGEGAELAALAEHGIVIRAFPEGARISVTNAEETD
KLLRAWEAINAG

>RXS00618 TRANSLATE of: RXS00618.seq check: 4181 from: 1 to: 1107
MQMLDRVHRRRREGKDTLMFCAGQPSTGAPEAVIEEAEIALRSGPLGYTEVIGDREFRERIADWHSATY
DVDTPNDNVIVTTGSSGGFVASFIATLDHGDYVAMPTPGYPAYRNILESLGAKVLNLRCTAETRFQPTA
QMLEELPHKPKAVIVTSPGNPTGTIIDPEELERIAKWCDNDNAVLISDEDYHGMSFGRPLATAHQFSKN
AIVVGTLSKYFSMTGWRVWGWIIVPDELVTPIENLQASLSLCPAIGQAAGRAAFTLEAGAELEDAHVEAY
REAREVFVDKLPEIGLGTADPDGGLYLWVDVSAYTDDSEEWALRLLD EAGVAVAPGVDFDPEEGHKWI
RLSLCASKEDTIEGVRKIGEFIKK

>RXS00838 TRANSLATE of: RXS00838.seq check: 1249 from: 1 to: 900
MKIAIVGAGAVGGYFGALLQESGADITMVARGRTLEALKSKGLHINDARGERYPPIPAVASVQELKDAD
VVMIAKALSRSRLDLAELLGGIPANSVVAITQNSIESADLAASKIGADRVWPGVVRGFFVHEGPASVSY
KGGPLSYTFGDSGELSROFASTLEQAGIDGVLHPDILVDVWEKAMFEVFGGLGAFVEKQLGTLRTHFR
ASLEALMEEVAEVARAAGVALPSDAVERTMNFADRMENSTSSMQRDLAAGVASELEAQTGAIVRAAHK
GVKTPHLHDLIYAGLKLKEEENSL

>RXS00870 TRANSLATE of: RXS00870.seq check: 4548 from: 1 to: 1512
MSEPQTISHWIDGAISPSTSGKTAPVYNPATGQVTANVALASQEEIDATIASATKAAKTWGNLSIAKRQ
AVLFNFRELLNARKGELAEIITAHEGKVLSDAMGEILRGQEVVELATGFPHLLKGAFNENVSTGIDVYS
LKQPLGVVGIIISPFNFPAMVPMWFFPIAIAAGNAVILKPSEKDPASALWMAQIWKEAGLPDGVFNVLQG
DKLAVDGLLNSPDVSAISFVGSTPIAKYIYETSAKNGKRVQALGGAKNHMLVLPDADLDLVADQAINAG
YGAAGERCMASVSVLAIESVADELIEKIKERIDTLRIGNGAGDEQGEPHLGLPLITDVHRDKVASVVDIA
EADGAKIIVDGRNCAVDGHEEGFFFGPTLIDDIPLTFRAYTEEIFGPVLSVVRVASFDEAIELINSGEF
GNGTAIFTNDGGAARRFQHEIEVGMIGINVPIPVVPVAYHSFGGWKNSLFGDAKAYGTQGFDFFTREKAI
TSRWLDPATHGGINLGFPPQND

>RXS00905 TRANSLATE of: RXS00905.seq check: 8965 from: 1 to: 801
MTQFENAQVLKENIENQREQIFTQLKEIVSFNSVHSDPNLLEDYAGAKEWVKETLTNAGLTVSEFAAED
GTTNFIGTRKRGSEGAPKVLVLYSHFDVVPSPGLDLWDTNPFELTERDAGHGTRWYGRGAADCKGNLVMHL
AALRAVEASGDTTLNLTYYVVEGSEEMGGGALSALIKDKPELFDADVILIADSGNASVGTPTLTTLTTLRG
GQVTVTVDTLEGAVHSGQNGGAAPDAVAALVRVLDTLRDEHGRTVIDGCQHHRKLEGRAL

>RXS00906 TRANSLATE of: RXS00906.seq check: 3597 from: 1 to: 504
MNTDAPLSTAVNTTANWKGEYPDPETFRSDAGILDGVDIMGDGDNPASMLWSRPAISITGFTSTPVAEA
LNAV PATASAKNLNRVPAGLEANDVAEKLKQHLINHTPWGAKITVEIDINQPFSTDITGPAMSTLASC
LSAAYEGKDLVTEGSGGSIPLCTELIEVNP

>RXS00907 TRANSLATE of: RXS00907.seq check: 9200 from: 1 to: 123
LALYGVEEPLTVIHSANESVDPNEIRDIATAEALFLLNYTK

>RXS00998 TRANSLATE of: RXS00998.seq check: 1808 from: 1 to: 462
MTSRDDQPQDLLSLAELAATRALTTDELEALNNANYGLDRNLGLRYTTIEPGRVVSSELHVASKHLQVVG
LVNGGVYAAIAESTGVSASMISAPGKMVVGINNTDFISAVSSGVIVAEATPIQLGGRTHLWQIECTHR
GEVVARTTLRTMVLNK

>RXS01105 TRANSLATE of: RXS01105.seq check: 6552 from: 1 to: 1098
MTKITLSDLPLREELRGEHAYGAPQLNVDIRLNTNENPYPPSEALVADLVATVDKIATELNRYPERDAV
ELRDELAAYITKQTGVAVTRDNLWAANGSNEILQQLLQAFGGPGRTALGFQPSYSMPILAKGTHTEFI
AVSRGADFRIDMDVALEEIRAKQPDIVFVTTNNPTGDTVSLDDVERIINVAPGIVIVDEAYAEFSPSP
SATTLLLEKYPTKLVVSRMTSKAFDFAGGRLGYFVANPAFIDAVMLVRLPYHLSALSQAAAI VALRHSAD
TLGTVEKLSVERVRVAARLEELGYAVVPSESNFVFFGDFSDQHAAWQAFLDRGVLIRDVGIAGHLRTTI
GVPEENDAFLDAAAEI IKLNL

>RXS01130 TRANSLATE of: RXS01130.seq check: 121 from: 1 to: 603
MDLARKLGLLAGKLVDAAPVSIEVEARGELSSEQVNALGLSAVRGLFSGIIEESVTFVNAPRIAEERGL
DISVKTNSSESVTHRSVLQVKVITGSGASATVVGALTGLERVEKITRINGRGLDLRAEGLNLFQYTDAP
GALGTVGTKLGAAGINIEAAALTQAEKGDGAVLILRVESAVSEELEAEINAELGATSFQVDLD

>RXS01145 TRANSLATE of: RXS01145.seq check: 748 from: 1 to: 1014
MAIELLYDADADLSLIQGRKVAIVGYGSQGHASQNLRDGVEVVIGLREGSKSAEKAKEAGFEVKTTA
EAAAWADVIMLLAPDTSQAEIFTNDIEPNLNAGDALLFGHGLNIHFDLIKPADDIIVGMVAPKGPGLHV
RRQFVDGKGVPCLIQVDQDPTGTQAALTSYAAAIGGARAGVIPTTFAETVTDLFGEQAVLCGGTEEL
VKVGFEVLTEAGYEPPEMAYFEVLHELKLIVDLMFEGGISNMNYSVSDTAEFGGYLSGPRVIDADTKSRM
KDILTDIQDGTFTKRLIANVENGNTLEGLRASYNHPIEETGAKLRDLMSWVKVDARAETA

>RXS01183 TRANSLATE of: RXS01183.seq check: 908 from: 1 to: 303
MAFSVEMPSELGESVTEGTITQWLKSVGDTVEVDEPLLEVSTDKVDTEIPSPVAGVILEIKAEDDTVDV
GGVIAIIGDADETPANEAPADEAPAPAEEEEP

>RXS01260 TRANSLATE of: RXS01260.seq check: 3260 from: 1 to: 1182
VTFNYEDAHKRSRGVSDKIVGGVHYLMKKNKIIEIHGLGNFKDAKTLEVTDGKDAGKTITFDDCIIATG
SVVNTLRGVDFSENVVSFEEQILNPVAPKKMVIVGAGAIMGEFAYVLGNYGVDVTVIEFMDRVLPNEDA
EVSKVIAKAYKKMGVKLLPGHATTAVRDNGDFVEVDYQKKGSDKTETLTVDVRVMVSVGFRPRVEGFGL
NTGVKLTERRGAIEIDDYMRNVDGIYAIGDVTAKLQLAHVAEAQGIVAAETIAGAETQTLGDYMMMPRA
TFCNPQVSSFGYTEEQAKEKWPDEIKVASFPFSANGKAVGLAETDGFAGKIVADADEFGLLGAHLVGN
ASELINELVLAQNWDLTTEEISRSVHIHPTLSEAVKEAAHGISHMINF

>RXS01261 TRANSLATE of: RXS01261.seq check: 5376 from: 1 to: 171
VTEHYDVVVLGAGPGGYVSARIAAQLGKKVAVIEKQYWGGVCLNVGCIPSKVSDQKR

>RXS01807 TRANSLATE of: RXS01807.seq check: 712 from: 1 to: 792
MPSAGEEILEQRAQLEFDQRRADVVMIGSQVYVGSVGLSAAIPVMHNEGLRVVAVPTVVLSSMPRYASS
HRQPMSDQWLADALQDLVDLGIIDEVSTISTGYFTSASQVRVVAWLQKIRETHPHVRIVVDPIMGDS
VGIYVADEIATAICQDLCLATGIIPNAFELSHMVSGDPRSLGPFGEWIIITSATETVGTTVTRIVT
RDSVQEIASATVDTTAKGAGDVYAAALIAALHKDFSLIDAASHASNTVCAGLQTKAL

>RXS02001 TRANSLATE of: RXS02001.seq check: 4280 from: 1 to: 1158
MPVINSIASFSDEMTRWRRHLHQNPEISFDCVETAFAEQLRSFGVDEIHTGIAKTGIIALIHGREAG
PVVGLRADMDALPLTEITGVYASTTPGKMHCAGHDGHTTMLGAAKYLAETRNFGTVALIFQPAEEN
GGGAGVMVDEGVLDRAFAIAEVYALHNQPLGLPHGFMTTAGPIMAADVDTFDINITGRGGHGAKPHQTRDP
IVAAGVIVQAFQTIIVSRNHNPNVEDLVSVTQIHTGSADNII PETAYINGTVRTFNKDVQAMVITRMEEI
VAGQAAAYGVEATLTYNRNYPATINDAAKAAIAAEVAGEVGLGVNPNGSRGMGAEDFSYFLEKRPAYL
FVGNGDSAGLHNPAYNFNDEAAPYGASFLARMAERPLPLKG

>RXS02021 TRANSLATE of: RXS02021.seq check: 9962 from: 1 to: 948
MSENIRGAQAVGIANIAMDGTILDTPWPEPQIFNPDQWAERYPLEVGTTRLGANELTPRMLQLVKLDQD
RLVEQVAVRTVIPDLSQPPVDAHDVYLRHLHLSHRLVRPHEMHMQNTLELLSDVWVTKGPCLPENFEW
VRGALRSRGLIHVYCVDRPLRMVDYVVPFGVRISEAERVRLGAYLAPGTSVLREGFVSFNSGTLGAAKV
EGRLLSSGVVIGEGSEIGLSSTIQSPREQRRRLPLSIGQNCNFGVSSGIIGVSLGDNCDIGNNIVLDGD
TPIWFAADEELRTIDSIEGQANWSIKRESGFHEPVARLKA

>RXS02101 TRANSLATE of: RXS02101.seq check: 3861 from: 1 to: 1263
MSRISELLNNHGVDLWSQEAAYQDFHEHPELSGFESSETADRIQKYLERFDCEVIPNVGGYGILAVFRNG
STDPGAPVALMRADFGLPVKEITGVPFSTRMRPHDGANVHVMHACGHDVHVTTALLGACAILDERRDA
WEGTFIALFPQSEENSQGANMKMVAGGLVDLIPRPDVCFGQHVVPGAAGTVMSMPGGALACDSIEIRIQ
GRSAHGSMPHNSIDPTYVAAMIVVRLQGVIGREVPEDFAVISVGTLSGNTNNTIPASARLVLCNCRFY
NDKVKKHVYRAIERVVRGECLASGIEEPVIEYFAHGDLTNNTPVVFDTVRPVDFDVFEDSIDAYRWT
ASEDFPSIPKAFNSPYLYWTIGVTPRDQWTEAVERDRVASDVPANHMGDFLPDYAPTMSAATRAAAAAL
LTYLGTN

>RXS02157 TRANSLATE of: RXS02157.seq check: 5341 from: 1 to: 1173
MSTLETWPQVIINTYGTTPVELVSGKGATVTDDQGNVYIDLLAGIAVNALGHAHPAIIIEAVTNQIGQLG
HVSNFLFASRPVVEVAEELIKRFSLLDATALAAQTRVFFCNSGAEANEAAFKIARLTGRSRILA AVHGFHG
RTMGSLALTGQPDKREAFPLMPSPGVFEFYPYGD TDYLRKMVETNPTDVA AIFLEPIQGETGVVPAPEGFL
KAVRELCDEY GILMITDEVQ TGVGRTGDFFAHQHDGVVPDVVTMAKGLGGGLPIGACLATGRAAELMTP
GKHGTTFGGNPVACAAAKAVLSVDDAFCAEVARKGELFKELLAKVDGVVDVRGRGLMLGVVLERDVAK
QAVLDGFKHGVILNAPADNIIRLTPPLVITDEEIA DAVKAI AETIA

>RXS02197 TRANSLATE of: RXS02197.seq check: 490 from: 1 to: 528
AERMRFSPRQQRGRFLCIADFIRPREQAVKDGQVDVMPFQLVTMGNPIADFANELFAANEYREYLEVH
GIGVQLTEALAEYWHSRVRSELKLNDDGGSVADFPEDKTKFFDL DYRGARFSFGYGSCPDLEDRAKLVE
LLEPGRIGVELSEELQLHPEQSTDAFVLYHPEAKYFNV

>RXS02234 TRANSLATE of: RXS02234.seq check: 4131 from: 1 to: 3339
MPKRSDINHVLVIGSGPIVIGQACEFDYSGTQACRVLKEEGLRVTLINSNPATIMTDPPEMADHTYVEPI
EPEYIDKIFAKEIEQGHPIDAVLATLGQTALNAAIQDLRLGILEKYGVELIGADIDA IERGEDRQKF
DIVTTIGGESARSRVCHNMEEVHETVAELGLPVVVRPSFTMGGLGSGLAYNTEDLERIAGGGLAASPEA
NVLIEESILGWKEFELELMRDTADNVVVICSIENVDALGVHTGDSVTVPALTLT DREFQKMRDQGIAI
IREVGVD TGGCNIQFAINPVDGR IIT IEMNPRVSRSSALASKATGFPIAKMAAKLAIGYTLDEITNDIT
GETPAAFEPTIDYVVKAPRFAFEKFVGADDTLT TTMKSVGEVMSLGRNYIAALNKALRSLETQKQGF
TKPDEFFAGERATDKAAVLEDLKRPTTEGRLYDVELAMRLGASVEELYEASSIDPWFLAELEALVQFRQK
LVDAPFLNEDLLREAKFMGLSDLQIAALRPEFAGEDGVRTLRLSLGIRPVFKTVDTCAA EF EAKTPYHY
SAYELDPAAESEVAPQTEREKVLILGSGPNRIGOGIEFDYSCVHALELSRVGYETVMVNCNPETVSTD
YDTADRLYFEPLTFEDVMEVYHAEAQSGTVAGVIVQELGGQTPGLGLADRLKKAGVPVIGTSPEAIDMAED
RGEFGALLNREQLPAPAFGTATSFEARTVADEISYPVLVRPSYVLGGRGMEIVYDEASLEDYINRATE
LSSDHPVLVDRFLDNAIEIDVDALCDGDEVYLAGVMEHIEEAGIHS GDSACALPPMTLGAQDIEKVREA
TKKLALGIGVQGLMNVQYALKDDILYVIEANPRASRTVPFVSKATGVNLAKAASRIAVGATIKDLQDEG
MIPTEYDGGSLPLDAPIAVKEAVLPFNRRFRPDGKTLDTLLSPMKSTGEVMGLANNFGAAYAKAEAGA

FGALPTEGTVFVTVANRDKRTLILPIQRLALMGYKILATEGTAGMLRRNGIECEVVLKASDIREGVEGK
SIVDRIREGVDLILNTPAGSAGARHDGYDIRAAAVTVGVPLITTVQGVTAADVQIEALREGVVSVRAL
QELDHAVKA

>RXS02262 TRANSLATE of: RXS02262.seq check: 7976 from: 1 to: 1146
MTATYTTTETAINFLFLSEPDMAAGVKDVAQCVDVMEETLVLLAQGDYKMAGLNSNSHGAMITFENPE
FEGMPKDGPDRRFMAMPAYLGGRFKNTGVKQWYGSNAENKASGLPRSIHTFVLNDTVTGAPKAISANLL
SAYRTGAVPGVGKHLAVADATTLAVVGPGVMAKTITEACIAERPGITTIIKIKRSEGINAFATWALE
KFPEIEVVAVGSEEDVVKDADIVIAATTTDAAGSSAFPYFKKEWLKPGALLLLPAAGRFDDAYLLDDAR
LVVDYMGLYEAWAEYGPQAYQLLGIPTGHWYDLALQGLDLAKISQIGDICSGLPGRTNDEEIIILYS
VGGMPVEDVAWATQVYENALEKGVGTTLNLWESPALA

>RXS02299 TRANSLATE of: RXS02299.seq check: 8495 from: 1 to: 408
MLRTILGSKIHRATVTQADLDYVGSVTIDADLVHAAGLIEGEKVAIVDITNGARLETYVIVGDAGTGN
CINGAAHLINPGDLVLIIMSYLQATDAEAKAYEPKIVHVDADNRIVALGNDLAEALPGSGLLTSRSI

>RXS02315 TRANSLATE of: RXS02315.seq check: 920 from: 1 to: 1629
MSSTPAQDLARAVIDSLAPHVTDVVLCPSRNSPLSLELLARQDLRVHVRIDERSASFLALSLARTQAR
PVAVVMTSGTAVANCLPAVAEAAHAHIPLIVLSADRPALHVGTVGASQTINQGTGIFGDLAPTGVITELDQ
VAQIAESLAQGASQIPRHFNLALDVPLVAPELPELHGEAVGASWTHRWINHGEVTVDLGEHTLVIAGDE
AWEVEGLEDDVPTIAEPTAPKPYNPVHPLAAEILLKEQVSAEGYVVNTRPDHVIIVVGHPTLHRGVKLMS
DPGIKLTVLSTRTDIITDPGRHADQVGSTVKVTGTQEKQWLKICSAASELAADGVRDVLNDQEFGFTGLH
VAAAVADTLGTGDTLFAAASNSIRDLVLGMPFDGVDTFSPRGVAGIDGSAQAIGTSLAVQSRHPDEI
RAPRTVALLGDLFLHDIGLLIGPDEPRPENLTIIVVSNNDGGGIFELLETGADGLRPNFERAFGTPHD
ASIADLCAGYGIEHQVVDNLQDLIIALVDTTEVSGFTIIEASTVRDTRRAQQQALMDTVH

>RXS02319 TRANSLATE of: RXS02319.seq check: 7220 from: 1 to: 957
MSNYSTDNPFDPQTQWATVPGFEEFTDITYHRHVGTTRADGIVRIAFDRPEVRNAFRPHTVDELYQALDH
ARRTPDVGTILLTGNGPSEKDGGAFCSSGQDQIRGRSGYQYATEHARDDATADVFTVDIARTKVEGGR
LHILEVQRLIRTPKVVIAVVGWAAAGGSHLVVCDLTIASRQEARFKQTDADVGSFDAGYGSAYLAK
MVGQKNAREIFFLGRTYDAERMQQMGAVNIVADHGDLEKEAIAQAREINTKSPTGQRMKLKFAFNLTDDG
LMGQQVFAGEATRLAYMTDEAVEGKEAFLEKREPWNNEFPYYY

>RXS02550 TRANSLATE of: RXS02550.seq check: 5515 from: 1 to: 1311
VTTDKRRTSKTTDTANKAVGADQAARPTRRTTRRIFDQSEKMKDVLVEIRGPVAAEAERMELDGHNLK
LNTGNPAVFGFDAPDVMIRDMIANLPTSQGYSTSKGIIIPARRAVVTRYEVVPGFPHFDVDDVFLNGVS
ELITMTTQALLNDGDEVLIAPADYPLWTAATSLAGGKPVHYLCDEEDDWNPSIEDIKSISEKTKAIVV
INPNNPTGAVYPRVLEQIVEIAREHDLILADEIYDRILYDDAEHISLATLAPDLLCITYNGLSKAYR
VAGYRAGWMVLTGPKQYARGFIEGLELLAGTRLCPNVPAQHAIQVALGGRQSIYDLTGEHGRLLQRMN
AWTKLNEIPGVSCVKPMGALYAFPKLDPNVYEIHDDTQMLDLRLAEKILMVQGTGFNWPVHHDHFRVVT
LPWASQLENAIERLGNFLSTYKQ

>RXS02556 TRANSLATE of: RXS02556.seq check: 1750 from: 1 to: 1158
LIVSTQPIITDRSALSAEHAIEVIKATLPLVGGKINEITPVFYKMFAAHPELIANTFNRGNQKQGDQKA
LAASIATFATMLVTPDAPDPVQLLSRIGHKHVSLGITADQYDIVHEHLFAAIVEVLGAETVTAPVAEAW
DAVYWIMANVLIGFENNLYASNDLEPGDVFREVTVTAKKQLSATVWEYTLAGELVAEPGQYTSIGVVL
DDGARQLRQYSLLGSDTEYRIAVEDNGEVSGFLDRVSVGDKIEATIAAGDLVLNKDTPNVVLISQGI
GSTPMVGMLAGMNPEDVVVLHADQAESTYAQVEEVQGLVEKLPKAAFEIFYRDNDQWLEVAGRIPSGA
SVYLCGGVEFLKNVREQIEALDEQPRDVNFELFAPNDWLIS

>RXS02560 TRANSLATE of: RXS02560.seq check: 4626 from: 1 to: 867
MQGNSLNLADNSERKKPMPSPGELLAARYGQPATWTPQWNETLDVIHQHRSVRRWLDKPVDDDTIRTI
ISAAQSAGTSSNKQVISIVVKDPELRKGLAGITRQMFPHLEQVPAVLIWLIDYSRISAVAAREDLPTG
ALDYLDEAAWGFLDAGIAAQNAAIAAESLGLTLYLGSVRNDAEAVHKLLGLPPEIVPVVVGLEMGHADP
PEPAGIKPPLPQEAIVHWDITYTEKNLELIDSYDRALDITYSRYGQHQLWSKQTAHRAASKSFSTNRF
LRGVFERAGFGLR

>RXS02565 TRANSLATE of: RXS02565.seq check: 9394 from: 1 to: 1266
VNDLTPDSGQEI RNAESLERFFEGTPNVKITKLEPHPGRTSIIIVTVPGSDPDAEPLTLLGHTDVVPVDL
PKWTKDPFGAEISDGQIWGRGSVDMLFITATQAAVTRQVAREGGLRGTLTFFVGVADEEARGGLGAKWLS
EEHQNLFSWKNCLSESGGSHLPVHDGSDAVVINVGEGKAAQRRIVHNGDAGHGSIPFDRDSAIVKIGE

ARRIAAADLKVAKDDIWQGFVQAHFRDPETEQALLSGTSPEAYAEFGGLSRFAHAVSHLTIAQTVVVRAG
QAINVLPSHAYLELDIRTLPGQTNQYVDDTLRAALGDLADEVEIEHLISEEATVSPTDSRLYNTLEKVL
GDDFFDAPVVPPIISSGGSDLRFGRRLGGVGYGFAVHARERTLAEAMQQLHSHDEALYLEDLTLTVRGYD
SVVREFLG

>RXS02908 TRANSLATE of: RXS02908.seq check: 6002 from: 1 to: 261
LKLHPEVLERAIAIDIKGVTAACVVGIPDPRLGQAIVAAAYSGSISPSEVIEGLDDLPWRQLPKRLKHLES
LPSIGPGKADRRRAIAKLF

>RXS02937 TRANSLATE of: RXS02937.seq check: 1915 from: 1 to: 402
VISNGEGPVVALRGDIDALPMAERSGKEYAATGVTQVDNTTGQETPVAHTCGHDVHISLLGAVQAFNS
HRELWNGTLMVAFQPAEETAAGARMMDQDNAPGNHSPAFAPDMQPTLDRGVEALVVAASAWLVK

>RXS02970 TRANSLATE of: RXS02970.seq check: 6259 from: 1 to: 1368
LALKGYTNFDGEFIEFGSVQAKEEEKRAFDNDRAHVHFSWSAQDKISPKVWAAAEGSTLYDFDGNAFID
MGSQVLVSANLGHNNPRLVEAIQRQAARLTNINPAFGNDVRSDDAAKIVSMARGEFSHVFFTTNGGADAIE
HSIRMARLHTGRNKILSAYRSYHGATGSAMMLTGEHRRLLGNPTTDPDIYHFVAPFLHSSFFATTQEEE
CERALKHLEDVIAFEGAGMIAAIVLEPVVGSSGIILPPAGYLVNGVRELCKHGIILFIADVEVMVGFGRGTG
KLFAYEHAGDDFQPDMITFAKGVNAGYAPLGGIVMTQSIRDFTGSEAYSGGLTYSCHPLAVAPAKAALE
IYAEGEIIPRVARLGAELIEPRLRELAENVAIADVRGIGFFWAVEFNADATAMAAGAAEFKERGVWPM
ISGNRFHIAAPLTTTDELVALLDAVEAAAQAVELTFAGALF

>RXS03003 TRANSLATE of: RXS03003.seq check: 6068 from: 1 to: 675
MTSRTPLVSVLPDFPWSLASAKAKAASHPDGIVNLSVGTVPDPVAPSIQIALAEAAGFSGYPTIGTP
ELRAAIRGALERRYNTKLVDASLLPVVGTKEAIALLPFALGISGTVVIPEIAYPTYEVAVVAAGCTVL
RSDSLFKLGPQIPSMMFINSNPTGKVLGIPHRLKVVKWAQENNVILADECYLGGLWDDENPPISIL
DPRVCDGDHTNLIAIHSL

>RXS03026 TRANSLATE of: RXS03026.seq check: 3330 from: 1 to: 267
MPGKILLNNGPNLNLGKREPDIYGHDTLEDVVALATAEAAKHGLEVEALQSNHQGELIDALHNARGTH
IGCVINPGGLTTLRWRFWML

>RXS03074 TRANSLATE of: RXS03074.seq check: 6105 from: 1 to: 498
MTQSAPEFIATADLVDIIGDNAQSCDTQFQNLGGATEFHGIITTVKCFQDNALLKSILSEDNPGGVLV
DGDASVHTALVGDIIAGLGKDHGWSGVIVNGAIRDSAVIGTMTFGCKALGTNPRKSTKTGSGERDVVVS
IGGIDFIPGHYVYADSDGIIIVTEAPIKQ

>RXS03112 TRANSLATE of: RXS03112.seq check: 9249 from: 1 to: 504
VEIFGKTVGIVGFGHIGQLFAQRLAAAFETTIVAYDPYANPARAAQLNVELVELDELMRSDFVTIHLPK
TKETAGMFDHLLAKSKKGQIIINAARGGLVDEQALADAIESGHIRGAGFDVYSTEPCTDSPLFKLPQV
VVTPLHGASTEAAQDRAGTDIADSVLKALA

>RXS03158 TRANSLATE of: RXS03158.seq check: 9521 from: 1 to: 564
LHSTTKYIEGHSDVVGGLVGTNDQEMDEELLFMQGGIGPIPSVFDAYLTARGLKTLAVRMDRHCDAEK
IAEFLDSRPEVSTVLYPGLKNHPGHEVAAQMKRFGGMISVRFAGGEEAAKKFCTSTKLICLAESLGGV
ESLLEHPATMTHQSAAGSQLEVPRDLVRISIGIEDIEDLLADVEQALNNL

>RXS03159 TRANSLATE of: RXS03159.seq check: 3925 from: 1 to: 738
LSFDPNTQGFSTASIHAGYEPDDYYGSINTPIYASTTFAQNAPNELRKGYEYTRVGNPTIVALEQTVA
LEKAKYGRAFFSSMAATDILFRIILKPGDHIVLGNDAYGGTYRLIDTVFTAWGVEYTVVDTSVVEEVKA
AIKDNTKLIWVETPTNPALGITDIEAVAKLTEGTNAKLVDNTLASPYLQQPLKLGAHASPTPPSTS
KDTPTLLAALWVPTTRKWTKNCCSCRAASDRSHQFSMHT

>RXS03183 TRANSLATE of: RXS03183.seq check: 124 from: 1 to: 417
EAEATAGKFEVQPLVGKGVSTLGGYNNGINVNSENKATARDFIEFIINEENQTFADNSFPPVLAS
IYDDESLVEQYPYLPALKESLENAAPRPVSPFYPAISKAIQDNAYAALNGNVDDVDQATDMKAAIENAS
S

>RXS03205 TRANSLATE of: RXS03205.seq check: 311 from: 2 to: 934
DSGIPTQLVEGSWFEPVRGRTFDRIIANPPFVVGPEIGHVYRDSGMDLDGATALVVKEACAHLPNGGT
AHLGAWVHSADQSWQQRVAEWLPDNGYVAWVIERDAVSPAQYVGTWLSDESLLDRSPEAAARTTAWLN

HFEKAKVQGVGFGFIATQRLLEEDEADEKSDILAESMTQYFEDPLGPEIEEYFTRTAWLREQTRDSILSS
RKFVRPGVAREQISLADAEQMGFSPTLRLTRTDGPRWSHDVDEHVASIVAGLNPHGLPFEEILEMYA
MAQGIIEGESLHNGAIAALVDLIRHGLVLPADLLDS

>RXS03223 TRANSLATE of: RXS03223.seq check: 402 from: 2 to: 1207
PEPVRIATAEALGLMCAEEVQASRALPGFAQAADIDGYAVRAVDVGGEKSFSQQLPVAPPEKSLPVVGEV
AAGSQQLRLQPKQAVMVHTGAPLPLADAVLPMAWSDRGRKRVTAQRPVRSGEFVRKEGDDIQPGDIA
VSAGAVLGPAAQIGLLAAVGRSKVLVYPRPRMSVISVGAELVDIDRQPGLGQVYDVNSYSLAAAGREAGA
DVYRYGIAAGEPRRIKEIIIESQMLRSEIIVITGAVGGAGSAGVRQVLNELGDDITERVAMHPGSGVQGF
LLGENKIPCFLLPSNPVASLVI FETFVRPVVRMSLGKSNAARRVVRARALNHVVSVAGRKGFIERSRLMR
DAETQDYLVEALGGATGAPSHLLAGLSEANGMIRIPEDVTEIRPGDVVDVIFLAQGR

>RXC00128 TRANSLATE of: RXC00128.seq check: 1749 from: 1 to: 1704
VSKISTKLKALTAVLSVTTLVAGCSTLPQNTDPQVLRFSGSQSTQEIAGPTPNQDPDLLIRGFFSAGA
YPTQQYEAAKAYLTEGTRSTWNPAASTRILDRIDLNTLPGSTNAERTIAIRGTQVGTLLSGGVYQPEN
EFAEITMRREDGEWRIDALPDGILLERNDLRNHYTPHDVYFFDPSGQVLVGDWRWLFNESQSMSTVLM
ALLVNGPSPAISPGVVNQLSTDASFVGFNDGEYQFTGLGNLDDARLRFAAQAVWTLAHADVAGPYTLV
ADGAPLLSEFPTLTDDLAEYNPEAYTNTVSTLTFALQDGSLSRVSSGNVSPQGIWSGGDIDSAAISS
ANVVAARHENNEAVLTVGSMEGVTS DALRSETITRPTFEYASSGLWAVVDGETPVRVARSAATTGELVQ
TEAEIVLPRDVTGPISFQLSRTGVRAAMIEGKVYVGVVTRPGPGERRVTNITEVAPSLGEAALSINW
RPDGILLVGT SIPETPLWRVEQDGS AISSMPSGNLSAPVVAVASSATTVYVTD SHAMLQLPTADNDIWR
EVPGLLGTRAAPVVAY

>RXC00152 TRANSLATE of: RXC00152.seq check: 9915 from: 1 to: 1296
MTGLILAIVFLVFVAVVVIKSIALIPQGEAAVIERLGSYTRTVSGGLTLLVPFVDRVRARIDTRERVVS
FPPQAVITQDNLTVADIVVTFQINEPERAIYGVNDNYIVGVEQISVATLRDVVGGMTLEETLTSRDVIN
RRLRGELDAATTKWGLRISRVELKAIDPPPSIQQSMKQMKADREKRATILTAEGQREADIKTAEGEKQ
AKILQAEGEKHASILNAEAERQAMILRAEGERAARYLQAQGEARAIQKVNAIKSAKLTPEVLAYQYLE
KLPKIAEGNASKMWVIPSQFSDSLEGFQKQFAGKDAEGVFRYEPNTVDEETRDIANADNVEDWFTESD
PEIAAAVAAANAVANKPVDPEPGEILSKKTARRVEPEAVLEALQNGTTTQPEVEAAPPTANFAQEFAP
QANPEDYSDQHRENPYGN

>RXC00164 TRANSLATE of: RXC00164.seq check: 2228 from: 1 to: 1689
VGRIPRAKWWFLGALVLLSAGAYASVLPQVLGRIVDLVSDGAQMRDFVELSVILIAVAIAGAVLSACG
FYVVSRISEKIIANLREDMVG TALGLPTHQVEDAGSGDLVSRSTDDVSEL SAAVTETVPILSSSLFTIA
ATIIALFSLDWQFVLIPVVVAPVYFASKHYLSKAPDRYAAERAAMAERARKVLEAIRGRATVRAYSME
DAMHNQIDQASWSVVVKGIRARTTMLILNMWMLFAEFLMLAVALVIGYKLVIDNALTIGAVTGAVLMI
RLRGPMNMFMRVLDTIQSGYASLARIVGVVADPPIPVPSDGVKAPQKGVELRNVSFSYGD SWAVKDIDI
TINSGETVALVGASGAGKTTVAALLAGLRVPDQGVLDVDDFPVSHLSDRERIARLAMVSQEVHVFSGTL
RQDLTLAKPDASDEELAHALGQVNALDWLES LPEGLD TVVGARGIQLEPVVAQQLALARVLLLNPAIVI
MDEATAEAGSAGASALEEAADAVSKNRSALVVAHRLDQASRADQILVMDKGEVVESGTHQELLDHGGIY
QRLWTAWSVGR

>RXC00416 TRANSLATE of: RXC00416.seq check: 8529 from: 1 to: 1650
LASYLSPTALVVAVLAIPLSATRILYLDGISVDQGFRTQFLTRMADDIGLSDMNYIDMPTFYFAGWFWLG
GRLANLLGLPGWEAFQPWAI VSMVAASVLPVWQRTIGSLPVATGIALVTTCIILAMNSEEPYAAIVA
MGIPAMLVLASRIAKGDKFALAGGIIYLGVSATFYTLFTGAIALS AVAVCIVVAAIVQRSIKPLLWLAV
LGGGSIVIALISWGPYLLASINGAERSGDSATHYLPLEGTQFPVPFLASSVVGLLCLVGLIYLVVRFHN
NEVRAMWVGIAVFYAWMGMSMAITLLGNTLLGFRLDTVLVLI FATAGVLGIADFRLASVYQLYPTQITE
RTATHLTNLIVVLVLLGGLYYAQDL PQKNARAIDLAYTDTDGYGERADLYPAGAARYYKDINDHLLDQG
FEPSETVVLTDDELDFMSYYPYRGYQFTSHYANPLGEFGNRNAFIEDLAIRSWDELADPQQFSDALNTS
PWTIPEVFIFRGSIDDPDAGWKYDVAEDLYPNNPNVRFRGVYFNPESFDQMWQTKQVGPFVVVTHNE

>RXC00540 TRANSLATE of: RXC00540.seq check: 3827 from: 1 to: 243
VARVVVNVMPKAEILD PQGQAVHRALGRIGVSGVSDVRQGRFELEVDDSVTEADLKKIAETLLANTVI
EDFDVVGVEVAK

>RXC00552 TRANSLATE of: RXC00552.seq check: 471 from: 1 to: 936
VATSKILLYYAFTPLSDPKAVQLWQRELCESLNLRGRILISTHGINGTVGGDIDDCKAYIKKTREYPGF
NRMQFKWSEGGAE DFPKLSVKVRDEIVAFGAPDELKVDENG VVGGGVHLKPQQVNELVEARGDEVVFFD

GRNAMEAQIGKFKDAVVPDVETTHDFIAEIESGKYDDLKDKPVVYCTGGIRCEILSSLMINRGFKEVY
QIDGGIVRYGEQFGNKGLWEGSLYVFDKRMHMEFGEDYKEVGHCIHCDTPTNKFEHCLNEDDCRELVL
CPDCFANVETRHCRRERCAIAADFAEQGIDPLVTS

>RXC00560 TRANSLATE of: RXC00560.seq check: 5757 from: 1 to: 375
MRIDPLETRQAVLAVKDWIEGEDVKKPGRAALAAATRLSVRLLAQHAPGNSVEVRVPPFVAVQCIEGP
KHTRGTPPNVVETDAKTWLRAPGQTTFDAEFESGKISASGTRAKEIADWLPVVKL

>RXC00657 TRANSLATE of: RXC00657.seq check: 8495 from: 1 to: 903
MSTEDIVVVAVDGSQAVRWAANTANKRGIPLRLASSYTMPQFLYAEGMVPPQELFDDDLQAEALEK
INEARDIAHEVAPEIKIGHTIAEGSPIDMLLEMSPDATMIVMGSRLGGLSGMVMGVSAGAVVSHAKCP
VVVVREDSAVNDESKYGPVVVGVDGSEVSQQATEYAFAEAEARGAELVAVHTWMDMQVQASLAGLAAQ
QQWDEVERQQTDMLIERLAPLVEKYPSVTVKIITRDRPVRALAEASENAQLLVGSHGRGGFKGMLLG
STSRALLQSAPCPMMVVRPPEKIKK

>RXC00733 TRANSLATE of: RXC00733.seq check: 1945 from: 1 to: 885
MSNTAGPRGRSHQADAAPNQKAQNFGPSAKRLFGILGHDRNTLIFVIFLAVLSVGLTVLGPWLLGKATN
VVFEGFLSKRMPAGASKEDIIAQLQAAGKHNOASMEDMNLVPGSGIDFEKLAMILGLVIGAYLIGSLL
SLFQARMLNRIVQSAMHRLRMEVEEKIHRLLPSYFDSIKRGDLLSRVTNDVDNIGQSLQQTLSQAITSL
LTVIGVLVMMFIISPLLALVALVSIPVTIVTVVVASRSQKLFAEQWKQTGILNARLEETYSGHAVVKV
FGHQKDVQEAFFEEENQACV

>RXC00861 TRANSLATE of: RXC00861.seq check: 5631 from: 1 to: 426
MAPHKVMLITTGTQGEPMALSRMARREHRQITVRDGLIILSSSLVPGNEEAVFGVINMLAQIGATVV
TGRDAKVHTSGHGYSGELLFLYNAARPKNAMPVHGEWRHLRANKELAISTGVNRDNVLAQNGVVVDMV
NGRA

>RXC00866 TRANSLATE of: RXC00866.seq check: 4209 from: 1 to: 966
MNDsrNRGRKVRKAGPPEAGQENHLDTPVFQAPDASSNQSAVKAETAGNDNRDAAQGAQGSQDSQGSQ
NAQGSQNRRESGNNNRNRNRRGGRGRRSGNANEGANNNSGNQNRQGGNRGNRGGRNRNVKSMQGA
DLTQRLPEPPKAPANGLRIYALGGISEIGRNMVFEYNNRLLIVDCGVLPSSGEPGVLDLILPDFGPIE
DHLHRVDALVVTHGHEDHIGAI PWLLKLRNDIPILASRFTLALIAAKCKEHRQRPKLIEVNEQSNEDRG
PFNIRFWAVNHSIPDCLGLAIKTPAGLVIHTGDIKLDQTPPDGRPT

>RXC00874 TRANSLATE of: RXC00874.seq check: 2465 from: 1 to: 1089
MSIGQHIIITERFYGAKSHTIDNVDIVLSRECGENTLAVVRINNALYQLLVNDDGKDVLDNHVEEVGASF
GAWTGSSAFFPIGPFTPLGTEQSNSSFITADNKAIVKYFRKLESGQNPDELISKISSCPNIAPILGFSS
AEISGANYTLVMAQQYVPGLDGWSHALTTTSGSFAEDAEEKIGEATRNVHTALASAFPTRVVPVEALADA
LTRLNELISQAPEIARFKEAAIDLYQSLEGEAHIQRIHGDHLHLGQLIKTPERYILIDFEGEPARPLNQ
RRLPDSPLKDLAGIIRSIDYAAFGEHTQWANEATALFLDGYGSIEDQELLNAYILDKALYEVAYEIN
NRPDWVKIPLEAVERLLD

>RXC00930 TRANSLATE of: RXC00930.seq check: 5911 from: 1 to: 753
MSGHSHKATTKHKKAANDAKRGKEFAKLIKNI EVAARTGGGDPSANPTLDDMIKKAKKASVPNDNIERA
RKRGSGEAEAGADWMNIMYEGYGPNGVAMLIECLTDNRNRAATEVRTAMTKNGGNLGESGSVSymFTRT
GVVTVQKGDLSEDDVLMAVLEAGAEVNDNGDLFEVTCAPTIDIQAVRDALVEAGIEVEDSESDFRASVQ
VPLDADGARKIFKLVDALSDSDVQNVYTNIDLSDEVLTLEND

>RXC00988 TRANSLATE of: RXC00988.seq check: 4588 from: 1 to: 423
MSKREESIEYGLGKGHDPLKDPKMGIRGVMAGTLVMEAITLGLVLTVILRVDDGIYWTTFNWVYVSAV
AIAHFVA AFLQRFSWSIPMNIVLQVLALAGFFVHPAMGFAAII FIIAWAYLFYLRNLIDRMKRGLLTT
QHS

>RXC01021 TRANSLATE of: RXC01021.seq check: 6144 from: 1 to: 522
MSSSESRSEGSQPAPSVQFERRADSTGAPAAASKEASQQMDAAGVLEWARTAVEQLSERRAEINALNV
FPVPDADTGSNMITYTMTAALDEALKLGELGDVARITEALAVGSVRGARGNSGVVLSQVLRATAQAADG
VIDGHTIQEALSIA RSLVDRAITDPVEGTVVTVLRS

>RXC01088 TRANSLATE of: RXC01088.seq check: 600 from: 1 to: 1182
MGLWIDATAGVAGDMLLGALIDAGAELEKIQQVVEAVIPGDVLLRTEEVVRQGGQRIKLHVDAQHEHHH
HRHLSTIKELLVNADIPEQTKQDALGVFELIAIAEGKVHGIEPEKIHFEVGAWDSIADIVGVCEAIRQ

LNPGLIAASPIALGFGRICAAHGDI PVPVPAVAELVKGWPTQTGALMESTEPVGELATPTGVALIRHFA
TQDGPFPGGIINEVGIGAGTKDTEGRPNIVRAILFNTSRSNPDTRTLVQLEANVDDQDPRLWPGVIEIL
FAAGAVDAWLTPILMKKGRPAHRVSALVDSSEVEAVKTALFAATTTFGIRSEVEREGLDRRFEQVEVD
GHTINIKIGSRDDQVISAQSEFEDIRSAVALGISEREVVARIPQGTTE

>RXC01096 TRANSLATE of: RXC01096.seq check: 6566 from: 1 to: 447
MKPRVLSALGIGAGALVWVWISSRMNVVTIEAFDDKSGSVTQSIVGATWSTEIMALALALLAAFAAALVL
KRMGRRIIGGISALIAVGASLSPLALLTQDPDAERARTLLTSGVASQKANSGLTLLSDWAEIINTTTHPL
AAVAMIGCAL

>RXC01158 TRANSLATE of: RXC01158.seq check: 5695 from: 1 to: 942
MSIVEHIKEFRRLRLIALAGILVGTIIGFIWYDFSFWQIPTLGELLRDPYCSLPAESRWAMSDSEECRL
LATGPFDPFMLRLKVAALVGMVLGSPVWLSQLWGFITPGLMKNERRYTAIFVTIAVVLVVGAVLAYFV
VAYGLEFLLTIGGDTQAAALTGDKYFGFLALLAIFGVSEFVPLVIGMLNIVGILPYDAIKDKRMIIM
ILFVFAAFMTPGQDPFTMLVLALSLTVLVELALQFCRFNDKRRDKRPEWLDGDDLSASPLDTSAGGED
APSPVETPEAVEPSRMLNPSGEASISYKPGRADFGDVL

>RXC01191 TRANSLATE of: RXC01191.seq check: 2562 from: 1 to: 1590
VGGLVDKLLATPSMRDVVVFALLIVAGGVVSSLGTWWGSALMARALEPAIAGLREDVLRAAVSLDANTI
ETAGRGDVISRIADDSREVSTAASTVVPMLVQAGFTVVISAFGMAAVDWRLGLVGLVAIPLYWTLRVY
LPRSGLPLYTREREAFVVRTQRLVGAVEGAETLRAFAEDTELKRIDAASGEARDISISVFRFLTWAFSR
NNRAECITLVLIILGTGYLVNIDLVTVGAVSTAALIFHRLFGPIGTLVGMFSDIQSASASLIRMVGVIN
AASNQVSGTSPASASTALTFLDVSHHYHTAPVIKNASVQLEPGEHIAIVGATGAGKSTLALIAAGLLSP
TSGQVALGGSSFSNVEPEALRQKIAMVSQEIHCFRGSVLNLRIRARPEATDADIHAVLADIGDSWLERL
PQGITDIVGDGAFRLTSVENQIMALARVHLADLAIVILDEATAESGSDHAKQLEDAALKVTENRSAILV
AHRNLQAKTADRIIVMDSGEIIESGTHEELRAIGGRYEQLWTAWSAR

>RXC01207 TRANSLATE of: RXC01207.seq check: 2212 from: 1 to: 648
VSRIYDCADQDSRAAGLKAAYDAVKAGQLVVLPTDTLYGLGCDAFNNEAVANLLATKHGPDMPVPVVLV
GSWDTIQGLVHSYSAQAKALVEAFWPGGLSIIVPQAPSLPWNLGDTRGTVMRLMPLHPVAIELLRQTGP
MAVSSANISGHTPPTTVLEARQQLNQNVAVYLDGGEALATPSTIVDISGPAPKILREGAISAERVGEV
LGVSAESLR

>RXC01434 TRANSLATE of: RXC01434.seq check: 1389 from: 1 to: 2952
VLGAVLTSLVIPVLTRAEKEDADGGSGFFRRLTSLSVTLLGGVTILSIIGAPLLTRMMLSSEGQVNVVM
STAFAYWLLPQIFFYGLFALFMAVLNTRVFKPGAWAPVVNNVITLTVLGVYMLPARLHPHEQVGIFD
PQIIFLGVGTTLGVVAQCLIMIPYLRRAGIDMRPLWGLIDARLKQFGGMAMAIIVYVAISQFGYIITRI
ASIADDAAPFIYQQHWMLLQVPYGIIGVTLLTAIMPRLSRNAADGDDRAVVSDDLQLGSKLTFIALIPV
VFTAFGVPIANGLEFAYGQFDANAANILGWTLSFSFAFTLIPYALVLLHLRVFYAREEVWTPTFIIAGIT
ATKVVLSSLAPLLSSSPERVVLLGAANGFSFITGAVIGAYLLRNKLGLLGMRLAKTSLWALGSAAVG
AAAAWALGWLIIQAVVGDFLLGLTLSSVGYLLNLAVLGVFFIFVTGIVLSRSLPEVQNLGQALTRIPGLS
RFIRPNTKISLDVGEVSEQDFSTQLVAPSEFAATPVPPPMMSAGIVRGPRLVPGAPVGDGRFLLADHGG
VQGAREWQAREIATGKEVALIFVDTSGNAPFAPLSSAAAAGIAYEVQRRTKKLASLGLAVAPNIHSEA
YRNGCLIVADWVPGSSLSAVAESGADPRAAFAALAELETETIGEHEMGI PAGLDNKRIRINTDGHAVL
ALPAILPDASELRDAKSLASAAEMLIDATLAPSDVKAMVTEAQGLATEDNPDYASLAMAMRTCGLFTEE
PTHLVVKKEKTPKPTRDGFASDYTVKGMAAIAAVVIIIVSLVAAGTAFLTSFFGSSTNEQSPLASVE
ATTSATPEPVGPPVYLDLDQARTWDDGAGTDVTDVTDGNTSTAWTSTGGDGLLDLSTPARLDRLVILT
GTGSDSNVTSTVKIYAFNDASPHSLSEGIEIGTVDYSGRSLSHSIRDSSKLPQVESVVLVDEVRSSQ
TSDTNPQMQUIAEVQLVGV

>RXC01518 TRANSLATE of: RXC01518.seq check: 9224 from: 1 to: 474
VAFMQKTSAGWLIATGGFLAAVSAILTWRIFYGSMTSISITVSITFWLLAVVCGFAGVKVQGRLEGLIG
QDKSQMNPVTIAYLAMLGRACAWGGAIFGGVYVIGISYVIPRAGELSAASNDLPGVACALGGIALSAA
GLYLERSCAAPPQSGEAS

>RXC01600 TRANSLATE of: RXC01600.seq check: 9748 from: 1 to: 669
MVSKMHIPGTHEFTVTDTELLLESPILGVRDRSLIMPGGSTARREVVEHFGAVAVVAFDGENIAMVKQY
RRSVGDSLWELPAGLLDIADEDELTAQRELMEEGLEASVSLTDLITSPGFCDEAVRVFLARGLTK
VERPKVMGDEEADMINQWVPLHEAVGMVFSGQLVNSIAIAGVMAADAVIAGRASARAVTAPFTYRPTAL
AQRRKAHGIVPDMKKL

>RXC01622 TRANSLATE of: RXC01622.seq check: 2066 from: 1 to: 603
MSDFYADRLFNAMERNEVAPGMLLVAAPDMASEDFERSIVLIIHSPATTFGVNISSRSDVAVANVLP
WVDLTSPQALYIGGPLSQQAVVGLGVTKPGVDIENSTSFNKLANRLVHVDLRSAPEDVADDLEGMRF
AGYAEWAPGQLNEEIEQGDWFTPALPSDIIAPGRVDIWDVMMRRQAMPLPLYSTFPSDPSDN

>RXC01656 TRANSLATE of: RXC01656.seq check: 8741 from: 1 to: 897
MTETQETQYQATTRVKRGLADMLKGGVIMDVVTPEQARIAEDAGASAVMALERVVPADIRSQGGVARMSP
DLIEGIVNAVSIIPVMAKARIGHFVEAQVLEALGVDFIDESEVLSPADYTHHINKWKFDVPFVCGATNLG
EALRRITEGAAMIRSKGEAGTGDVSEAVRHLRTIRGDINRLRSLDEDELFAAKEFQAPYDLVREVAST
GKLPVVTFVAGGVATPADAAALVRQMGAEVFGVSGIFKSGNPAARAAAIVKAATLFDDPSVIADVSRGL
GEAMVGINVSVDVPAPHRLAERGW

>RXC01709 TRANSLATE of: RXC01709.seq check: 6991 from: 1 to: 432
VFEQALGLTTLAQTAGAGAAGGLGFMAALLSAGMRSGVDMILNETGGEKMLAQADLVITGEGRIDAQT
LSGKAPTGIARARAKGIPVLAVCGQSLGPAISNELFEDIYSFTDFESDINECIRNPLPILEGIGFNI
AKHHLS

>RXC01711 TRANSLATE of: RXC01711.seq check: 1589 from: 1 to: 1158
MLLMAHREFFVLAINGAVTDDFTTVYSALRRFEVGEIPVYNEVYHFVDPHYLYNPGATLLLAPLGYYTHFT
LARWMFIAVNLLAIVLAFGLLTRLSGWALRSMVWPIAIALAMLTETVQNTLIFSNINGILLMLAIFLW
CJVHKKSWLGGVLIGLAILIKPMFLPLLFLPLVKKQWGSILGILTPVIFNAVAVFLVPGASEYVTRTM
PYLGETRDFANSSLPGLAIYFGMPTWMEITWFLIFGAMVGLAVLALLRFRNTEPYFWAATTTGVLLTGV
FFLSSSLGQMYYSMMIFPMIFTLTLLGSRSVFHNWVAWVAAYFLLSPDTFTSQRLPDVARWMEFFSATVGWG
LLIVVTFVSALIWFIDIRAKGTPSSPITTDPTHDLERTA

>RXC01715 TRANSLATE of: RXC01715.seq check: 5867 from: 1 to: 696
VSELDIKQLNKLQRYSQWAVFRAIPGALDDDRTEVTDQAAKFFADLEAEGKVTVRGIYNASGLRADADY
MIWWHAEEFEDIQKAFADFRRTTILGQVSEVFWIGNALHRPSEFNKAHLPSFIMGEEAKDWITVYPFVR
SYDWYIMEPLKRSRILREHGQAAVEFPDVRANTVPALFALGDYEWVLAFAEDELHRIVDLMHKMRYTEAR
LHVREELPFISGQVRDIADLIKVL

>RXC01796 TRANSLATE of: RXC01796.seq check: 303 from: 1 to: 774
LLLGGNPAEIDQVLGGDQQTQIESGESTGAGDFDHCQTGADANASDDCRLYTSFSVNMWQTLLPAQAG
IEYTEPTLTLFKNSTQTGCGFASASTGPFYCPSDQDAYFDLTFFDQMRQFGAENAPLAQMYIVAHEYGH
HVQNLEGTGLLSNYNDPGADSNVAKIELQADCYAGIWANHSSSEGPDPQLPITESELDSALLAASAVGD
DNIQQRSGGDVNPESWTHGSSQQRKDAFLAGYNTGQMSACDFLGRGVYND

>RXC01942 TRANSLATE of: RXC01942.seq check: 8026 from: 1 to: 600
MLRIGLTGGIGSGKSTVADLLSSEGFLIVDADQVARDIVEPGQPALAEAEAFQDILKPDGTLDRAGL
AAKAFVSEEQTALLNAITHPRIAESARRFNEAEDQGAQVAVYDMPLLVEKGLDRKMDLVVVVDVVEE
RVRRLVEKRGLTEDDVRRIASQVPDDVRLKAADIVVDNNGTLEDLHAEASKLIAEILSRVN

>RXC01946 TRANSLATE of: RXC01946.seq check: 7246 from: 1 to: 1275
IRKYSRLEEQFQSLGGYEADAEAAQICDNLGLEARILDQQLKTLGGQRRRVELAQILFAATNGSGKSK
TTLLEDEPTNHLDAISITWLRDFLAKHEGGLIMISHDVELLGAVCNKIWYLDVAVRSEADVNMGFSKYV
DARALDEARRRRERANAEEKKAGALKDQAARLGAKATKAAAKQMIARAERMIDNLDEIRVADRAANIVF
PEPAPCGKTPLNAKGLTKMYGSLEVFAVDLAIDKGSRVVVLGFNGAGKTTLLKLLAGVERTDGEGLIV
TGYGLKIGYFAQEHDITIDPKSVWQNTIEACADADQQSLRSLLSGFSMFSGEQLDQAPGTLGSGEKTRLA
LATLVSSSRANVLLLEDEPTNNLDPIISREQVLDALRTYTGAUVLVTHDPGAVKALEPERVIVLPDGTEDLW
NDQYMEIVELA

>RXC02080 TRANSLATE of: RXC02080.seq check: 2711 from: 1 to: 807
MSIEWLQIVELGAIFGAGFLAGSIINVIVGAGTLVSFPILVFLGLPPLTATIANIGIVPGSISGVVAYR
RELHAHVKTIRFLLPASILGGITGASLLLHFSADVFTAVIPWLIGFGTLLVIAGPSIKKHVGAHTSGGI
SAGFRQLPFPSRTTFIVSVCGALLLGMYYGGYFSAAQGILLIALLGITSTLQMQLNAIKNLTVAAVNLI
AASVFIIISPELISWPTVALIALGSALGGYIGGRYARRLRPSVFRFVIVGITTIVIVMTIG

>RXC02095 TRANSLATE of: RXC02095.seq check: 6468 from: 1 to: 1404
MKTEQSQAQLAPKKAPEKPQRIRQLISVAWQRPWLTSFTVISALAATLFEFLTPLLTGGAIIDIALGNT
GDTLTDLDRFTPSGLSVLTSVIALIVLLALLRYASQFGRRYTAGKLSMGVQHDVRLKTMRSLLQNLG
PGQDSIRTGQVVSRSISDINMVQSLVAMLPMLIGNVVKLVLTVMIMLAISPPLTIIAAVLVPLLLWAVA

YSRKALFASTWSAQKKAADLTTHVEETVTGIRVVKAFAQEDRETDKDLTARELFAQRMRTARLTAKFI
PMVEQLPQLALVVNIVGGGYLAMTGHITVGTFFAFSSYLTSLSAVARSLSGMLMRVQLALSSVERIFEV
IDLQPERTDPAHPLSLPDTPLGLSFNNVDFRGILNGFELGVQAGETVVVLVGPPGSGKTMVQLAGNFYQ
PDSGHIAFDSNGHRTRFDDLTTHSDIRRNLIASFDEPFYSSSIPREHLDFGFCQ

>RXC02206 TRANSLATE of: RXC02206.seq check: 8771 from: 1 to: 936
MVGSSGLRVSRLLGLTSTWGSGETELAEAGDIFKAFINSGGTLIDVSPNYTTGVAEEMLTMLDAEVSRS
AVVISSSAGVNPALPLGRRVDCSRRNLIAQLDVTLRALNTDYLDLWSVGWDEGTPPHEVADTLDYAVR
TGRVRYAGVRGYSQWQLAVTHAASNHAASARPVVVAQNEYSLLERRAEQELLPATQHLGVGFFAGAPL
GQGVLTAKYRSEIPHDSRAASTGRDAEVQSYLDNRGRIIVDALDTAAKGLGISPAVTATTWVRDRPGVT
AVIVGARTHEQLSHLLKAESVTLPTPITQALDDVSL

>RXC02207 TRANSLATE of: RXC02207.seq check: 6831 from: 1 to: 798
MRRRSRVSRLLPATALLASTALLSACTQGVTDSPDMGKATPAVSPAASNPDGQVIEFGNITDMEVTDG
DILGVRTEDALAIGTVSDFEAGSQVELDVVKQCGDLTATGGTFVLPCADGVYLIDAKDPDLDELRAATDK
PVTVAALTSDDQLLVGNGEDEELTIYREGEEPETFTVAGPNTQLIAPVIDRHDVAVRTWNENTTIQDV
DYPNDREGATLRVGLGVGMAGGEDGLLVVSDMGGQIAIYNADDVIRLQNDRPHRRGT

>RXC02238 TRANSLATE of: RXC02238.seq check: 4471 from: 1 to: 285
VTNVSNETNATKAVFDPPVGITAPPIDELLDKVTISKYALVIFAARARQINSFYHQADEGVFEFIGPLV
TPQPGKPLSIALREINAGLLDHEEG

>RXC02295 TRANSLATE of: RXC02295.seq check: 491 from: 1 to: 780
MGLELAASGWGILIAGAAVAGWIDAVIGGGGLVLIPLILAVMPQLAPVTALASNKLAAVTGTASAAFTL
VRRVKPDKKLLALYVLVAAVCSGAGALAASLIDKQIMRPLIIVLMLVVGLIVVFKPNFGTGESKALPTG
WKRWAAIVAVGLIAAYDGIIFGPGTGMFLIMAFTALLSQNFLSSAAMAKVVNTATNLGALIVFIIGGHMW
WTLGLVLAVANVAGAQLGARTVLGGGTRLIRYALLTLVVVMSVYLTWQQIQGM

>RXC02380 TRANSLATE of: RXC02380.seq check: 4082 from: 1 to: 654
MTTTVKRRARIGIMGGTFDPIHNGHLVAGSEVADRFDLDLVYVPTGQPWQKANKKVSPAEDRYLMTVI
ATASNPRFMVSRVDIDRGGDYTTIDTLQDLKQYPDAQLYFITGADALAQIVTWRDWEKTFELAHFVG
TRPGYELDGNIIPEMHQDRVSLVDIPAMASSTDCRERSSEERPWWYLVDPGVVQYIAKRQLYRPEGSD
KMDPKGQONQA

>RXC02390 TRANSLATE of: RXC02390.seq check: 7081 from: 1 to: 669
VEWTAFTGLILLNLVGLSLSPGPDFTFLRLATRSRAHAIAGVAGIVTGLTVVWTLTVVGAALLTTPS
ILGIIQLVGGTYLSFIGYKLLRSASRELIDARQFRFNADARPIPDVEALGTRTQVYRQGLATNLSNPK
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Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar

Haberhauer, Gregor

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Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
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Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
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Ile	Leu	Gly	Ile	Ile	Gln	Leu	Val	Gly	Gly	Thr	Tyr	Leu	Ser	Phe	Ile		
	70				75					80					85		
ggg	tac	aag	ttg	ctg	cgc	tcg	gcg	tcg	aga	gag	ctt	atc	gac	gcc	cgc		403
Gly	Tyr	Lys	Leu	Leu	Arg	Ser	Ala	Ser	Arg	Glu	Leu	Ile	Asp	Ala	Arg		
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cag	ttc	cgt	ttc	aac	gcc	gat	gcc	cga	cct	atc	ccg	gat	gcg	gta	gaa		451
Gln	Phe	Arg	Phe	Asn	Ala	Asp	Ala	Arg	Pro	Ile	Pro	Asp	Ala	Val	Glu		
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Leu	Ser	Asn	Pro	Lys	Val	Val	Met	Tyr	Phe	Ala	Ala	Ile	Leu	Ala	Pro		
	135					140					145						
ttg	atg	cca	gcg	cac	cca	tca	ccg	gtg	ctg	gcg	ttc	tct	atc	atc	gtg		595
Leu	Met	Pro	Ala	His	Pro	Ser	Pro	Val	Leu	Ala	Phe	Ser	Ile	Ile	Val		
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gcg	att	tta	gtg	cag	acc	ttt	gtt	acc	ttc	tct	gct	gtg	tgc	ctc	att		643
Ala	Ile	Leu	Val	Gln	Thr	Phe	Val	Thr	Phe	Ser	Ala	Val	Cys	Leu	Ile		
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gtc	tct	acg	gag	cgt	gtg	cgc	aaa	gca	atg	ctg	cgt	gca	ggt	ccc	tgg		691
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 Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
 65 70 75 80
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 Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
 115 120 125
 Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
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 Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
 145 150 155 160
 Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
 165 170 175
 Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
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 Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
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 Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
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ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259
 Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
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 Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
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 Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
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 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
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 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
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 120 125 130

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 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
 135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595
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 150 155 160 165

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 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
 170 175 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
 185 190 195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga 739
 Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
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Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
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 35 40 45

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Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
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Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
 130 135 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
 145 150 155 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
 165 170 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
 180 185 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
 195 200 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
 210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
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Val Ser Arg Ile Tyr
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Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
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gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
25 30 35
tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
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ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
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Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
70 75 80 85
gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
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Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
105 110 115
acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
120 125 130
cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
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 gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
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 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
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 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
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 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
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 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
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 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala

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Leu Ala Thr	Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys				
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 Met Ser Thr Glu Asp
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 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
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 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
 25 30 35
 gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259
 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
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 Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
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 Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
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 Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
 90 95 100
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 Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
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 Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser
 120 125 130

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His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
135 140 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu
150 155 160 165

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Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg
170 175 180

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag 691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
185 190 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
200 205 210

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Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
215 220 225

gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
230 235 240 245

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
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Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
265 270 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
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35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala

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Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu 130 135 140		
Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly 145 150 155 160		
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Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met 180 185 190		
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Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly 260 265 270		
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Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg																
25 30 35																
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Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile																
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Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro																
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Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His																
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Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val																
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Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu																
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215 220 225																
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Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
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 Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
 250 255 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
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tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc 1027
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Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
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Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
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Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95

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Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
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Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
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Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
 145 150 155 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu

165										170					175						
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Ile	Leu	Ser	Ser	Leu	Met	Ile	Asn	Arg	Gly	Phe	Lys	Glu	Val	Tyr	Gln						
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225					230					235					240						
Phe	Gly	Glu	Asp	Tyr	Lys	Glu	Val	Gly	His	Cys	Ile	His	Cys	Asp	Thr						
			245					250						255							
Pro	Thr	Asn	Lys	Phe	Glu	His	Cys	Leu	Asn	Glu	Asp	Asp	Cys	Arg	Glu						
			260					265					270								
Leu	Val	Leu	Met	Cys	Pro	Asp	Cys	Phe	Ala	Asn	Val	Glu	Thr	Arg	His						
		275					280					285									
Cys	Lys	Arg	Glu	Arg	Cys	Ala	Ala	Ile	Ala	Ala	Asp	Phe	Ala	Glu	Gln						
	290					295					300										
Gly	Ile	Asp	Pro	Leu	Val	Thr	Ser														
305					310																

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<211> 1578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1555)

<223> RXN00351

<400> 17

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cgcaaagaag	accacaaaga	agtcttaagc	cggatcttat	atg	gat	gat	tcc	aat	115
				Met	Asp	Asp	Ser	Asn	
				1				5	

agc	ttt	gta	gtt	gtt	gct	aac	cgt	ctg	cca	gtg	gat	atg	act	gtc	cac	163
Ser	Phe	Val	Val	Val	Ala	Asn	Arg	Leu	Pro	Val	Asp	Met	Thr	Val	His	
			10					15						20		

cca	gat	ggt	agc	tat	agc	atc	tcc	ccc	agc	ccc	ggt	ggc	ctt	gtc	acg	211
Pro	Asp	Gly	Ser	Tyr	Ser	Ile	Ser	Pro	Ser	Pro	Gly	Gly	Leu	Val	Thr	
		25					30						35			

ggg	ctt	tcc	ccc	gtt	ctg	gaa	caa	cat	cgt	gga	tgt	tgg	gtc	gga	tgg	259
Gly	Leu	Ser	Pro	Val	Leu	Glu	Gln	His	Arg	Gly	Cys	Trp	Val	Gly	Trp	
		40				45					50					

cct	gga	act	gta	gat	gtt	gca	ccc	gaa	cca	ttt	cga	aca	gat	acg	ggg	307
Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe	Arg	Thr	Asp	Thr	Gly	

55	60	65	
gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc			355
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe			
70	75	80	85
tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg			403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu			
	90	95	100
att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag			451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu			
	105	110	115
gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt			499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly			
	120	125	130
gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att			547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile			
	135	140	145
ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att			595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile			
	150	155	160
ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag			643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu			
	170	175	180
att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt			691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val			
	185	190	195
caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act			739
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr			
	200	205	210
gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa			787
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu			
	215	220	225
gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg			835
Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg			
	230	235	240
cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt			883
Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe			
	250	255	260
ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac			931
Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp			
	265	270	275
gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag			979
Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys			
	280	285	290
ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc			1027
Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly			
	295	300	305

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gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg 1075
Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser
310 315 320 325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa 1123
Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg 1171
Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
345 350 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg 1219
Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu
360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg 1267
Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met
375 380 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt 1315
Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly
390 395 400 405

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt 1363
Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg 1411
Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
425 430 435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg 1459
Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg 1507
Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac tca 1555
Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn Ser
470 475 480 485

tgaaccgcgc acgaatcgcg acc 1578

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<210> 18

<211> 485

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 18

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Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
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Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
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Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly

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35					40					45					
Cys	Trp	Val	Gly	Trp	Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe
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Arg	Thr	Asp	Thr	Gly	Val	Leu	Leu	His	Pro	Val	Val	Leu	Thr	Ala	Ser
65					70					75					80
Asp	Tyr	Glu	Gly	Phe	Tyr	Glu	Gly	Phe	Ser	Asn	Ala	Thr	Leu	Trp	Pro
				85					90					95	
Leu	Phe	His	Asp	Leu	Ile	Val	Thr	Pro	Val	Tyr	Asn	Thr	Asp	Trp	Trp
			100					105					110		
His	Ala	Phe	Arg	Glu	Val	Asn	Leu	Lys	Phe	Ala	Glu	Ala	Val	Ser	Gln
			115				120					125			
Val	Ala	Ala	His	Gly	Ala	Thr	Val	Trp	Val	Gln	Asp	Tyr	Gln	Leu	Leu
			130				135					140			
Leu	Val	Pro	Gly	Ile	Leu	Arg	Gln	Met	Arg	Pro	Asp	Leu	Lys	Ile	Gly
145					150					155					160
Phe	Phe	Leu	His	Ile	Pro	Phe	Pro	Ser	Pro	Asp	Leu	Phe	Arg	Gln	Leu
			165						170					175	
Pro	Trp	Arg	Glu	Glu	Ile	Val	Arg	Gly	Met	Leu	Gly	Ala	Asp	Leu	Val
			180					185					190		
Gly	Phe	His	Leu	Val	Gln	Asn	Ala	Glu	Asn	Phe	Leu	Ala	Leu	Thr	Gln
			195				200					205			
Gln	Val	Ala	Gly	Thr	Ala	Gly	Ser	His	Val	Gly	Gln	Pro	Asp	Thr	Leu
			210				215					220			
Gln	Val	Ser	Gly	Glu	Ala	Leu	Val	Arg	Glu	Ile	Gly	Ala	His	Val	Glu
225					230					235					240
Thr	Ala	Asp	Gly	Arg	Arg	Val	Ser	Val	Gly	Ala	Phe	Pro	Ile	Ser	Ile
			245						250					255	
Asp	Val	Glu	Met	Phe	Gly	Glu	Ala	Ser	Lys	Ser	Ala	Val	Leu	Asp	Leu
			260					265					270		
Leu	Lys	Thr	Leu	Asp	Glu	Pro	Glu	Thr	Val	Phe	Leu	Gly	Val	Asp	Arg
			275				280					285			
Leu	Asp	Tyr	Thr	Lys	Gly	Ile	Leu	Gln	Arg	Leu	Leu	Ala	Phe	Glu	Glu
			290				295					300			
Leu	Leu	Glu	Ser	Gly	Ala	Leu	Glu	Ala	Asp	Lys	Ala	Val	Leu	Leu	Gln
305					310					315					320
Val	Ala	Thr	Pro	Ser	Arg	Glu	Arg	Ile	Asp	His	Tyr	Arg	Val	Ser	Arg
			325						330					335	
Ser	Gln	Val	Glu	Glu	Ala	Val	Gly	Arg	Ile	Asn	Gly	Arg	Phe	Gly	Arg
			340					345					350		
Met	Gly	Arg	Pro	Val	Val	His	Tyr	Leu	His	Arg	Ser	Leu	Ser	Lys	Asn
			355				360					365			

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
370 375 380

Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
385 390 395 400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
405 410 415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
420 425 430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
435 440 445

Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
450 455 460

His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
465 470 475 480

Ser Gly Glu Asn Ser
485

<210> 19

<211> 1546

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1546)

<223> FRXA00351

<400> 19

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cgcaaagaag accacaaaga agtcttaagc cggatcttat atg gat gat tcc aat 115
Met Asp Asp Ser Asn
1 5

agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac 163
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His
10 15 20

cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg 211
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr
25 30 35

ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg 259
Gly Leu Ser Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp
40 45 50

cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt 307
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly
55 60 65

gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc 355
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe

70	75	80	85	
tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg				403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu	90	95	100	
att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag				451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu	105	110	115	
gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt				499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly	120	125	130	
gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att				547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile	135	140	145	
ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att				595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile	150	155	160	165
ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag				643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu	170	175	180	
att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt				691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val	185	190	195	
caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act				739
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr	200	205	210	
gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa				787
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu	215	220	225	
gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg				835
Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg	230	235	240	245
cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt				883
Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe	250	255	260	
ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac				931
Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp	265	270	275	
gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag				979
Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys	280	285	290	
ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc				1027
Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly	295	300	305	
gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg				1075
Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser	310	315	320	325

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cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa 1123
Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg 1171
Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
345 350 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg 1219
Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu
360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg 1267
Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met
375 380 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt 1315
Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly
390 395 400 405

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt 1363
Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg 1411
Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
425 430 435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg 1459
Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg 1507
Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga 1546
Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly
470 475 480

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<210> 20

<211> 482

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 20

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Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
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Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
20 25 30

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Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
35 40 45

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Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
50 55 60

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Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser

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Asp	Tyr	Glu	Gly	Phe	Tyr	Glu	Gly	Phe	Ser	Asn	Ala	Thr	Leu	Trp	Pro
				85					90					95	
Leu	Phe	His	Asp	Leu	Ile	Val	Thr	Pro	Val	Tyr	Asn	Thr	Asp	Trp	Trp
			100					105					110		
His	Ala	Phe	Arg	Glu	Val	Asn	Leu	Lys	Phe	Ala	Glu	Ala	Val	Ser	Gln
		115					120					125			
Val	Ala	Ala	His	Gly	Ala	Thr	Val	Trp	Val	Gln	Asp	Tyr	Gln	Leu	Leu
	130					135					140				
Leu	Val	Pro	Gly	Ile	Leu	Arg	Gln	Met	Arg	Pro	Asp	Leu	Lys	Ile	Gly
145					150					155					160
Phe	Phe	Leu	His	Ile	Pro	Phe	Pro	Ser	Pro	Asp	Leu	Phe	Arg	Gln	Leu
				165					170					175	
Pro	Trp	Arg	Glu	Glu	Ile	Val	Arg	Gly	Met	Leu	Gly	Ala	Asp	Leu	Val
			180					185					190		
Gly	Phe	His	Leu	Val	Gln	Asn	Ala	Glu	Asn	Phe	Leu	Ala	Leu	Thr	Gln
		195					200					205			
Gln	Val	Ala	Gly	Thr	Ala	Gly	Ser	His	Val	Gly	Gln	Pro	Asp	Thr	Leu
	210					215					220				
Gln	Val	Ser	Gly	Glu	Ala	Leu	Val	Arg	Glu	Ile	Gly	Ala	His	Val	Glu
225					230					235					240
Thr	Ala	Asp	Gly	Arg	Arg	Val	Ser	Val	Gly	Ala	Phe	Pro	Ile	Ser	Ile
				245					250					255	
Asp	Val	Glu	Met	Phe	Gly	Glu	Ala	Ser	Lys	Ser	Ala	Val	Leu	Asp	Leu
			260					265					270		
Leu	Lys	Thr	Leu	Asp	Glu	Pro	Glu	Thr	Val	Phe	Leu	Gly	Val	Asp	Arg
		275					280					285			
Leu	Asp	Tyr	Thr	Lys	Gly	Ile	Leu	Gln	Arg	Leu	Leu	Ala	Phe	Glu	Glu
	290					295					300				
Leu	Leu	Glu	Ser	Gly	Ala	Leu	Glu	Ala	Asp	Lys	Ala	Val	Leu	Leu	Gln
305					310					315					320
Val	Ala	Thr	Pro	Ser	Arg	Glu	Arg	Ile	Asp	His	Tyr	Arg	Val	Ser	Arg
				325					330					335	
Ser	Gln	Val	Glu	Glu	Ala	Val	Gly	Arg	Ile	Asn	Gly	Arg	Phe	Gly	Arg
		340						345					350		
Met	Gly	Arg	Pro	Val	Val	His	Tyr	Leu	His	Arg	Ser	Leu	Ser	Lys	Asn
		355					360					365			
Asp	Leu	Gln	Val	Leu	Tyr	Thr	Ala	Ala	Asp	Val	Met	Leu	Val	Thr	Pro
	370					375					380				
Phe	Lys	Asp	Gly	Met	Asn	Leu	Val	Ala	Lys	Glu	Phe	Val	Ala	Asn	His
385					390					395					400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
 405 410 415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
 420 425 430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
 435 440 445

Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
 450 455 460

His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
 465 470 475 480

Ser Gly

<210> 21
 <211> 779
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(756)
 <223> RXA00873

<400> 21
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gaa atg gtc tcc gat gag gaa cgc agc tac atg tac tcc caa ttc gcc 96
 Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala
 20 25 30

tcc gaa cct cgc atg cgc gcc aac gta gga atc cgc agg cgc ctt tcc 144
 Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser
 35 40 45

cca ctg ctt gaa ggc gac cgc aac cag ctg gaa ctc ctt cac ggt ttg 192
 Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
 50 55 60

ttg ctg tct cta cct ggc tca ccc gtg ttg tat tac ggt gat gaa att 240
 Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile
 65 70 75 80

ggc atg ggc gac aat atc tgg ctc cac gac cgc gac gga gtg cgc acc 288
 Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr
 85 90 95

ccc atg cag tgg tcc aac gac cgc aac ggt ggt ttc tcc aaa gct gat 336
 Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
 100 105 110

cct gaa cgc ctg tac ctt cca gcg atc caa aat gat caa tac ggc tac 384
 Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr

115	120	125	
gcc caa gta aac gtg gaa agc caa ctc aac cgc gaa aac tcc ctg ctg			432
Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu			
130	135	140	
cgc tgg ctc cga aac caa atc ctt atc cgc aag cag tac cgc gca ttt			480
Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe			
145	150	155	160
ggg gcc gga acc tac cgt gaa gtg tcc tcc acc aat gag tca gtg ttg			528
Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu			
	165	170	175
aca ttt tta cga gaa cac aag ggc caa acc att ttg tgt gtc aac aac			576
Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn			
	180	185	190
atg agc aaa tat cct cag gca gtc tcg ctt gat ttg cgt gaa ttt gca			624
Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala			
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Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile			
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Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp			
225	230	235	240
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<213> Corynebacterium glutamicum

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Ser	Glu	Pro	Arg	Met	Arg	Ala	Asn	Val	Gly	Ile	Arg	Arg	Arg	Leu	Ser
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Pro	Leu	Leu	Glu	Gly	Asp	Arg	Asn	Gln	Leu	Glu	Leu	Leu	His	Gly	Leu
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Leu	Leu	Ser	Leu	Pro	Gly	Ser	Pro	Val	Leu	Tyr	Tyr	Gly	Asp	Glu	Ile
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Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
 115 120 125

Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu
 130 135 140

Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe
 145 150 155 160

Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
 165 170 175

Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn
 180 185 190

Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala
 195 200 205

Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile
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<223> RXA00891

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 Val Leu Gln Thr Ser
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tgg cat ttc tct atc ctg gca ggc atg act gat acc tct ccg ttg aat 163
 Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp Thr Ser Pro Leu Asn
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 Ser Gln Pro Ser Ala Asp His His Pro Asp His Ala Ala Arg Pro Val
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ctt gat gcc cac ggc ttg atc gtt gag cac gaa tcg gaa gag ttt cca 259
 Leu Asp Ala His Gly Leu Ile Val Glu His Glu Ser Glu Glu Phe Pro
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Tyr	Asp	Pro	Glu	Gly	Asn	Gly	Val	Gly	Ser	Leu	Lys	Gly	Leu	Thr	Glu		
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Ala Ala Arg Pro Val Leu Asp Ala His Gly Leu Ile Val Glu His Glu
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Ser Glu Glu Phe Pro Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp
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Glu Lys Lys Asn Arg Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val
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Leu Val Arg Ala Phe Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu
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Lys Gly Leu Thr Glu Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp
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Cys Ile Trp Ile Pro Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly
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Asp Asp Phe Val Glu Leu Val Asp His Ala His Arg Arg Gly Leu Arg
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Val Ile Thr Asp Leu Val Met Asn His Thr Ser Asp Gln His Ala Trp
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Val Asp Thr Glu Glu Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln
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Tyr Phe Trp His Arg Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp
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<223> RXA00534

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 Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
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Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
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 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
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 aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc 1267
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 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
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 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
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 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
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 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
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 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
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 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
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 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
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 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
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 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
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 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
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<212> DNA

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 250 255 260

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 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
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 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
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 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn

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Ala	Val	Gly	Asp	His	Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	
180					185					190						
Asp	Ala	Gly	Asp	Val	Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	
195					200					205						
Leu	Pro	Phe	Ala	Gly	Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	
210					215					220						
Glu	Glu	Gln	Lys	Leu	Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	
225					230					235					240	
Asp	Leu	Lys	Val	Ser	Gly	Thr	Cys	Val	Arg	Val	Pro	Val	Phe	Thr	Gly	
245					250					255						
His	Thr	Leu	Thr	Ile	His	Ala	Glu	Phe	Asp	Lys	Ala	Ile	Thr	Val	Asp	
260					265					270						
Gln	Ala	Gln	Glu	Ile	Leu	Gly	Ala	Ala	Ser	Gly	Val	Lys	Leu	Val	Asp	
275					280					285						
Val	Pro	Thr	Pro	Leu	Ala	Ala	Ala	Gly	Ile	Asp	Glu	Ser	Leu	Val	Gly	
290					295					300						
Arg	Ile	Arg	Gln	Asp	Ser	Thr	Val	Asp	Asp	Asn	Arg	Gly	Leu	Val	Leu	
305					310					315					320	
Val	Val	Ser	Gly	Asp	Asn	Leu	Arg	Lys	Gly	Ala	Ala	Leu	Asn	Thr	Ile	
325					330					335						
Gln	Ile	Ala	Glu	Leu	Leu	Val	Lys									
340																

<210> 29

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 29

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tggacgcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

1

5

10

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acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

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<210> 30

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

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Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
165 170 175

Ala Ser Met Val
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<210> 31

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1207)

<223> RXA02022

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cttccatcat gttttaacta aggtttgtag gcttaaactc gtg aac tct gaa ctc 115
Val Asn Ser Glu Leu
1 5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
10 15 20

ttg gta gat ata ccg agt ccg tcg ggt cag gaa aag cag att gct gat 211
Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
25 30 35

gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
40 45 50

ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala
55 60 65

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	1027
Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val	
295 300 305	
ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt	1075

Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
 310 315 320 325

 ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca 1123
 Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
 330 335 340

 agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg 1171
 Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
 345 350 355

 gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt 1217
 Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
 360 365

 cgggggttattc gtg 1230

 <210> 32
 <211> 369
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 32
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 Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
 20 25 30

 Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
 35 40 45

 Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
 50 55 60

 Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
 65 70 75 80

 Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
 85 90 95

 Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
 100 105 110

 His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
 115 120 125

 Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
 130 135 140

 Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
 145 150 155 160

 Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
 165 170 175

 Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
 180 185 190

 Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile

195	200	205
Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly 210	215	220
Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val 225	230	235 240
Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg 245	250	255
Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu 260	265	270
Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp 275	280	285
Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly 290	295	300
Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp 305	310	315 320
Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe 325	330	335
Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro 340	345	350
Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser 355	360	365
Glu		

<210> 33
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXA00044

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 Met Ala Ser Ala Thr
 1 5
 ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
 10 15 20
 agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat 211
 Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn
 25 30 35

ggt ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca	259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala	
40 45 50	
ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag	307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu	
55 60 65	
cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc	355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr	
70 75 80 85	
act gct cgc gtg att gag ctc gtg gaa gat gcc ctg gag gct ggt gcc	403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala	
90 95 100	
gaa ggc ctc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg	451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val	
105 110 115	
gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt	499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Pro Glu Leu	
120 125 130	
cca ctg ttt gcc tac aac atc cca gtg tgg gtg cac tcc aac ctc aac	547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn	
135 140 145	
cca gtc atg ctt ttg acg ctg gcc aag gat ggc gtt ctt gca ggc acc	595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr	
150 155 160 165	
aag gat tcc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct	643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala	
170 175 180	
cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc ggc agc	691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser	
185 190 195	
gaa acc acc gtt gat ttc gcc tac ctt gcg ggt gcc gat gga gtt gtc	739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val	
200 205 210	
cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa	787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys	
215 220 225	
ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc	835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg	
230 235 240 245	
atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg	883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met	
250 255 260	
tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac	931
Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His	
265 270 275	
ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc	979

Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
 280 285 290

agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg 1027
 Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
 295 300 305

tac acc gct taaggccac acctcatgac tga 1059
 Tyr Thr Ala
 310

<210> 34

<211> 312

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 34

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Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
 20 25 30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
 35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
 50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
 65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
 85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
 100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
 115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
 130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
 145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
 165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
 180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
 195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
 210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala

225	230	235	240
Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly			
	245	250	255
Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys			
	260	265	270
Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val			
	275	280	285
Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile			
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Val Asp Glu Phe Leu Tyr Thr Ala			
305	310		

<210> 35

<211> 867

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(844)

<223> RXA00863

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				Met	Gly	Ile	Lys	Val	
				1				5	

ggc	gtt	ctc	gga	gcc	aaa	ggc	cgt	gtt	ggt	caa	act	att	gtg	gca	gca	163
Gly	Val	Leu	Gly	Ala	Lys	Gly	Arg	Val	Gly	Gln	Thr	Ile	Val	Ala	Ala	
			10					15					20			

gtc	aat	gag	tcc	gac	gat	ctg	gag	ctt	gtt	gca	gag	atc	ggc	gtc	gac	211
Val	Asn	Glu	Ser	Asp	Asp	Leu	Glu	Leu	Val	Ala	Glu	Ile	Gly	Val	Asp	
			25				30						35			

gat	gat	ttg	agc	ctt	ctg	gta	gac	aac	ggc	gct	gaa	gtt	gtc	gtt	gac	259
Asp	Asp	Leu	Ser	Leu	Leu	Val	Asp	Asn	Gly	Ala	Glu	Val	Val	Val	Asp	
		40				45						50				

ttc	acc	act	cct	aac	gct	gtg	atg	ggc	aac	ctg	gag	ttc	tgc	atc	aac	307
Phe	Thr	Thr	Pro	Asn	Ala	Val	Met	Gly	Asn	Leu	Glu	Phe	Cys	Ile	Asn	
	55				60				65							

aac	ggc	att	tct	gcg	gtt	gtt	gga	acc	acg	ggc	ttc	gat	gat	gct	cgt	355
Asn	Gly	Ile	Ser	Ala	Val	Val	Gly	Thr	Thr	Gly	Phe	Asp	Asp	Ala	Arg	
	70				75					80				85		

ttg	gag	cag	gtt	cgc	gac	tgg	ctt	gaa	gga	aaa	gac	aat	gtc	ggt	gtt	403
Leu	Glu	Gln	Val	Arg	Asp	Trp	Leu	Glu	Gly	Lys	Asp	Asn	Val	Gly	Val	
			90					95					100			

ctg	atc	gca	cct	aac	ttt	gct	atc	tct	gcg	gtg	ttg	acc	atg	gtc	ttt	451
Leu	Ile	Ala	Pro	Asn	Phe	Ala	Ile	Ser	Ala	Val	Leu	Thr	Met	Val	Phe	

105	110	115	
tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg			499
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu			
120	125	130	
cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act			547
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr			
135	140	145	
gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag			595
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln			
150	155	160	165
cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta			643
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val			
170	175	180	
gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac			691
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His			
185	190	195	
gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag			739
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln			
200	205	210	
gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg			787
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val			
215	220	225	
cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac			835
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr			
230	235	240	245
cta ggc ctg taaaggctca ttccagcagc ggg			867
Leu Gly Leu			

<210> 36

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
1 5 10 15

Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
20 25 30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
65 70 75 80

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys

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<210> 37
<211> 873
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(850)  
<223> RXA00864
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<400> 37
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agcagcgggt ggaatttttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt 115
Val Ala Glu Gln Val
1 5

aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163
Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
10 15 20

gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag 211
Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
25 30 35

ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
40 45 50

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act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac 307
Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
    55                60                65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 355
Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
    70                75                80                85

tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403
Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
                90                95                100

tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg 451
Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
                105                110                115

gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg 499
Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
                120                125                130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg 547
His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
                135                140                145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag 595
Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
    150                155                160                165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc 643
Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
                170                175                180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691
Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
                185                190                195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta 739
Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
                200                205                210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787
Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
    215                220                225

ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg 835
Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
    230                235                240                245

tat gtc atg gac ttt taacgcaaag ctcacaccca cga 873
Tyr Val Met Asp Phe
                250

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<210> 38

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 38

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Glu Ala Leu	Val Glu Phe Ala	Gly Arg Ala Cys	Tyr Glu Thr Phe Asp
	35	40	45
Lys Pro Asn	Pro Arg Thr Ala	Ser Asn Ala Ala	Tyr Leu Arg His Ile
	50	55	60
Met Glu Val	Gly His Thr Ala	Leu Leu Glu His	Ala Asn Ala Thr Met
	65	70	75
Tyr Ile Arg	Gly Ile Ser Arg	Ser Ala Thr His	Glu Leu Val Arg His
	85	90	95
Arg His Phe	Ser Phe Ser Gln	Leu Ser Gln Arg	Phe Val His Ser Gly
	100	105	110
Glu Ser Glu	Val Val Val Pro	Thr Leu Ile Asp	Glu Asp Pro Gln Leu
	115	120	125
Arg Glu Leu	Phe Met His Ala	Met Asp Glu Ser	Arg Phe Ala Phe Asn
	130	135	140
Glu Leu Leu	Asn Ala Leu Glu	Glu Lys Leu Gly	Asp Glu Pro Asn Ala
	145	150	155
Leu Leu Arg	Lys Lys Gln Ala	Arg Gln Ala Ala	Arg Ala Val Leu Pro
	165	170	175
Asn Ala Thr	Glu Ser Arg Ile	Val Val Ser Gly	Asn Phe Arg Thr Trp
	180	185	190
Arg His Phe	Ile Gly Met Arg	Ala Ser Glu His	Ala Asp Val Glu Ile
	195	200	205
Arg Glu Val	Ala Val Glu Cys	Leu Arg Lys Leu	Gln Val Ala Ala Pro
	210	215	220
Thr Val Phe	Gly Asp Phe Glu	Ile Glu Thr Leu	Ala Asp Gly Ser Gln
	225	230	235
Met Ala Thr	Ser Pro Tyr Val	Met Asp Phe	
	245	250	

<210> 39

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 39

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Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
1 5 10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

<210> 40
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 40
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
20 25 30

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Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
 35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175

Ala Ser Met Val
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<210> 41
 <211> 1143
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1120)
 <223> RXN00355

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ggtcctgatg aaagagatgt cctgaatca tcataaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307

Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val		
55						60					65						
gcc	gac	gtg	gac	aag	cac	gcc	gac	gac	gtg	gac	gtg	ctg	ttc	ctg	tgc	355	
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys	85	
70					75					80							
atg	ggc	tcc	gcc	acc	gac	atc	cct	gag	cag	gca	cca	aag	ttc	gcg	cag	403	
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln	100	
				90					95								
ttc	gcc	tgc	acc	gta	gac	acc	tac	gac	aac	cac	cgc	gac	atc	cca	cgc	451	
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Arg	115	
			105					110									
cac	cgc	cag	gtc	atg	aac	gaa	gcc	gcc	acc	gca	gcc	ggc	aac	gtt	gca	499	
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala	130	
		120					125										
ctg	gtc	tct	acc	ggc	tgg	gat	cca	gga	atg	ttc	tcc	atc	aac	cgc	gtc	547	
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val	145	
	135					140											
tac	gca	gcg	gca	gtc	tta	gcc	gag	cac	cag	cag	cac	acc	ttc	tgg	ggc	595	
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly	165	
	150				155					160							
cca	ggt	ttg	tca	cag	ggc	cac	tcc	gat	gct	ttg	cga	cgc	atc	cct	ggc	643	
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly	180	
				170				175									
gtt	caa	aag	gca	gtc	cag	tac	acc	ctc	cca	tcc	gaa	gac	gcc	ctg	gaa	691	
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu	195	
			185					190									
aag	gcc	cgc	cgc	ggc	gaa	gcc	ggc	gac	ctt	acc	gga	aag	caa	acc	cac	739	
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His	210	
		200					205										
aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	gcg	gcc	gat	cac	gag	cgc	atc	787	
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile	225	
	215					220											
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	gtt	ggc	tac	gaa	gtc	835	
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val	245	
	230				235					240							
gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttc	gac	tcc	gag	cac	acc	ggc	883	
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly	260	
			250						255								
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	ttc	931	
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe	275	
			265					270									
aac	cac	acc	gtg	gaa	tac	atc	ctc	aag	ctg	gac	cga	aac	cca	gat	ttc	979	
Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	Arg	Asn	Pro	Asp	Phe	290	
		280					285										
acc	gct	tcc	tca	cag	atc	gct	ttc	ggt	cgc	gca	gct	cac	cgc	atg	aag	1027	
Thr	Ala	Ser	Ser	Gln	Ile	Ala	Phe	Gly	Arg	Ala	Ala	His	Arg	Met	Lys		

295 300 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac 1075
 Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
 310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc 1120
 Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
 330 335 340

taatttagct cgaggggcaa gga 1143

<210> 42
 <211> 340
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 42
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Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
 20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
 35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
 50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
 85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
 100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
 115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
 130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
 145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 180 185 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 260 265 270
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
 275 280 285
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
 290 295 300
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
 305 310 315 320
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
 325 330 335
 Ala Arg Asp Val
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<210> 43

<211> 958

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> FRXA00352

<400> 43

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ggtcctgatg aaagagatgt cctgaatca tcatctaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
 55 60 65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc 355
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70 75 80 85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag 403
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
 90 95 100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc 451
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
 105 110 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca 499
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
 120 125 130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc 547
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
 135 140 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc 595
 Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
 150 155 160 165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc 643
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
 170 175 180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa 691
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
 185 190 195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac 739
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
 200 205 210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc 787
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
 215 220 225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
 230 235 240 245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc 883
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
 250 255 260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc 931
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
 265 270 275

aac cac acc gtg gaa tac atc ctc aag 958
 Asn His Thr Val Glu Tyr Ile Leu Lys
 280 285

<210> 44

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu

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Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met	35	40	45
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr	50	55	60
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp	65	70	75
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala	85	90	95
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His	100	105	110
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala	115	120	125
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe	130	135	140
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln	145	150	155
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu	165	170	175
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser	180	185	190
Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr	195	200	205
Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala	210	215	220
Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe	225	230	235
Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp	245	250	255
Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly	260	265	270
Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys	275	280	285

<210> 45

<211> 1400

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1377)

<223> RXA00972

<400> 45

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aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat	96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn	
20 25 30	
gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg	144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu	
35 40 45	
cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag	192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu	
50 55 60	
gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga	240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly	
65 70 75 80	
cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att	288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile	
85 90 95	
gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc	336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile	
100 105 110	
aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc	384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile	
115 120 125	
acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt	432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val	
130 135 140	
caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa	480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu	
145 150 155 160	
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg	528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu	
165 170 175	
atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc	576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala	
180 185 190	
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc	624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser	
195 200 205	
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg	672
Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu	
210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc	720

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly	
225 230 235 240	
ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac	768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His	
245 250 255	
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac	816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr	
260 265 270	
ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt	864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val	
275 280 285	
gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc	912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly	
290 295 300	
atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc	960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly	
305 310 315 320	
ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac	1008
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His	
325 330 335	
gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg	1056
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met	
340 345 350	
tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc	1104
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg	
355 360 365	
gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg	1152
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val	
370 375 380	
ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac	1200
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr	
385 390 395 400	
cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc	1248
Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly	
405 410 415	
gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc	1296
Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro	
420 425 430	
gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc	1344
Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg	
435 440 445	
gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga	1397
Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala	
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ccc	1400

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 <213> Corynebacterium glutamicum

<400> 46

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Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
      35          40          45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
      50          55          60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
      65          70          75          80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
      85          90          95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
      100          105          110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
      115          120          125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
      130          135          140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
      145          150          155          160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
      165          170          175

Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
      180          185          190

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
      195          200          205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
      210          215          220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
      225          230          235          240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
      245          250          255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
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Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
      275          280          285

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Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
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Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
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Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
 325 330 335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340 345 350

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
 355 360 365

Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
 370 375 380

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
 405 410 415

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
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Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2098)

<223> RXA02653

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 Met Ile Pro Lys Pro
 1 5

gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tcg gaa 163
 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
 10 15 20

aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
 25 30 35

gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259
 Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu

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tgg gga atg ggg gcc act tgg cgg gag ctg tac ccc agc atc gtg gaa			307
Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu			
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cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cac tta			355
Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu			
70	75	80	85
gcc cgg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt			403
Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe			
	90	95	100
gaa tac ctc caa gaa ctc gta aaa tcc gga gtg gta gac atc act cac			451
Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His			
	105	110	115
ctg cat cgt ggc cgg gaa cca ctg aca gat tta gtt cgt gaa ctt gaa			499
Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu			
	120	125	130
ata act gtg gtg ata gac gct gtt ctt ccc ccg ccg gga gta gtg cca			547
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro			
	135	140	145
ggc aca ttg gtg cac aat ttg gta aaa gag gga tat gcc aga atg cgt			595
Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg			
150	155	160	165
cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg			643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly			
	170	175	180
caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg			691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu			
	185	190	195
ggt aat gac aca ttg tcg cga tca tta cat gac ata atc ccg aag tgg			739
Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp			
	200	205	210
gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat			787
Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His			
	215	220	225
ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc			835
Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu			
230	235	240	245
act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt			883
Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser			
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cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag			931
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu			
	265	270	275
ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt			979
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe			
	280	285	290

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acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val 310 315 320 325	1075
ctt aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile 330 335 340	1123
aaa ccg gac aga cta ttg gca tta gcg atc gaa aat ggc gtg atc atc Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile 345 350 355	1171
tct gtg gat tcg cgt gat gaa tta gat cgc att tcg gct ttg gtt ggt Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly 360 365 370	1219
gac cgc gtt gca cga gtt gcg cct aga gta gct cca gat cct gca gtc Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val 375 380 385	1267
tta cct cca act aga ttt ggt gag cgt gct gca gac tgg ggt aat cgg Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg 390 395 400 405	1315
ctt acc gag gtg ata ccc ggc gtg gat att gtg ggt ctt cac gtt cac Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His 410 415 420	1363
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aag ggg gta gct cag atg ctc att gac ccg gga ttg ccg tta cac ata Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile 520 525 530	1699

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa 1747
 Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu
 535 540 545

gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctg 1795
 Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu
 550 555 560 565

gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att 1843
 Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile
 570 575 580

gat ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca 1891
 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
 585 590 595

tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg 1939
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg
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cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att 1987
 Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
 615 620 625

cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac 2035
 Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
 630 635 640 645

caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac 2083
 Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
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gat atc gat gcg gat taagacataa ccattcgcta atc 2121
 Asp Ile Asp Ala Asp
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 35 40 45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
 50 55 60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
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Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
 85 90 95

Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
 100 105 110
 Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
 115 120 125
 Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
 130 135 140
 Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
 145 150 155 160
 Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
 165 170 175
 Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr
 180 185 190
 Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp
 195 200 205
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
 210 215 220
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
 225 230 235 240
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
 245 250 255
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
 260 265 270
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
 275 280 285
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
 290 295 300
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
 305 310 315 320
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
 325 330 335
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
 340 345 350
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
 355 360 365
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
 370 375 380
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
 385 390 395 400
 Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
 405 410 415
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu

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His	Ser	Pro	Gln	Phe	Ile	Asp	Leu	Gly	Gly	Gly	Val	Pro	Met	Ser	Tyr															
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Ile	Glu	Ser	Glu	Glu	Asp	Trp	Ile	Arg	Tyr	Gln	Ser	Ala	Lys	Ser	Ala															
465					470					475					480															
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Lys	Asp	Val	Leu	Ser	Lys	Gly	Val	Ala	Gln	Met	Leu	Ile	Asp	Arg	Gly															
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Leu	Arg	Leu	His	Ile	Glu	Pro	Gly	Arg	Ser	Leu	Leu	Asp	Gly	Cys	Gly															
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Val	Thr	Leu	Ala	Glu	Val	Ala	Phe	Val	Lys	Thr	Arg	Ser	Asp	Gly	Leu															
545					550					555					560															
Pro	Leu	Val	Gly	Leu	Ala	Met	Asn	Arg	Thr	Gln	Cys	Arg	Thr	Thr	Ser															
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Asp	Asp	Phe	Leu	Ile	Asp	Pro	Leu	His	Ile	Thr	Asp	Gly	Asp	Val	Gly															
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Glu	Glu	Ile	Glu	Ala	Tyr	Leu	Val	Gly	Ala	Tyr	Cys	Ile	Glu	Asp	Glu															
		595					600					605																		
Leu	Ile	Leu	Arg	Arg	Arg	Ile	Arg	Phe	Pro	Arg	Gly	Val	Lys	Pro	Gly															
		610				615					620																			
Asp	Ile	Ile	Gly	Ile	Pro	Asn	Thr	Ala	Gly	Tyr	Phe	Met	His	Ile	Leu															
625					630					635					640															
Glu	Ser	Ala	Ser	His	Gln	Ile	Pro	Leu	Ala	Lys	Asn	Val	Val	Trp	Pro															
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Glu	Gly	Gln	Leu	Asp	Asp	Ile	Asp	Ala	Asp																					
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<213> Corynebacterium glutamicum

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<222> (101)..(970)

<223> RXA01393

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Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
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Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
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gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa 307
Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
                55                60                65

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Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu
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gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca 403
Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr
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Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr
                105                110                115

ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg 499
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg
                120                125                130

cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg 547
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala
                135                140                145

gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca 595
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
                150                155                160                165

acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg 643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp
                170                175                180

gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
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cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Val
                200                205                210

tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc 787
Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly
                215                220                225

ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa 835

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Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys
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 gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg 883
 Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met
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 tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca 931
 Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr
 265 270 275
 gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc 980
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 35 40 45
 Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60
 Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80
 Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95
 Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110
 Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125
 Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140
 Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160
 His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175
 Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190
 Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val

195	200	205
Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu		
210	215	220
Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala		
225	230	235 240
Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro		
	245	250 255
Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser		
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Arg Pro		
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 <223> RXA00241

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 Val Asn Thr Gln Ser
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gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Thr Ser Arg Thr Val Ser
 10 15 20

att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga 211
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
 25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
 40 45 50

atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
 55 60 65

ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc 355
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
 70 75 80 85

gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc 403
 Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser
 90 95 100

tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac 451
 Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr
 105 110 115

gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc 499
 Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser
 120 125 130

caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg 547
 Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp
 135 140 145

ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg 595
 Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu
 150 155 160 165

aca acg gtc acc acc gtg gcc aaa att ctg cct ctg ttg tgc ttc atc 643
 Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile
 170 175 180

atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat 691
 Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp
 185 190 195

tta tgg gcg cgt gat ggt ggc gtg ggc agc att ttt gat cag gtg cgc 739
 Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg
 200 205 210

ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca 787
 Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala
 215 220 225

tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct 835
 Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala
 230 235 240 245

acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct 883
 Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Val Ser Ile Ser
 250 255 260

tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca 931
 Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro
 265 270 275

gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt 979
 Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly
 280 285 290

gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat 1027
 Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr
 295 300 305

gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg 1075
 Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met
 310 315 320 325

gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct 1123
 Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
 330 335 340

gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc 1171
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
 345 350 355

atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg 1219
 Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
 360 365 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg 1267
 Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
 375 380 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc 1315
 Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
 390 395 400 405

aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc 1363
 Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg
 410 415 420

aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg 1411
 Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
 425 430 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg 1459
 Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
 440 445 450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa 1507
 Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
 455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt 1555
 Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
 470 475 480 485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt 1603
 Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
 490 495 500

taaacaccga aaccttcctg cta 1626

<210> 52

<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
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Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
 20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
 35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
 50 55 60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
 65 70 75 80
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
 85 90 95
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
 100 105 110
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
 115 120 125
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
 130 135 140
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
 145 150 155 160
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
 165 170 175
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu
 180 185 190
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
 195 200 205
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
 210 215 220
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
 225 230 235 240
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
 245 250 255
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
 260 265 270
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
 275 280 285
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
 290 295 300
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
 305 310 315 320
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
 325 330 335
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
 340 345 350
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
 355 360 365
 Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
 370 375 380
 Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr

385 390 395 400
 His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser
 405 410 415
 Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
 420 425 430
 Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
 435 440 445
 Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg
 450 455 460
 Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
 465 470 475 480
 Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
 485 490 495
 Gly Ser Leu Ser Leu
 500

<210> 53
 <211> 822
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(799)
 <223> RXA01394

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 Met Glu Ile Phe Ile
 1 5
 aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
 10 15 20
 aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
 25 30 35
 gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259
 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
 40 45 50
 acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307
 Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
 55 60 65
 att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70 75 80 85

gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att 403
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
 90 95 100

gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tgc 451
 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
 105 110 115

gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc 499
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
 120 125 130

gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg 547
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
 135 140 145

acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc 595
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
 150 155 160 165

ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct 643
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
 170 175 180

ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc 691
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
 185 190 195

gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg 739
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
 200 205 210

atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg 787
 Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu
 215 220 225

atg ttg atg ggt tagttttcgc gggtttttggga atc 822
 Met Leu Met Gly
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<210> 54

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
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Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
 20 25 30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
 35 40 45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala
 50 55 60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
 65 70 75 80

Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu
85 90 95

Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr
100 105 110

Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg
115 120 125

Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu
130 135 140

Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala
145 150 155 160

Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg
165 170 175

Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro
180 185 190

Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro
195 200 205

Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala
210 215 220

Leu Ala Ile Lys Leu Met Leu Met Gly
225 230

<210> 55

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00865

<400> 55

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tttaaccccc aaatgagggga agaaggtaac cttgaactct atg agc aca ggt tta 115
Met Ser Thr Gly Leu
1 5

aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
10 15 20

gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
25 30 35

gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc 259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu
40 45 50

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta 307
 Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu
 55 60 65

gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc 355
 Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu
 70 75 80 85

atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg 403
 Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala
 90 95 100

gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct 451
 Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro
 105 110 115

tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca 499
 Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala
 120 125 130

att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt 547
 Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly
 135 140 145

cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa 595
 Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu
 150 155 160 165

tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca 643
 Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala
 170 175 180

gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat 691
 Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp
 185 190 195

gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att 739
 Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile
 200 205 210

tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca 787
 Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr
 215 220 225

agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa 835
 Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys
 230 235 240 245

cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg 883
 Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu
 250 255 260

gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga 931
 Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg
 265 270 275

ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa 979
 Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
 280 285 290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccga aat 1026

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<210> 56
<211> 301
<212> PRT
<213> Corynebacterium glutamicum
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<400> 56

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
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Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
 275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
 290 295 300

<210> 57
 <211> 1071
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1048)
 <223> RXS02021

<400> 57
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aaaccttagt taaaacatga tggaagcggg cgattaaaaa atg agt gaa aac att 115
 Met Ser Glu Asn Ile
 1 5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163
 Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
 10 15 20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211
 Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
 25 30 35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259
 Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
 40 45 50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307
 Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
 55 60 65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355
 Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
 70 75 80 85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403
 Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
 90 95 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451
 Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
 105 110 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499
 Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
 120 125 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547
 Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
 135 140 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595

His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165

 ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180

 tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195

 aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210

 ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225

 cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

 caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

 gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

 ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

 cca gtt gcc cgc ctc aaa gct tgaccatttt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 58

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
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Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
 35 40 45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
 50 55 60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65 70 75 80
 Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
 85 90 95
 Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
 100 105 110
 Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
 115 120 125
 Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
 130 135 140
 Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
 145 150 155 160
 Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
 165 170 175
 Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
 180 185 190
 Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
 195 200 205
 Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
 210 215 220
 Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
 225 230 235 240
 Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
 245 250 255
 Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
 260 265 270
 Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
 275 280 285
 Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
 290 295 300
 Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
 305 310 315

<210> 59

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1273)

<223> RXS02157

<400> 59

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Met Ser Thr Leu Glu																
1 5																
act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag																163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu																
10 15 20																
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc																211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val																
25 30 35																
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc																259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala																
40 45 50																
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt																307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly																
55 60 65																
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag																355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu																
70 75 80 85																
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa																403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln																
90 95 100																
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct																451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala																
105 110 115																
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt																499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val																
120 125 130																
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag																547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln																
135 140 145																
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc																595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe																
150 155 160 165																
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac																643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn																
170 175 180																
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg																691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr																
185 190 195																
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg																739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu																
200 205 210																
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc																787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly																
215 220 225																

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245
 ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260
 ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275
 aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290
 aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
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<210> 60

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
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Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
 355 360 365
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys

370

375

380

Ala Ile Ala Glu Thr Ile Ala
385 390

<210> 61
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXC00733

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gtgaaattgt tgaatcccaa gagactgcgc aggcgcgaatc atg agt aat act gca 115
Met Ser Asn Thr Ala 5

ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag 163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys 20

gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc 211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly 35

cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc 259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn 65

gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca 355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser 85

aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag 403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln 90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca ggc tca ggc att gat 451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp 105 110 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu 120 125 130

atc ggt agc ctg ttg tcg ttg ttc cag gcg cgg atg ctc aac cgc atc 547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile 135 140 145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile

150	155	160	165	
cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg				643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu				
	170	175	180	
ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa				691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln				
	185	190	195	
caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg				739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val				
	200	205	210	
ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg				787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu				
	215	220	225	
gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt				835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg				
	230	235	240	245
tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat				883
Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn				
	250	255	260	
gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc				931
Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe				
	265	270	275	
gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct				979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala				
	280	285	290	
tgt gta taaggccagc tttggtgccc agt				1008
Cys Val				
	295			

<210> 62

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

Met	Ser	Asn	Thr	Ala	Gly	Pro	Arg	Gly	Arg	Ser	His	Gln	Ala	Asp	Ala
1				5				10					15		

Ala	Pro	Asn	Gln	Lys	Ala	Gln	Asn	Phe	Gly	Pro	Ser	Ala	Lys	Arg	Leu
		20						25					30		

Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe
		35					40					45			

Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu
	50					55					60				

Gly	Lys	Ala	Thr	Asn	Val	Val	Phe	Glu	Gly	Phe	Leu	Ser	Lys	Arg	Met
65					70					75					80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala

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<210> 63
<211> 426
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (1)..(426)  
<223> RXC00861
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<400> 63																
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Met	Ala	Pro	His	Lys	Val	Met	Leu	Ile	Thr	Thr	Gly	Thr	Gln	Gly	Glu	
1				5					10					15		
cct	atg	gct	gcg	ctg	tct	cgc	atg	gcg	cgt	cgt	gag	cac	cga	cag	atc	96
Pro	Met	Ala	Ala	Leu	Ser	Arg	Met	Ala	Arg	Arg	Glu	His	Arg	Gln	Ile	
			20					25					30			

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
130 135 140

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<221> CDS
<222> (101)..(1066)
<223> RXC00866
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[illegible]

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Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp			
185	190	195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc			739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val			
200	205	210	
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att			787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile			
215	220	225	
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt			835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg			
230	235	240	245
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt			883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg			
250	255	260	
ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg			931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro			
265	270	275	
ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt			979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu			
280	285	290	
ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac			1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp			
295	300	305	
atc aag ctg gat cag act cct cct gat gga cgc cca act			1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr			
310	315	320	

<210> 66

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1					5				10					15	

Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50						55				60				

Ser	Gln	Gly	Ser	Gln	Asn	Ala	Gln	Gly	Ser	Gln	Asn	Arg	Glu	Ser	Gly
	65				70					75				80	

Asn	Asn	Asn	Arg	Asn	Arg	Ser	Asn	Asn	Asn	Arg	Arg	Gly	Gly	Arg	Gly
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[illegible]

<210> 67
<211> 1527
<212> DNA
<213> Corynebacterium glutamicum

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<220>  
<221> CDS  
<222> (101)..(1504)  
<223> RXC02095
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<400> 67
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tactccccca	acagggtcaa	aaatactgaa	agggtcacgc	atg	aaa	act	gag	caa	115							
				Met	Lys	Thr	Glu	Gln								
				1				5								
tcc	caa	aaa	gca	caa	tta	gcc	cct	aag	aaa	gca	cct	gaa	aag	cca	caa	163
Ser	Gln	Lys	Ala	Gln	Leu	Ala	Pro	Lys	Lys	Ala	Pro	Glu	Lys	Pro	Gln	
				10				15						20		
cgc	atc	cgc	caa	ctt	att	tcc	gtg	gcg	tgg	cag	cga	cct	tgg	ctc	acc	211
Arg	Ile	Arg	Gln	Leu	Ile	Ser	Val	Ala	Trp	Gln	Arg	Pro	Trp	Leu	Thr	
			25				30						35			
tca	ttc	acc	gta	atc	agc	gct	tta	gct	gca	acg	ttg	ttt	gaa	ctt	aca	259
Ser	Phe	Thr	Val	Ile	Ser	Ala	Leu	Ala	Ala	Thr	Leu	Phe	Glu	Leu	Thr	
		40					45					50				
ctt	cct	ctt	ttg	acc	ggg	ggc	gcc	atc	gat	atc	gcg	ctc	gga	aat	acc	307
Leu	Pro	Leu	Leu	Thr	Gly	Gly	Ala	Ile	Asp	Ile	Ala	Leu	Gly	Asn	Thr	
	55					60					65					
gga	gat	act	tta	acc	act	gac	ctg	ctg	gac	cgg	ttc	act	ccg	agt	gga	355
Gly	Asp	Thr	Leu	Thr	Thr	Asp	Leu	Leu	Asp	Arg	Phe	Thr	Pro	Ser	Gly	
	70					75				80					85	
tta	agc	gtg	ttg	acc	agc	gtc	att	gcc	ctt	atc	gtg	ctt	ctc	gcg	ttg	403
Leu	Ser	Val	Leu	Thr	Ser	Val	Ile	Ala	Leu	Ile	Val	Leu	Leu	Ala	Leu	
			90						95					100		
ctt	cgc	tat	gcc	agt	caa	ttt	gga	cgg	cga	tac	acc	gca	ggc	aag	ctc	451
Leu	Arg	Tyr	Ala	Ser	Gln	Phe	Gly	Arg	Arg	Tyr	Thr	Ala	Gly	Lys	Leu	
			105					110					115			
agc	atg	ggg	gta	cag	cat	gat	gtc	cgg	ctt	aaa	acg	atg	cgc	tca	ttg	499
Ser	Met	Gly	Val	Gln	His	Asp	Val	Arg	Leu	Lys	Thr	Met	Arg	Ser	Leu	
		120					125					130				
cag	aac	ctc	gat	ggg	cca	ggg	cag	gac	tct	att	cgc	aca	ggc	caa	gta	547
Gln	Asn	Leu	Asp	Gly	Pro	Gly	Gln	Asp	Ser	Ile	Arg	Thr	Gly	Gln	Val	
	135					140						145				
gtc	agt	cgg	tcc	att	tcg	gat	atc	aac	atg	gtg	caa	agc	ctt	gtg	gcg	595
Val	Ser	Arg	Ser	Ile	Ser	Asp	Ile	Asn	Met	Val	Gln	Ser	Leu	Val	Ala	
	150				155					160				165		
atg	ttg	ccg	atg	ttg	atc	gga	aat	gtg	gtc	aag	ctt	gtg	ctc	act	ttg	643
Met	Leu	Pro	Met	Leu	Ile	Gly	Asn	Val	Val	Lys	Leu	Val	Leu	Thr	Leu	
				170				175						180		
gtg	atc	atg	ctg	gct	att	tcc	ccg	ccg	ctg	acc	atc	atc	gct	gca	gtg	691
Val	Ile	Met	Leu	Ala	Ile	Ser	Pro	Pro	Leu	Thr	Ile	Ile	Ala	Ala	Val	
			185					190					195			
ttg	gtg	cct	ttg	ctg	ttg	tgg	gcc	gtg	gcc	tat	tcg	cga	aaa	gcg	ctt	739
Leu	Val	Pro	Leu	Leu	Leu	Trp	Ala	Val	Ala	Tyr	Ser	Arg	Lys	Ala	Leu	
		200					205					210				
ttt	gcg	tcc	acg	tgg	tcg	gcc	cag	caa	aag	gct	gcg	gat	ctg	acc	act	787
Phe	Ala	Ser	Thr	Trp	Ser	Ala	Gln	Gln	Lys	Ala	Ala	Asp	Leu	Thr	Thr	
	215					220					225					
cat	gtg	gaa	gaa	act	gtc	acg	ggg	atc	cgc	gtg	gtc	aag	gca	ttt	gcg	835

His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala	
230 235 240 245	
cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta	883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu	
250 255 260	
ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc	931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro	
265 270 275	
atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc	979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly	
280 285 290	
ggg ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg	1027
Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val	
295 300 305	
gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg	1075
Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu	
310 315 320 325	
tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc	1123
Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg	
330 335 340	
atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac	1171
Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His	
345 350 355	
ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta	1219
Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val	
360 365 370	
gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt	1267
Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly	
375 380 385	
gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct	1315
Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala	
390 395 400 405	
gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc	1363
Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala	
410 415 420	
ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc	1411
Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser	
425 430 435	
gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac	1459
Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr	
440 445 450	
tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag	1504
Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln	
455 460 465	
tgatgagcag atcgaacacg cag	1527

<210> 68
 <211> 468
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 68
 Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala
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 Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
 20 25 30
 Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45
 Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60
 Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
 85 90 95
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
 145 150 155 160
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
 165 170 175
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
 180 185 190
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
 195 200 205
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
 210 215 220
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
 225 230 235 240
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
 245 250 255
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
 260 265 270
 Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320

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Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
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Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
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Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
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 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
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gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
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gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
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Met Lys Pro Gln Gly
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Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
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gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
25 30 35

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
40 45 50

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
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Thr	Gly	Ile	Ala	Phe	Leu	Pro	Arg	Gly	Arg	Met	Ala	Met	Met	Asp	Ala	
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Gln	Lys	Glu	Ile	Glu	Arg	Ile	Ala	Lys	Gln	Glu	Gly	Ala	Asp	Val	Leu	
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Glu	Glu	Ala	Met	Pro	Ser	Phe	Ala	Gln	Ile	Phe	Leu	Thr	Val	Pro	Gly	
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Pro	Ser	Leu	Ser	Ser	Arg	Thr	Ile	Ile	Tyr	Lys	Gly	Met	Leu	Thr	Thr	
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Leu	Gln	Leu	Glu	Gly	Phe	Phe	Glu	Asp	Leu	Gly	Asp	Ala	Arg	Leu	Glu	
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Ser	Ala	Ile	Ala	Ile	Val	His	Ser	Arg	Phe	Ser	Thr	Asn	Thr	Phe	Pro	
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Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe	Asp	Glu	Ala	Leu	Glu	
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Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His	Ala	Val	Ala	Met	Met	
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Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro	
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Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp	
345 350 355	
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Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu	
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Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser	
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Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp	
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Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu	
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Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His	
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Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg	
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Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met	
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Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg	
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Lys	Thr	Leu	Ile	Val	Leu	Ser	Asp	Arg	Glu	Ser	Asp	Glu	Arg	Met	Ala		
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Arg	His	Arg	Ser	Ala	Phe	Leu	Pro	Arg	Pro	Glu	Glu	His	Ala	His	Arg		
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gaa	ttg	gat	ttg	ggt	ggt	gaa	tac	aag	tgg	cgc	cgc	gaa	ggt	gaa	tac	2515	
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His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg	810	815	820	
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Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp	825	830	835	
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Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr	840	845	850	
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Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile	855	860	865	
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Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala	870	875	880	885
gaa gcc cat gag gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg				2803
Glu Ala His Glu Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met	890	895	900	
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Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu	905	910	915	
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Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly	920	925	930	
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Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln	935	940	945	
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Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro	950	955	960	965
cca aac aag gtg tac cca tgg gtt gca gaa gtc cgc atc acc acc cca				3043
Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro	970	975	980	
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Gly Val Gly Leu Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile	985	990	995	
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Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg	1000	1005	1010	
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Ala Arg Ile His Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val	1015	1020	1025	
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Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly	1030	1035	1040	1045

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 1335 1340 1345

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 Ser
 1510

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Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala
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Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln
          50           55           60

Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu
          65           70           75           80

Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met
          85           90           95

Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu
          100          105          110

Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp
          115          120          125

Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe
          130          135          140

Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe
          145          150          155          160

Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg
          165          170          175

Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys
          180          185          190

Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly
          195          200          205

Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser
          210          215          220

Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val
          225          230          235          240

Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
          245          250          255

Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser
          260          265          270

Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe
          275          280          285

Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His

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290					295					300					
Ala	Val	Ala	Met	Met	Ile	Pro	Gln	Ala	Trp	Glu	His	Asn	Lys	Thr	Leu
305					310					315					320
Ser	Pro	Glu	Leu	Arg	Asp	Phe	Tyr	Glu	Tyr	His	Ser	Cys	Leu	Met	Glu
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Pro	Trp	Asp	Gly	Pro	Ala	Ala	Leu	Ala	Phe	Thr	Asp	Gly	Arg	Phe	Val
			340					345					350		
Gly	Ala	Val	Leu	Asp	Arg	Asn	Gly	Leu	Arg	Pro	Gly	Arg	Ile	Thr	Ile
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Thr	Asp	Ser	Gly	Leu	Val	Val	Met	Ala	Ser	Glu	Ser	Gly	Val	Leu	Asp
	370					375					380				
Leu	Arg	Glu	Glu	Ser	Val	Val	Lys	Arg	Thr	Arg	Val	Gln	Pro	Gly	Arg
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Met	Phe	Leu	Val	Asp	Thr	Ala	Glu	Gly	Arg	Ile	Val	Glu	Asp	Glu	Glu
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Ile	Lys	Gln	Lys	Leu	Ser	Glu	Ala	Gln	Pro	Tyr	Gly	Glu	Trp	Ile	Arg
			420					425					430		
Asp	Asn	Phe	Val	His	Leu	Asp	Arg	Leu	Pro	Gln	Thr	Arg	Tyr	Asn	Tyr
		435					440					445			
Met	Ala	His	Ser	Arg	Ala	Val	Leu	Arg	Gln	Arg	Val	Phe	Gly	Ile	Thr
		450				455					460				
Glu	Glu	Asp	Val	Asp	Leu	Leu	Leu	Leu	Pro	Met	Ala	Arg	Gln	Gly	Ala
465					470					475					480
Glu	Ala	Ile	Gly	Ser	Met	Gly	Ser	Asp	Thr	Pro	Ile	Ala	Ala	Leu	Ser
			485						490					495	
Gln	Arg	Pro	Arg	Met	Leu	Tyr	Asp	Phe	Phe	Ala	Gln	Arg	Phe	Ala	Gln
			500					505					510		
Val	Thr	Asn	Pro	Pro	Leu	Asp	Ser	Ile	Arg	Glu	Lys	Pro	Val	Thr	Ser
		515					520					525			
Met	Phe	Thr	Leu	Leu	Gly	Ala	Gln	Ser	Asp	Val	Leu	Asn	Pro	Gly	Pro
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Asp	Ala	Ala	Arg	Arg	Ile	Arg	Leu	Glu	Ser	Pro	Ile	Ile	Asp	Asn	His
545					550					555					560
Glu	Leu	Ala	Thr	Leu	Ile	Asn	Ala	Asn	Ala	His	Gly	Glu	Trp	Asp	Ser
			565						570					575	
Phe	Gly	Ala	Ala	Val	Ile	Ser	Gly	Leu	Tyr	Pro	Val	Ala	His	His	Gly
			580					585					590		
Ala	Gly	Met	Lys	Ala	Ala	Ile	Ala	Arg	Val	Arg	Arg	Glu	Val	Ser	Glu
		595					600					605			
Ala	Ile	Arg	Asn	Gly	Lys	Thr	Leu	Ile	Val	Leu	Ser	Asp	Arg	Glu	Ser
		610				615					620				

Asp Glu Arg Met Ala Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val
 625 630 635 640
 His Gln Tyr Leu Val Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val
 645 650 655
 Val Glu Ser Gly Asp Ala Arg Glu Val His His Leu Ala Met Leu Ile
 660 665 670
 Gly Phe Gly Ala Asp Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile
 675 680 685
 Asp Glu Leu Arg Met Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu
 690 695 700
 Ala Ser Arg Asn Tyr Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val
 705 710 715 720
 Met Ser Lys Met Gly Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln
 725 730 735
 Leu Ala Asp Val Thr Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe
 740 745 750
 Gly Gly Ile Ala Ser Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala
 755 760 765
 Ala Asp Val Glu Ala Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu
 770 775 780
 Glu His Ala His Arg Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg
 785 790 795 800
 Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu
 805 810 815
 Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr
 820 825 830
 Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu
 835 840 845
 Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu
 850 855 860
 Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr
 865 870 875 880
 Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu Ala Ile Ala Met Asn
 885 890 895
 Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg
 900 905 910
 Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys
 915 920 925
 Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn
 930 935 940

Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu
 945 950 955 960
 Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val
 965 970 975
 Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser Pro Pro Pro His His
 980 985 990
 Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys
 995 1000 1005
 Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys Leu Val Ala Glu Gln
 1010 1015 1020
 Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys Ala His Ala Asp Val
 1025 1030 1035 1040
 Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr
 1045 1050 1055
 Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr
 1060 1065 1070
 Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln
 1075 1080 1085
 Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu
 1090 1095 1100
 Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu
 1105 1110 1115 1120
 Gly Cys Ile Met Met Arg Val Cys His Leu Asp Thr Cys Pro Val Gly
 1125 1130 1135
 Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala
 1140 1145 1150
 Glu His Val Val Asn Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu
 1155 1160 1165
 Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln
 1170 1175 1180
 Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala
 1185 1190 1195 1200
 Ala His Leu Asp Leu Ser Pro Ile Phe His Arg Pro Glu Thr Pro His
 1205 1210 1215
 Phe Pro Thr Gln Asp Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu
 1220 1225 1230
 Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile
 1235 1240 1245
 Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser
 1250 1255 1260
 Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val

1265 1270 1275 1280
 Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu
 1285 1290 1295
 Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg
 1300 1305 1310
 Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys
 1315 1320 1325
 Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro
 1330 1335 1340
 Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly
 1345 1350 1355 1360
 Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu
 1365 1370 1375
 Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile
 1380 1385 1390
 Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu
 1395 1400 1405
 Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala
 1410 1415 1420
 Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu
 1425 1430 1435 1440
 Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu
 1445 1450 1455
 Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg
 1460 1465 1470
 Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu
 1475 1480 1485
 Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys
 1490 1495 1500
 Ile Met Glu Ala Val Ser
 1505 1510

<210> 73

<211> 1906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1906)

<223> FRXA00007

<400> 73

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gaacgattga tagaaacagg attaaagtga ggtatccgc	atg	aaa	cca	caa	gga	115
	Met	Lys	Pro	Gln	Gly	
	1				5	
ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att						163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile						
gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt						211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu						
gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag						259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys						
aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt						307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe						
tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc						355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala						
act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct						403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala						
cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt						451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu						
ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct						499
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala						
gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga						547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly						
aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt						595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg						
tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc						643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe						
ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act						691
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr						
ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag						739
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu						
tcg gcc att gct att gtg cac tcg cgt ttc tcc acg aac act ttc cca						787
Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser Thr Asn Thr Phe Pro						
agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag						835

Ser	Trp	Pro	Leu	Ala	His	Pro	Tyr	Arg	Phe	Val	Ala	His	Asn	Gly	Glu	
230					235					240					245	
atc	aac	act	gtg	cgt	ggc	aat	gaa	aac	tgg	atg	cgc	gcc	cgc	gag	gcg	883
Ile	Asn	Thr	Val	Arg	Gly	Asn	Glu	Asn	Trp	Met	Arg	Ala	Arg	Glu	Ala	
				250				255						260		
ctt	atc	aaa	aac	gac	aag	ctg	ggc	aat	ttg	agc	agc	gtg	ctg	cct	atc	931
Leu	Ile	Lys	Asn	Asp	Lys	Leu	Gly	Asn	Leu	Ser	Ser	Val	Leu	Pro	Ile	
			265					270					275			
tgc	acc	ccg	gag	ggc	tcg	gat	acc	gcg	cgt	ttc	gac	gag	gct	ttg	gag	979
Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe	Asp	Glu	Ala	Leu	Glu	
		280					285					290				
ctt	ttg	cac	ctg	ggc	gga	tac	tca	ctt	ccg	cat	gct	gtt	gcg	atg	atg	1027
Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His	Ala	Val	Ala	Met	Met	
	295					300					305					
atc	cct	cag	gcg	tgg	gaa	cac	aac	aag	acg	ctg	agc	cct	gag	ctg	cgt	1075
Ile	Pro	Gln	Ala	Trp	Glu	His	Asn	Lys	Thr	Leu	Ser	Pro	Glu	Leu	Arg	
310					315					320					325	
gat	ttc	tac	gaa	tac	cac	tct	tgt	ctg	atg	gag	cca	tgg	gat	ggc	cct	1123
Asp	Phe	Tyr	Glu	Tyr	His	Ser	Cys	Leu	Met	Glu	Pro	Trp	Asp	Gly	Pro	
				330					335					340		
gca	gcg	ctg	gca	ttt	act	gac	ggc	cgt	ttt	gtg	ggt	gcc	gtg	ctg	gac	1171
Ala	Ala	Leu	Ala	Phe	Thr	Asp	Gly	Arg	Phe	Val	Gly	Ala	Val	Leu	Asp	
			345					350					355			
cgt	aat	ggc	ctg	cga	cct	ggg	cga	atc	acc	att	act	gat	tcg	ggc	ttg	1219
Arg	Asn	Gly	Leu	Arg	Pro	Gly	Arg	Ile	Thr	Ile	Thr	Asp	Ser	Gly	Leu	
		360					365					370				
gtt	gtg	atg	gct	tct	gaa	tcg	gga	gtg	ttg	gac	ttg	agg	gag	gag	agc	1267
Val	Val	Met	Ala	Ser	Glu	Ser	Gly	Val	Leu	Asp	Leu	Arg	Glu	Glu	Ser	
	375					380					385					
gtc	gta	aag	cgt	act	cgc	gta	cag	cct	gga	cgc	atg	ttc	ctt	gtt	gac	1315
Val	Val	Lys	Arg	Thr	Arg	Val	Gln	Pro	Gly	Arg	Met	Phe	Leu	Val	Asp	
390					395					400					405	
act	gcc	gag	ggc	cgc	atc	gtt	gaa	gac	gag	gaa	atc	aag	cag	aaa	tta	1363
Thr	Ala	Glu	Gly	Arg	Ile	Val	Glu	Asp	Glu	Glu	Ile	Lys	Gln	Lys	Leu	
				410				415						420		
agc	gaa	gcg	cag	cca	tat	ggc	gag	tgg	att	cgc	gat	aat	ttt	gtg	cat	1411
Ser	Glu	Ala	Gln	Pro	Tyr	Gly	Glu	Trp	Ile	Arg	Asp	Asn	Phe	Val	His	
			425					430					435			
ctg	gat	cgt	ctg	cct	cag	aca	cgc	tac	aac	tac	atg	gcg	cac	tct	cgt	1459
Leu	Asp	Arg	Leu	Pro	Gln	Thr	Arg	Tyr	Asn	Tyr	Met	Ala	His	Ser	Arg	
		440					445					450				
gct	gtg	ttg	cgt	cag	cgt	gtt	ttc	gga	atc	act	gaa	gaa	gat	gtg	gat	1507
Ala	Val	Leu	Arg	Gln	Arg	Val	Phe	Gly	Ile	Thr	Glu	Glu	Asp	Val	Asp	
	455					460					465					
ttg	ttg	ctg	ctg	ccg	atg	gcc	cgc	cag	ggc	gct	gag	gcg	att	ggc	tcc	1555
Leu	Leu	Leu	Leu	Pro	Met	Ala	Arg	Gln	Gly	Ala	Glu	Ala	Ile	Gly	Ser	

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470              475              480              485
atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg 1603
Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met
              490              495              500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg 1651
Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro
              505              510              515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg 1699
Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu
              520              525              530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt 1747
Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg
              535              540              545

att cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg 1795
Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu
              550              555              560              565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta 1843
Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val
              570              575              580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct 1891
Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala
              585              590              595

gcg att gct cgt gtg
Ala Ile Ala Arg Val
              600

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<210> 74

<211> 602

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 74

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Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys
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Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile
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Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala
              35              40              45

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln
              50              55              60

Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu
              65              70              75              80

Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met
              85              90              95

Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu
              100              105              110

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Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp
 115 120 125
 Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe
 130 135 140
 Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe
 145 150 155 160
 Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg
 165 170 175
 Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys
 180 185 190
 Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly
 195 200 205
 Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser
 210 215 220
 Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val
 225 230 235 240
 Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
 245 250 255
 Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser
 260 265 270
 Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe
 275 280 285
 Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His
 290 295 300
 Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu
 305 310 315 320
 Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu
 325 330 335
 Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val
 340 345 350
 Gly Ala Val Leu Asp Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile
 355 360 365
 Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp
 370 375 380
 Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg
 385 390 395 400
 Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu
 405 410 415
 Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg
 420 425 430

Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr
435 440 445

Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr
450 455 460

Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala
465 470 475 480

Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser
485 490 495

Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln
500 505 510

Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser
515 520 525

Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro
530 535 540

Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His
545 550 555 560

Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser
565 570 575

Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly
580 585 590

Ala Gly Met Lys Ala Ala Ile Ala Arg Val
595 600

<210> 75

<211> 1362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (70)..(1362)

<223> FRXA00364

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gcgcattttttg cca cgc cct gaa gag cac gct cac cgt gaa ttg gat ttg 111
Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu
1 5 10

ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac cac ctg ttc aac 159
Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn
15 20 25 30

cca gaa acc atc ttc aag ctg cag cat gca acg cgt tct ggc agc tac 207
Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr
35 40 45

gag att ttc aag gat tac acc cgc aag gtt gat gat caa tcc act cgc 255
Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg

50										55										60										
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Leu	Gly	Thr	Ile	Arg	Gly	Leu	Phe	Glu	Phe	Ser	Thr	Asp	Arg	Lys	Pro															
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Ile	Ser	Val	Ser	Glu	Val	Glu	Pro	Val	Ser	Glu	Ile	Val	Lys	Arg	Phe															
80					85					90																				
tcc	act	ggt	gcg	atg	tct	tat	ggc	tcg	att	tct	gct	gaa	gcc	cat	gag	399														
Ser	Thr	Gly	Ala	Met	Ser	Tyr	Gly	Ser	Ile	Ser	Ala	Glu	Ala	His	Glu															
95					100					105					110															
gtc	ttg	gcc	atc	gcc	atg	aac	cga	ctg	ggc	ggt	atg	tcc	aac	tcc	ggc	447														
Val	Leu	Ala	Ile	Ala	Met	Asn	Arg	Leu	Gly	Gly	Met	Ser	Asn	Ser	Gly															
115					120					125																				
gaa	ggt	ggc	gag	gac	gcc	cgc	cga	ttt	gat	gtg	gaa	ccc	aac	ggt	gac	495														
Glu	Gly	Gly	Glu	Asp	Ala	Arg	Arg	Phe	Asp	Val	Glu	Pro	Asn	Gly	Asp															
130					135					140																				
tgg	aag	cgc	tct	gcc	att	aag	cag	gtg	gcc	tcg	gga	cgt	ttc	ggc	gtg	543														
Trp	Lys	Arg	Ser	Ala	Ile	Lys	Gln	Val	Ala	Ser	Gly	Arg	Phe	Gly	Val															
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acc	agc	cac	tac	ttg	aac	aac	tgc	acc	gat	att	cag	atc	aag	atg	gca	591														
Thr	Ser	His	Tyr	Leu	Asn	Asn	Cys	Thr	Asp	Ile	Gln	Ile	Lys	Met	Ala															
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cag	ggc	gca	aag	ccc	ggt	gaa	ggt	ggc	cag	ctg	cca	cca	aac	aag	gtg	639														
Gln	Gly	Ala	Lys	Pro	Gly	Glu	Gly	Gly	Gln	Leu	Pro	Pro	Asn	Lys	Val															
175					180					185					190															
tac	cca	tgg	gtt	gca	gaa	gtc	cgc	atc	acc	acc	cca	ggc	gtt	ggt	ctg	687														
Tyr	Pro	Trp	Val	Ala	Glu	Val	Arg	Ile	Thr	Thr	Pro	Gly	Val	Gly	Leu															
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att	tcc	cct	cca	cca	cac	cac	gat	att	tac	tcc	att	gag	gat	ctg	gct	735														
Ile	Ser	Pro	Pro	Pro	His	His	Asp	Ile	Tyr	Ser	Ile	Glu	Asp	Leu	Ala															
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cag	ctg	atc	cac	gac	ctg	aag	aac	gct	aac	cca	cgc	gca	cga	atc	cac	783														
Gln	Leu	Ile	His	Asp	Leu	Lys	Asn	Ala	Asn	Pro	Arg	Ala	Arg	Ile	His															
225					230					235																				
gtg	aag	cta	gtg	gca	gaa	caa	ggc	gtg	ggc	acc	gtt	gcc	gca	ggt	gtg	831														
Val	Lys	Leu	Val	Ala	Glu	Gln	Gly	Val	Gly	Thr	Val	Ala	Ala	Gly	Val															
240					245					250																				
tcc	aaa	gca	cac	gct	gat	gtg	gtg	ctt	att	tcc	ggc	cac	gat	ggc	gga	879														
Ser	Lys	Ala	His	Ala	Asp	Val	Val	Leu	Ile	Ser	Gly	His	Asp	Gly	Gly															
255					260					265					270															
act	ggc	gca	tct	cct	ttg	acc	tcc	ctg	aag	cat	gcc	ggt	ggt	cca	tgg	927														
Thr	Gly	Ala	Ser	Pro	Leu	Thr	Ser	Leu	Lys	His	Ala	Gly	Gly	Pro	Trp															
275					280					285																				
gag	ttg	ggc	ttg	gct	gaa	acc	cag	caa	acg	ttg	ctg	ctc	aac	ggc	ctg	975														
Glu	Leu	Gly	Leu	Ala	Glu	Thr	Gln	Gln	Thr	Leu	Leu	Leu	Asn	Gly	Leu															
290					295					300																				

cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg aaa act ggc cga 1023
 Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg
 305 310 315
 gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa ttc ggt ttt gcc 1071
 Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala
 320 325 330
 acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg cgc gtc tgc cac 1119
 Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His
 335 340 345 350
 ctg gac acc tgc ccg gtg ggt atc gct acc cag aac ccg gat ttg cgt 1167
 Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg
 355 360 365
 tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac ttc ttc acc ttc 1215
 Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe
 370 375 380
 atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt ggt ttc cgc tct 1263
 Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser
 385 390 395
 att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc aag cgt tcc gga 1311
 Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly
 400 405 410
 atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc 1359
 Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe
 415 420 425 430
 atc 1362
 Ile

<210> 76

<211> 431

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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 20 25 30
 Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile
 35 40 45
 Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly
 50 55 60
 Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser
 65 70 75 80
 Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr
 85 90 95

Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu
 100 105 110
 Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly
 115 120 125
 Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys
 130 135 140
 Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser
 145 150 155 160
 His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly
 165 170 175
 Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro
 180 185 190
 Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser
 195 200 205
 Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu
 210 215 220
 Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys
 225 230 235 240
 Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys
 245 250 255
 Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly
 260 265 270
 Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu
 275 280 285
 Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp
 290 295 300
 Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val
 305 310 315 320
 Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala
 325 330 335
 Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp
 340 345 350
 Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys
 355 360 365
 Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala
 370 375 380
 Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp
 385 390 395 400
 Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro
 405 410 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile
 420 425 430

<210> 77

<211> 866

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(843)

<223> FRXA00367

<400> 77

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His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser	
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gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att	96
Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile	
20 25 30	
gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt	144
Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly	
35 40 45	
tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc	192
Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr	
50 55 60	
atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc	240
Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe	
65 70 75 80	
atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt	288
Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe	
85 90 95	
gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct	336
Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala	
100 105 110	
cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac	384
Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn	
115 120 125	
gtg ctt gga tac ggc gca acc agt ggt gaa ttg ttc att cgt ggc cag	432
Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln	
130 135 140	
gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt	480
Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val	
145 150 155 160	
gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc	528
Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val	
165 170 175	
ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt	576
Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly	

180	185	190	
ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat			624
Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn			
195	200	205	
ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg			672
Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp			
210	215	220	
gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc			720
Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr			
225	230	235	240
aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa			768
Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln			
245	250	255	
aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca			816
Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro			
260	265	270	
gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga			863
Ala Ile Lys Ile Met Glu Ala Val Ser			
275	280		
ttc			866
<210> 78			
<211> 281			
<212> PRT			
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<400> 78			
His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser			
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Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile			
20	25	30	
Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly			
35	40	45	
Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr			
50	55	60	
Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe			
65	70	75	80
Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe			
85	90	95	
Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala			
100	105	110	
Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn			
115	120	125	
Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln			
130	135	140	

Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
 145 150 155 160

Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
 165 170 175

Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
 180 185 190

Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
 195 200 205

Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
 210 215 220

Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
 225 230 235 240

Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
 245 250 255

Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
 260 265 270

Ala Ile Lys Ile Met Glu Ala Val Ser
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<210> 79
 <211> 1494
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1471)
 <223> RXN00076

<400> 79
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 Met Thr Thr Pro Leu
 1 5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163
 Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
 10 15 20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211
 Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu
 25 30 35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259
 Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
 40 45 50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307
 His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
 55 60 65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc	355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile	
70 75 80 85	
acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc	403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr	
90 95 100	
ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa	451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu	
105 110 115	
ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca	499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro	
120 125 130	
cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc	547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca	595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
150 155 160 165	
ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc	643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc	691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac	739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
200 205 210	
tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac	787
Ser Pro Thr Ile Asn Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc	835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg	883
Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro	
250 255 260	
cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa	931
His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln	
265 270 275	
aag gac ggc aag gtt gtt ggc ctg cgc acc gaa cgc acc tca ctt gat	979
Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp	
280 285 290	
ggc aac ggc ggc gta aac gga acc ggc gaa ttc aag gac tgg cca gtc	1027
Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val	
295 300 305	

cag gct gtc tac cgc gca gtc ggc tac aag tcc gac ccc atc gac ggc 1075
 Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly
 310 315 320 325

 gtc cca ttc gat gag aac aag cac gtc atc cct aat gac ggc gga cat 1123
 Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His
 330 335 340

 gtc ctc acc gct cca ggc gca gaa cca gta cca ggc ctc tat gca acc 1171
 Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr
 345 350 355

 ggc tgg atc aag cgt gga cca atc ggt cta atc ggc aac acc aag tcc 1219
 Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser
 360 365 370

 gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt 1267
 Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly
 375 380 385

 gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt 1315
 Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu
 390 395 400 405

 ctc gat tcc cgc aac atc cca ttc acc acc tgg gaa ggc tgg tac aaa 1363
 Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp Glu Gly Trp Tyr Lys
 410 415 420

 ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc 1411
 Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg
 425 430 435

 aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct 1459
 Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala
 440 445 450

 cca gca att gtc taaattgttt taacgcgtga agc 1494
 Pro Ala Ile Val
 455

<210> 80

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

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 20 25 30

 Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
 35 40 45

 Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
 50 55 60

 His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Gly Asn Ile Glu
 65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
 85 90 95
 Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
 100 105 110
 Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
 115 120 125
 Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
 130 135 140
 Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
 145 150 155 160
 Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
 165 170 175
 Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val
 180 185 190
 Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu
 195 200 205
 Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu
 210 215 220
 Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys
 225 230 235 240
 Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu
 245 250 255
 Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro
 260 265 270
 Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu
 275 280 285
 Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe
 290 295 300
 Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser
 305 310 315 320
 Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro
 325 330 335
 Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro
 340 345 350
 Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile
 355 360 365
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 370 375 380
 Asp Ala Val Ala Gly Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu
 385 390 395 400

<400> 81																		
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cgc	gta	gcc	gtc	atc	gga	gct	ggc	cct	gct	ggc	att	tac	gca	tcc	gac	163		
Arg	Val	Ala	Val	Ile	Gly	Ala	Gly	Pro	Ala	Gly	Ile	Tyr	Ala	Ser	Asp			
				10					15					20				
ctc	ctc	atc	cgc	aat	gaa	gag	cgc	gaa	gtg	ttc	gtt	gac	ctt	ttc	gag	211		
Leu	Leu	Ile	Arg	Asn	Glu	Glu	Arg	Glu	Val	Phe	Val	Asp	Leu	Phe	Glu			
			25					30					35					
caa	atg	cct	gca	ccg	ttc	gga	ctc	atc	cgt	tac	ggc	gtt	gct	cca	gac	259		
Gln	Met	Pro	Ala	Pro	Phe	Gly	Leu	Ile	Arg	Tyr	Gly	Val	Ala	Pro	Asp			
		40					45					50						
cac	cca	cgc	atc	aag	ggc	atc	gtt	aag	tcc	ctg	cac	aac	gtg	ttg	gac	307		
His	Pro	Arg	Ile	Lys	Gly	Ile	Val	Lys	Ser	Leu	His	Asn	Val	Leu	Asp			
	55					60					65							
aag	cca	cgc	ctg	cgc	ctg	ctc	ggc	aac	att	gaa	atc	ggc	aaa	gac	atc	355		
Lys	Pro	Arg	Leu	Arg	Leu	Leu	Gly	Asn	Ile	Glu	Ile	Gly	Lys	Asp	Ile			
	70				75					80				85				
acc	gtc	gaa	gaa	ctc	cgc	gac	tac	tac	gat	gca	gtc	gtg	ttc	tcc	acc	403		
Thr	Val	Glu	Glu	Leu	Arg	Asp	Tyr	Tyr	Asp	Ala	Val	Val	Phe	Ser	Thr			
				90					95				100					
ggc	gca	gtt	gca	gac	cgc	gac	ctc	aac	atc	ccc	gga	att	gaa	gca	gaa	451		
Gly	Ala	Val	Ala	Asp	Arg	Asp	Leu	Asn	Ile	Pro	Gly	Ile	Glu	Ala	Glu			
			105					110					115					
ggc	tcc	ttc	ggc	gcc	ggc	gag	ttc	gtt	ggc	ttc	tac	gac	ggc	aac	cca	499		
Gly	Ser	Phe	Gly	Ala	Gly	Glu	Phe	Val	Gly	Phe	Tyr	Asp	Gly	Asn	Pro			
		120					125					130						

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc 547
 Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile
 135 140 145

ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca 595
 Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr
 150 155 160 165

ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc 643
 Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser
 170 175 180

ctc aaa gaa aac aag gyc wct gaa gtg cac gtt ttc gga cgt cgg tgg 691
 Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val Phe Gly Arg Arg Trp
 185 190 195

ccc agc aca ggt caa gtt cac ccc aca gga act maa aga act cgr cca 739
 Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr Xaa Arg Thr Xaa Pro
 200 205 210

ctc ccc cac cat caa cgt ggt tgt tgatccagaa gacatcgact acg 786
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 215 220

<210> 82

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly
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 20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
 35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
 50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
 65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
 85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
 100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
 115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
 130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
 145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
 165 170 175

Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val
 180 185 190

Phe Gly Arg Arg Trp Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr
 195 200 205

Xaa Arg Thr Xaa Pro Leu Pro His His Gln Arg Gly Cys
 210 215 220

<210> 83
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(649)
 <223> RXN00198

<400> 83
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cgcgcctcct ttccagcgcg ccgattccac tccatggccg atg tac ccc aac ctc 115
 Met Tyr Pro Asn Leu
 1 5

ttc cgc acc gca acg gct cac gaa gaa ggc gaa tac atc atc act ggc 163
 Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly
 10 15 20

gat gaa tca gcc gat gaa atc gca gcc ctg ggc ctc gcc gaa cgt gcc 211
 Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala
 25 30 35

gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259
 Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu
 40 45 50

ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307
 Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile
 55 60 65

cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355
 Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro
 70 75 80 85

ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403
 Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu
 90 95 100

caa ggc gga ttg gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc 451
 Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly
 105 110 115

cgc atc ctc cgc gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt 499
 Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val

120	125	130	
tac atc gca ggc gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca			547
Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala			
135	140	145	
atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg			595
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met			
150	155	160	165
ggg gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg			643
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu			
	170	175	180
gct gtc tagcttgggt agaaaatgct aga			672
Ala Val			

<210> 84

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Tyr Pro Asn Leu Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu			
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Tyr Ile Ile Thr Gly Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly			
	20	25	30
Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala			
	35	40	45
Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu			
	50	55	60
Thr Gly Asn Gln Ile Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu			
	65	70	75
Gly Thr Glu Phe Pro Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly			
	85	90	95
Phe Thr Gly Ala Glu Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly			
	100	105	110
Phe Asp Asp Arg Gly Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro			
	115	120	125
Thr Asn Ser Arg Val Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser			
	130	135	140
Leu Ile Val Trp Ala Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile			
	145	150	155
Asp Ala Asp Leu Met Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro			
	165	170	175
Gln Asp Val Pro Leu Ala Val			
	180		

<210> 85
 <211> 305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(282)
 <223> FRXA00198

<400> 85
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 Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu
 1 5 10 15
 gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc cgc atc ctc cgc 96
 Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
 20 25 30
 gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt tac atc gca ggc 144
 Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
 35 40 45
 gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc 192
 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
 50 55 60
 cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca 240
 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
 65 70 75 80
 ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc 282
 Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val
 85 90
 tagcttgggt agaaaatgct aga 305

<210> 86
 <211> 94
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 86
 Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu
 1 5 10 15
 Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
 20 25 30
 Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
 35 40 45
 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
 50 55 60
 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
 65 70 75 80
 Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val

85

90

<210> 87
 <211> 727
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(727)
 <223> RXN00365

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 ccgcaccct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115
 Met Ile Leu Ser Pro
 1 5
 tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
 10 15 20
 tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
 25 30 35
 gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
 40 45 50
 cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
 55 60 65
 ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp
 70 75 80 85
 atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403
 Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln
 90 95 100
 gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451
 Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile
 105 110 115
 ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499
 Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly
 120 125 130
 cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547
 His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln
 135 140 145
 aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595
 Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys
 150 155 160 165
 ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643

Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
 170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
 Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
 185 190 195

atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727
 Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser
 200 205

<210> 88

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys
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Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr
 20 25 30

Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala
 35 40 45

Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
 50 55 60

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
 65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
 85 90 95

Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
 100 105 110

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
 165 170 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
 180 185 190

Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
 195 200 205

Ser

<210> 89
 <211> 727
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(727)
 <223> FRXA00365

<400> 89
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cccgccacct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115
 Met Ile Leu Ser Pro
 1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
 10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
 25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
 40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
 55 60 65

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp
 70 75 80 85

atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403
 Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln
 90 95 100

gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451
 Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile
 105 110 115

ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499
 Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly
 120 125 130

cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547
 His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln
 135 140 145

aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595
 Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys
 150 155 160 165

ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643
 Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
 170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
 Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
 185 190 195

atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727
 Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser
 200 205

<210> 90

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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 20 25 30

Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala
 35 40 45

Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
 50 55 60

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
 65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
 85 90 95

Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
 100 105 110

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
 165 170 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
 180 185 190

Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
 195 200 205

Ser

<210> 91

<211> 480

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(457)

<223> RXA00366

<400> 91

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gccaagaccc agcaatcaag atcatggagg cagtgaagcta atg gcc gac cca caa 115
                                         Met Ala Asp Pro Gln
                                         1           5

gga ttc atc aaa tac tcc cga cgc gag cct gca cac cgc ccg gtc ccg 163
Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala His Arg Pro Val Pro
                        10                15                20

ctg cgc ctc atg gac cac tcc gag gtc tac gaa aag gca ccg gca ggt 211
Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu Lys Ala Pro Ala Gly
                        25                30                35

cag atc gag gaa cag gct gcc cgc tgc atg gat tgc ggt gtc ccg ttc 259
Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe
                        40                45                50

tgc cac gaa ggc tgc cca ctg ggc aac atc atc cct gag tgg aat gat 307
Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile Pro Glu Trp Asn Asp
                        55                60                65

ctg gta cgc caa ggt cgg tgg aag gaa gcc tac gat cgc ttg cac gcg 355
Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr Asp Arg Leu His Ala
                        70                75                80                85

acc aac aat ttc ccc gag ttc acc ggc cgt ttg tgc ccc gca ccc tgc 403
Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu Cys Pro Ala Pro Cys
                        90                95                100

gaa ggc gcc tgc gtg ctc ggt atc aac gat gat tct gtc acc atc aaa 451
Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp Ser Val Thr Ile Lys
                        105                110                115

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Asn Val

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<210> 92

<211> 119

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

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His Arg Pro Val Pro Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu
  20           25           30

Lys Ala Pro Ala Gly Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp
  35           40           45

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Cys Gly Val Pro Phe Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile
 50 55 60
 Pro Glu Trp Asn Asp Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr
 65 70 75 80
 Asp Arg Leu His Ala Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu
 85 90 95
 Cys Pro Ala Pro Cys Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp
 100 105 110
 Ser Val Thr Ile Lys Asn Val
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<210> 93

<211> 1464

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1441)

<223> RXA02072

<400> 93

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 Met Thr Val Asp Glu
 1 5

 cag gtc tct aac tat tac gac atg ctt ctg aag cgc aat gct ggc gag 163
 Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys Arg Asn Ala Gly Glu
 10 15 20

 cct gaa ttt cac cag gca gtg gca gag gtt ttg gaa tct ttg aag atc 211
 Pro Glu Phe His Gln Ala Val Ala Glu Val Leu Glu Ser Leu Lys Ile
 25 30 35

 gtc ctg gaa aag gac cct cat tac gct gat tac ggt ctc atc cag cgc 259
 Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr Gly Leu Ile Gln Arg
 40 45 50

 ctg tgc gag cct gag cgt cag ctc atc ttc cgt gtg cct tgg gtt gat 307
 Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg Val Pro Trp Val Asp
 55 60 65

 gac cag ggc cag gtc cac gtc aac cgt ggt ttc cgc gtg cag ttc aac 355
 Asp Gln Gly Gln Val His Val Asn Arg Gly Phe Arg Val Gln Phe Asn
 70 75 80 85

 tct gca ctt gga cca tac aag ggc ggc ctg cgc ttc cac cca tct gta 403
 Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val
 90 95 100

 aac ctg ggc att gtg aag ttc ctg ggc ttt gag cag atc ttt aaa aac 451
 Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn
 105 110 115

tcc cta acc ggc ctg cca atc ggt ggt ggc aag ggt gga tcc gac ttc	499
Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys Gly Gly Ser Asp Phe	
120 125 130	
gac cct aag ggc aag tcc gat ctg gaa atc atg cgt ttc tgc cag tcc	547
Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met Arg Phe Cys Gln Ser	
135 140 145	
ttc atg acc gag ctg cac cgc cac atc ggt gag tac cgc gac gtt cct	595
Phe Met Thr Glu Leu His Arg His Ile Gly Glu Tyr Arg Asp Val Pro	
150 155 160 165	
gca ggt aac atc gga gtt ggt ggc cac gag atc ggt tac ctg ttt ggc	643
Ala Gly Asn Ile Gly Val Gly Gly His Glu Ile Gly Tyr Leu Phe Gly	
170 175 180	
cac tac cgt cgc atg gct aac cag cac gag tcc ggc gtt ttg acc ggt	691
His Tyr Arg Arg Met Ala Asn Gln His Glu Ser Gly Val Leu Thr Gly	
185 190 195	
aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc acc gag gca act ggc	739
Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg Thr Glu Ala Thr Gly	
200 205 210	
tac ggc tgc gtt tac ttc gtg agt gaa atg atc aag gct aag ggc gag	787
Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile Lys Ala Lys Gly Glu	
215 220 225	
agc atc agc ggc cag aag atc atc gtt tcc ggt tcc ggc aac gta gca	835
Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly Ser Gly Asn Val Ala	
230 235 240 245	
acc tac gcg att gaa aag gct cag gaa ctc ggc gca acc gtt att ggt	883
Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly Ala Thr Val Ile Gly	
250 255 260	
ttc tcc gat tcc agc ggt tgg gtt cat acc cct aac ggc gtt gac gtg	931
Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro Asn Gly Val Asp Val	
265 270 275	
gct aag ctc cgc gaa atc aag gaa gtt cgt cgc gca cgc gta tcc gtg	979
Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg Ala Arg Val Ser Val	
280 285 290	
tac gcc gac gaa gtt gaa ggc gca acc tac cac acc gac ggt tcc atc	1027
Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His Thr Asp Gly Ser Ile	
295 300 305	
tgg gat ctc aag tgc gat atc gct ctt cct tgt gca act cag aac gag	1075
Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu	
310 315 320 325	
ctc aac ggc gag aac gct aag act ctt gca gac aac ggc tgc cgt ttc	1123
Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp Asn Gly Cys Arg Phe	
330 335 340	
gtt gct gaa ggc gcg aac atg cct tcc acc cct gag gct gtt gag gtc	1171
Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro Glu Ala Val Glu Val	
345 350 355	

ttc cgt gag cgc gac atc cgc ttc gga cca ggc aag gca gct aac gct 1219
 Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly Lys Ala Ala Asn Ala
 360 365 370

ggt ggc gtt gca acc tcc gct ctg gag atg cag cag aac gct tcg cgc 1267
 Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln Gln Asn Ala Ser Arg
 375 380 385

gat tcc tgg agc ttc gag tac acc gac gag cgc ctc cag gtg atc atg 1315
 Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg Leu Gln Val Ile Met
 390 395 400 405

aag aac atc ttc aag acc tgt gca gag acc gca gca gag tat gga cac 1363
 Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala Ala Glu Tyr Gly His
 410 415 420

gag aac gat tac gtt gtc ggc gct aac att gct ggc ttc aag aag gta 1411
 Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala Gly Phe Lys Lys Val
 425 430 435

gct gac gcg atg ctg gca cag ggc gtc atc taagaccct gcgctttact 1461
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 440 445

taa 1464

<210> 94

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 94

Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
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Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
 20 25 30

Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
 35 40 45

Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
 50 55 60

Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe
 65 70 75 80

Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
 85 90 95

Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
 100 105 110

Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
 115 120 125

Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met
 130 135 140

Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu

145		150		155		160
Tyr Arg Asp Val	Pro Ala Gly Asn Ile	Gly Val Gly Gly His Glu Ile				
	165		170			175
Gly Tyr Leu Phe	Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser					
	180		185			190
Gly Val Leu Thr	Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg					
	195		200			205
Thr Glu Ala Thr	Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile					
	210		215			220
Lys Ala Lys Gly	Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly					
	225		230			235
Ser Gly Asn Val	Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly					
	245		250			255
Ala Thr Val Ile	Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro					
	260		265			270
Asn Gly Val Asp	Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg					
	275		280			285
Ala Arg Val Ser	Val Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His					
	290		295			300
Thr Asp Gly Ser	Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys					
	305		310			315
Ala Thr Gln Asn	Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp					
	325		330			335
Asn Gly Cys Arg	Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro					
	340		345			350
Glu Ala Val Glu	Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly					
	355		360			365
Lys Ala Ala Asn	Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln					
	370		375			380
Gln Asn Ala Ser	Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg					
	385		390			395
Leu Gln Val Ile	Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala					
	405		410			415
Ala Glu Tyr Gly	His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala					
	420		425			430
Gly Phe Lys Lys	Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile					
	435		440			445

<210> 95

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXA00323

<400> 95

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                                         Met Asn Ser Glu Gln
                                         1 5

gaa ttt gta ctc agc gcc att gaa gaa cgc gac att aag ttt gtg cgt 163
Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg
          10          15          20

cta tgg ttc act gac att ctt ggc cac ttg aag tca gtg gtt gtg gct 211
Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys Ser Val Val Val Ala
          25          30          35

cct gca gaa cta gag tct gcg ttg gaa gaa ggc atc gga ttc gat ggc 259
Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly Ile Gly Phe Asp Gly
          40          45          50

tca gcc att gag ggc tac gcg cgt atc tcg gaa gcg gac acc att gcc 307
Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu Ala Asp Thr Ile Ala
          55          60          65

cgc cca gat cca tcg aca ttc cag gtc ctc cca cta gaa gcg ggc atc 355
Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro Leu Glu Ala Gly Ile
          70          75          80          85

tca aaa ctg cag gca gca cgc ctg ttt tgc gat gtc acg atg cca gac 403
Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp Val Thr Met Pro Asp
          90          95          100

gga cag cca tct ttt tct gac ccg cgc caa gtg ctg cgc agg cag gtc 451
Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val Leu Arg Arg Gln Val
          105          110          115

caa cta gct gca gat gaa ggc ttg acc tgc atg atc tca cca gag att 499
Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met Ile Ser Pro Glu Ile
          120          125          130

gag ttc tat ttg gtg caa agc ctt cgc acc aac gga ctg cca cct gtg 547
Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn Gly Leu Pro Pro Val
          135          140          145

ccc act gac aac ggc gga tat ttc gac caa gcc aca ttc aat gag gcg 595
Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala Thr Phe Asn Glu Ala
          150          155          160          165

ccg aat ttc cgt cga aac gcg atg gta gcg ctg gag gaa ctc ggc atc 643
Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu Glu Glu Leu Gly Ile
          170          175          180

cct gtc gag ttc tcc cac cat gaa act gca cct ggc cag caa gaa atc 691
Pro Val Glu Phe Ser His His Glu Thr Ala Pro Gly Gln Gln Glu Ile
          185          190          195

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gat tta cgc cat gcg gat gcg ctc acc atg gcc gac aac atc atg acc	739
Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala Asp Asn Ile Met Thr	
200 205 210	
ttc cgc tac atc atg aaa cag gtg gca agg gac caa ggc gtc ggg gca	787
Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp Gln Gly Val Gly Ala	
215 220 225	
tca ttt atg ccc aag cca ttc caa gaa cat gca ggc tcc gcc atg cac	835
Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala Gly Ser Ala Met His	
230 235 240 245	
acg cac atg tcc tta ttt gag ggc gat acc aac gcg ttc cac gat cca	883
Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn Ala Phe His Asp Pro	
250 255 260	
gac gat tct tac atg ctg tcc aaa acc gca aaa cag ttc atc gct gga	931
Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys Gln Phe Ile Ala Gly	
265 270 275	
atc ttg cat cac gct cca gaa ttc acc gct gtg acc aac cag tgg gtc	979
Ile Leu His His Ala Pro Glu Phe Thr Ala Val Thr Asn Gln Trp Val	
280 285 290	
aat tcc tac aaa cgc atc gtg tac gga aac gaa gct cca act gcg gca	1027
Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala	
295 300 305	
acc tgg ggt gta tct aat cgt tct gcg ctg gtt cgt gtt cct acc tac	1075
Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr	
310 315 320 325	
cgt ttg aat aag gag gag tcg cgc cgg gtg gag gtg cgt ctt cct gat	1123
Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp	
330 335 340	
acc gct tgt aac cca tat ttg gcg ttt tca gtg atg ctc ggc gct ggt	1171
Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val Met Leu Gly Ala Gly	
345 350 355	
ttg aaa ggc att aaa gaa ggt tat gag ctc gac gag cca gct gag gac	1219
Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp Glu Pro Ala Glu Asp	
360 365 370	
gat atc tcc aac ttg agc ttc cgg gaa cgt cgc gcc atg ggc tac aac	1267
Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg Ala Met Gly Tyr Asn	
375 380 385	
gat ctg cca agc agc ctt gat cag gca ctg cgc caa atg gaa aag tca	1315
Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg Gln Met Glu Lys Ser	
390 395 400 405	
gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg	1363
Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu	
410 415 420	
cgc aat aag tgg cgt gaa tgg cgt gac tac caa gag cag atc act ccg	1411
Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln Glu Gln Ile Thr Pro	
425 430 435	
tgg gag ctc cga aac aat ctt gat tac tagacttttg cactccaatg	1458

gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg
Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu

Trp Glu Leu Arg Asn Asn Leu Asp Tyr
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gaa

1461

<210> 96

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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Ser Val Val Val Ala Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly
 35 40 45

Ile Gly Phe Asp Gly Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu
 50 55 60

Ala Asp Thr Ile Ala Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
 65 70 75 80

Leu Glu Ala Gly Ile Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp
 85 90 95

Val Thr Met Pro Asp Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val
 100 105 110

Leu Arg Arg Gln Val Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met
 115 120 125

Ile Ser Pro Glu Ile Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn
 130 135 140

Gly Leu Pro Pro Val Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala
 145 150 155 160

Thr Phe Asn Glu Ala Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu
 165 170 175

Glu Glu Leu Gly Ile Pro Val Glu Phe Ser His His Glu Thr Ala Pro
 180 185 190

Gly Gln Gln Glu Ile Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala
 195 200 205

Asp Asn Ile Met Thr Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp
 210 215 220

Gln Gly Val Gly Ala Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala
 225 230 235 240

Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn
 245 250 255

Ala Phe His Asp Pro Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys

260					265					270						
Gln	Phe	Ile	Ala	Gly	Ile	Leu	His	His	Ala	Pro	Glu	Phe	Thr	Ala	Val	
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Thr	Asn	Gln	Trp	Val	Asn	Ser	Tyr	Lys	Arg	Ile	Val	Tyr	Gly	Asn	Glu	
290					295					300						
Ala	Pro	Thr	Ala	Ala	Thr	Trp	Gly	Val	Ser	Asn	Arg	Ser	Ala	Leu	Val	
305					310					315					320	
Arg	Val	Pro	Thr	Tyr	Arg	Leu	Asn	Lys	Glu	Glu	Ser	Arg	Arg	Val	Glu	
325					330					335						
Val	Arg	Leu	Pro	Asp	Thr	Ala	Cys	Asn	Pro	Tyr	Leu	Ala	Phe	Ser	Val	
340					345					350						
Met	Leu	Gly	Ala	Gly	Leu	Lys	Gly	Ile	Lys	Glu	Gly	Tyr	Glu	Leu	Asp	
355					360					365						
Glu	Pro	Ala	Glu	Asp	Asp	Ile	Ser	Asn	Leu	Ser	Phe	Arg	Glu	Arg	Arg	
370					375					380						
Ala	Met	Gly	Tyr	Asn	Asp	Leu	Pro	Ser	Ser	Leu	Asp	Gln	Ala	Leu	Arg	
385					390					395					400	
Gln	Met	Glu	Lys	Ser	Glu	Leu	Val	Ala	Asp	Ile	Leu	Gly	Glu	His	Val	
405					410					415						
Phe	Glu	Phe	Phe	Leu	Arg	Asn	Lys	Trp	Arg	Glu	Trp	Arg	Asp	Tyr	Gln	
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Glu	Gln	Ile	Thr	Pro	Trp	Glu	Leu	Arg	Asn	Asn	Leu	Asp	Tyr			
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<210> 97

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA00335

<400> 97

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				Val	Ala	Phe	Glu	Thr	
				1				5	

ccg	gaa	gaa	att	gtc	aag	ttc	atc	aag	gat	gaa	aac	gtc	gag	ttc	gtt	163
Pro	Glu	Glu	Ile	Val	Lys	Phe	Ile	Lys	Asp	Glu	Asn	Val	Glu	Phe	Val	
				10				15					20			

gac	gtt	cga	ttc	acc	gac	ctt	ccc	ggc	acc	gag	cag	cac	ttc	agc	atc	211
Asp	Val	Arg	Phe	Thr	Asp	Leu	Pro	Gly	Thr	Glu	Gln	His	Phe	Ser	Ile	
				25				30					35			

cca gct gcc agc ttc gat gca gat aca atc gaa gaa ggt ctc gca ttc 259
 Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu Glu Gly Leu Ala Phe
 40 45 50

gac gga tcc tcg atc cgt ggc ttc acc acg atc gac gaa tct gac atg 307
 Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile Asp Glu Ser Asp Met
 55 60 65

aat ctc ctg cca gac ctc gga acg gcc acc ctt gat cca ttc cgc aag 355
 Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu Asp Pro Phe Arg Lys
 70 75 80 85

gca aag acc ctg aac gtt aag ttc ttc gtt cac gat cct ttc acc cgc 403
 Ala Lys Thr Leu Asn Val Lys Phe Phe Val His Asp Pro Phe Thr Arg
 90 95 100

gag gca ttc tcc cgc gac cca cgc aac gtg gca cgc aag gca gag cag 451
 Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala Arg Lys Ala Glu Gln
 105 110 115

tac ctg gca tcc acc ggc att gca gac acc tgc aac ttc ggc gcc gag 499
 Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys Asn Phe Gly Ala Glu
 120 125 130

gct gag ttc tac ctc ttc gac tcc gtt cgc tac tcc acc gag atg aac 547
 Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr Ser Thr Glu Met Asn
 135 140 145

tcc ggc ttc tac gaa gta gat acc gaa gaa ggc tgg tgg aac cgt ggc 595
 Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly Trp Trp Asn Arg Gly
 150 155 160 165

aag gaa acc aac ctc gac ggc acc cca aac ctg ggc gca aag aac cgc 643
 Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu Gly Ala Lys Asn Arg
 170 175 180

gtc aag ggt ggc tac ttc cca gta gca cca tac gac caa acc gtt gac 691
 Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr Asp Gln Thr Val Asp
 185 190 195

gtg cgc gat gac atg gtt cgc aac ctc gca gct tcc ggc ttc gct ctt 739
 Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala Ser Gly Phe Ala Leu
 200 205 210

gag cgt ttc cac cac gaa gtc ggt ggc gga cag cag gaa atc aac tac 787
 Glu Arg Phe His His Glu Val Gly Gly Gly Gln Gln Glu Ile Asn Tyr
 215 220 225

cgc ttc aac acc atg ctc cac gcg gca gat gat atc cag acc ttc aag 835
 Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp Ile Gln Thr Phe Lys
 230 235 240 245

tac atc atc aag aac acc gct cgc ctc cac ggc aag gct gca acc ttc 883
 Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly Lys Ala Ala Thr Phe
 250 255 260

atg cct aag cca ctg gct ggc gac aac ggt tcc ggc atg cac gct cac 931
 Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser Gly Met His Ala His
 265 270 275

cag tcc ctc tgg aag gac ggc aag cca ctc ttc cac gat gag tcc ggc 979

Gln	Ser	Leu	Trp	Lys	Asp	Gly	Lys	Pro	Leu	Phe	His	Asp	Glu	Ser	Gly		
		280					285					290					
tac	gca	ggc	ctg	tcc	gac	atc	gcc	cgc	tac	tac	atc	ggc	ggc	atc	ctg	1027	
Tyr	Ala	Gly	Leu	Ser	Asp	Ile	Ala	Arg	Tyr	Tyr	Ile	Gly	Gly	Ile	Leu		
	295					300					305						
cac	cac	gca	ggc	gct	gtt	ctg	gcg	ttc	acc	aac	gca	acc	ctg	aac	tcc	1075	
His	His	Ala	Gly	Ala	Val	Leu	Ala	Phe	Thr	Asn	Ala	Thr	Leu	Asn	Ser		
310					315					320					325		
tac	cac	cgt	ctg	gtt	cca	ggc	ttc	gag	gct	cca	atc	aac	ctg	gtg	tac	1123	
Tyr	His	Arg	Leu	Val	Pro	Gly	Phe	Glu	Ala	Pro	Ile	Asn	Leu	Val	Tyr		
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Ser	Gln	Arg	Asn	Arg	Ser	Ala	Ala	Val	Arg	Ile	Pro	Ile	Thr	Gly	Ser		
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aac	ccg	aag	gca	aag	cgc	atc	gaa	ttc	cgc	gct	cca	gac	cca	tca	ggc	1219	
Asn	Pro	Lys	Ala	Lys	Arg	Ile	Glu	Phe	Arg	Ala	Pro	Asp	Pro	Ser	Gly		
		360					365				370						
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Asn	Pro	Tyr	Leu	Gly	Phe	Ala	Ala	Met	Met	Met	Ala	Gly	Leu	Asp	Gly		
		375				380					385						
atc	aag	aac	cgc	atc	gag	cca	cac	gct	cca	gtg	gac	aag	gac	ctc	tac	1315	
Ile	Lys	Asn	Arg	Ile	Glu	Pro	His	Ala	Pro	Val	Asp	Lys	Asp	Leu	Tyr		
390					395				400					405			
gaa	cta	cca	cca	gag	gaa	gct	gca	tcc	att	cca	cag	gca	cca	acc	tcc	1363	
Glu	Leu	Pro	Pro	Glu	Glu	Ala	Ala	Ser	Ile	Pro	Gln	Ala	Pro	Thr	Ser		
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ctg	gaa	gca	tcc	ctg	aag	gca	ctg	cag	gaa	gac	acc	gac	ttc	ctc	acc	1411	
Leu	Glu	Ala	Ser	Leu	Lys	Ala	Leu	Gln	Glu	Asp	Thr	Asp	Phe	Leu	Thr		
			425					430					435				
gag	tct	gac	gtc	ttc	acc	gag	gat	ctc	atc	gag	gcg	tac	atc	cag	tac	1459	
Glu	Ser	Asp	Val	Phe	Thr	Glu	Asp	Leu	Ile	Glu	Ala	Tyr	Ile	Gln	Tyr		
		440					445					450					
aag	tac	gac	aac	gag	atc	tcc	cca	gtt	cgc	ctg	cgc	cca	acc	ccg	cag	1507	
Lys	Tyr	Asp	Asn	Glu	Ile	Ser	Pro	Val	Arg	Leu	Arg	Pro	Thr	Pro	Gln		
	455					460					465						
gaa	ttc	gaa	ttg	tac	ttc	gac	tgc	taattcactt	agctagccga	tag						1554	
Glu	Phe	Glu	Leu	Tyr	Phe	Asp	Cys										
470					475												

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<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

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Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu
 35 40 45

Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
 50 55 60

Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu
 65 70 75 80

Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His
 85 90 95

Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala
 100 105 110

Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
 115 120 125

Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr
 130 135 140

Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly
 145 150 155 160

Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu
 165 170 175

Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
 180 185 190

Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala
 195 200 205

Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln
 210 215 220

Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp
 225 230 235 240

Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly
 245 250 255

Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser
 260 265 270

Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe
 275 280 285

His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr
 290 295 300

Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn
 305 310 315 320

Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro
 325 330 335

Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

340	345	350
Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala 355 360 365		
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met 370 375 380		
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val 385 390 395 400		
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro 405 410 415		
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp 420 425 430		
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu 435 440 445		
Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu 450 455 460		
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<210> 99

<211> 3258

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3235)

<223> RXA00324

<400> 99

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                                         1 5

aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa 163
Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys
          10          15          20

gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag 211
Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu
          25          30          35

cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg 259
His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu
          40          45          50

tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg 307
Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu
          55          60          65

tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat 355

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Tyr	Gln	Ala	Leu	Glu	Ala	Ile	Gly	Glu	Asp	Ala	Arg	Asn	Glu	Leu	Asp	
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Gln	Glu	Ile	Arg	Gln	Asp	Glu	Lys	Leu	Arg	Val	Arg	Leu	Phe	Ala	Leu	
				90					95					100		
ttg	ggg	ggg	tcc	tcg	gct	gtc	ggg	gat	cac	ttg	gtc	gcc	aat	cct	ttg	451
Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu	Val	Ala	Asn	Pro	Leu	
			105					110					115			
cag	tgg	aaa	ctc	tta	aaa	ctt	gat	gcg	cca	tcg	agg	gaa	gag	atg	ttt	499
Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser	Arg	Glu	Glu	Met	Phe	
		120					125					130				
cag	gcg	ctg	ctg	gaa	tct	gtg	aaa	gct	cag	cct	gct	gtg	ctt	gag	ggt	547
Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro	Ala	Val	Leu	Glu	Val	
		135				140					145					
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Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg	Asp	Asp	Leu	Ser	Thr	
		150			155				160						165	
cct	ggg	ttt	tac	acg	gct	agt	gtt	acc	ggg	cct	gaa	gca	gag	cga	gtc	643
Pro	Gly	Phe	Tyr	Thr	Ala	Ser	Val	Thr	Gly	Pro	Glu	Ala	Glu	Arg	Val	
				170					175					180		
ttg	aaa	tgg	act	tat	cgc	acg	ttg	ctg	acc	cgg	att	gct	gcg	cat	gat	691
Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg	Ile	Ala	Ala	His	Asp	
				185				190					195			
tta	gcg	ggg	acc	tat	ccc	acc	gac	atg	cgg	aga	aaa	ggg	ggc	gat	cct	739
Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg	Lys	Gly	Gly	Asp	Pro	
		200					205					210				
gtt	ccg	ttt	agc	aca	gtg	acc	atg	cag	ctc	agc	gac	cta	gct	gat	gct	787
Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser	Asp	Leu	Ala	Asp	Ala	
		215				220					225					
gct	ttg	act	gct	gct	tta	gct	gtg	gca	att	gcc	aat	gtt	tat	ggg	gaa	835
Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala	Asn	Val	Tyr	Gly	Glu	
					235					240					245	
aag	ccg	gtt	gat	tca	gct	tta	tct	gtc	atc	gcg	atg	ggc	aaa	tgt	ggc	883
Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala	Met	Gly	Lys	Cys	Gly	
				250				255						260		
gcg	cag	gaa	ttg	aac	tac	att	tca	gat	gtg	gac	gtg	gtg	ttt	gtt	gca	931
Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp	Val	Val	Phe	Val	Ala	
			265					270					275			
gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	gca	gag	ctc	att	cgc	979
Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala	Ala	Glu	Leu	Ile	Arg	
		280					285					290				
atc	ggg	agc	aac	tcg	ttc	ttt	gag	gtg	gat	gca	gca	ctt	cgc	cca	gaa	1027
Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala	Ala	Leu	Arg	Pro	Glu	
		295				300					305					
ggg	aaa	agt	ggc	gct	ctt	gtg	cgc	tct	ttg	gat	tcc	cat	atg	gcg	tat	1075
Gly	Lys	Ser	Gly	Ala	Leu	Val	Arg	Ser	Leu	Asp	Ser	His	Met	Ala	Tyr	

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act	gct	ctt	gca	tca	gga	gct	agc	cgt	aaa	gcc	aag	att	cag	gcg	atg	1843
Thr	Ala	Leu	Ala	Ser	Gly	Ala	Ser	Arg	Lys	Ala	Lys	Ile	Gln	Ala	Met	
			570							575				580		
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Leu	Leu	Pro	Thr	Leu	Met	Glu	Trp	Leu	Ser	Gln	Thr	Ala	Glu	Pro	Asp	
			585							590				595		
gcg	gga	ttg	ctg	aat	tac	cgc	aag	ctt	tct	gat	gct	tcc	tat	gat	cgc	1939
Ala	Gly	Leu	Leu	Asn	Tyr	Arg	Lys	Leu	Ser	Asp	Ala	Ser	Tyr	Asp	Arg	
			600							605				610		
agc	tgg	ttt	ttg	cgc	atg	ctg	cgt	gat	gag	ggc	gta	gtg	ggg	cag	cgg	1987
Ser	Trp	Phe	Leu	Arg	Met	Leu	Arg	Asp	Glu	Gly	Val	Val	Gly	Gln	Arg	
			615							620				625		
ttg	atg	cgt	att	ttg	gga	aat	tct	ccc	tat	att	tct	gaa	ctg	att	atc	2035
Leu	Met	Arg	Ile	Leu	Gly	Asn	Ser	Pro	Tyr	Ile	Ser	Glu	Leu	Ile	Ile	
			630							635				640		
tcc	act	ccg	gac	ttt	atg	aaa	cag	ctg	ggg	gat	gcg	gcg	tct	ggg	cct	2083
Ser	Thr	Pro	Asp	Phe	Met	Lys	Gln	Leu	Gly	Asp	Ala	Ala	Ser	Gly	Pro	
			650							655				660		
aaa	ttg	ctt	gct	act	gca	ccg	act	cag	gtt	gtg	aaa	gca	atc	aag	gca	2131
Lys	Leu	Leu	Ala	Thr	Ala	Pro	Thr	Gln	Val	Val	Lys	Ala	Ile	Lys	Ala	
			665							670				675		
acg	gtg	tcg	cgt	cat	gag	tca	cct	gat	cgg	gcg	atc	cag	gct	gca	cga	2179
Thr	Val	Ser	Arg	His	Glu	Ser	Pro	Asp	Arg	Ala	Ile	Gln	Ala	Ala	Arg	
			680							685				690		
tcg	ctg	agg	agg	cag	gag	ctg	gca	cgc	att	gcc	tct	gct	gat	ttg	ctc	2227
Ser	Leu	Arg	Arg	Gln	Glu	Leu	Ala	Arg	Ile	Ala	Ser	Ala	Asp	Leu	Leu	
			695							700				705		
aac	atg	ctc	act	gtt	cag	gaa	gta	tgc	caa	agc	ttg	tca	cta	gtc	tgg	2275
Asn	Met	Leu	Thr	Val	Gln	Glu	Val	Cys	Gln	Ser	Leu	Ser	Leu	Val	Trp	
			710							715				720		
gat	gcg	gtg	ttg	gat	gct	gcc	ttg	gat	gcg	gaa	atc	cgt	gct	gca	ctt	2323
Asp	Ala	Val	Leu	Asp	Ala	Ala	Leu	Asp	Ala	Glu	Ile	Arg	Ala	Ala	Leu	
			730							735				740		
aac	gat	cca	cag	aaa	cca	gat	cag	cct	ctg	gcc	aat	att	tct	gtg	atc	2371
Asn	Asp	Pro	Gln	Lys	Pro	Asp	Gln	Pro	Leu	Ala	Asn	Ile	Ser	Val	Ile	
			745							750				755		
ggc	atg	ggc	cgt	ttg	ggg	gga	gca	gaa	ctt	gga	tac	ggg	tct	gat	gcc	2419
Gly	Met	Gly	Arg	Leu	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Ser	Asp	Ala	
			760							765				770		
gat	gtg	atg	ttt	gta	tgc	gag	ccg	gta	gcc	ggg	gtg	gaa	gag	cat	gag	2467
Asp	Val	Met	Phe	Val	Cys	Glu	Pro	Val	Ala	Gly	Val	Glu	Glu	His	Glu	
			775							780				785		
gcc	gtc	aca	tgg	tct	att	gct	atc	tgt	gat	tcc	atg	cgg	tcg			

gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt 2563
 Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg
 810 815 820

cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg 2611
 Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val
 825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg 2659
 Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu
 840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg 2707
 Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu
 855 860 865

gag tgc att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg 2755
 Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala
 870 875 880 885

cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg 2803
 Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg
 890 895 900

ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga 2851
 Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly
 905 910 915

gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat 2899
 Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His
 920 925 930

gct cat gag att ccg gag ctg cac aat acg tgc acg ttg gaa gtt ctt 2947
 Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu
 935 940 945

gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg 2995
 Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr
 950 955 960 965

ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg 3043
 Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Arg Asn Ala Leu Val
 970 975 980

ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac 3091
 Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro His
 985 990 995

ctt gcg cag gtg gct ggt gcg tct ggt tgg gat cca aat gag tac cag 3139
 Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln
 1000 1005 1010

gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt 3187
 Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val
 1015 1020 1025

gtt gat gaa gtc ttc tgg ggt gtg gac tct atg gag caa cgt gag ttt 3235
 Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe
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taggtaggtg gtgggagccc caa 3258

<210> 100

<211> 1045

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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Asp Pro Leu Pro Lys Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala
 20 25 30

Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp
 35 40 45

Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn
 50 55 60

Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala
 65 70 75 80

Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val
 85 90 95

Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu
 100 105 110

Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser
 115 120 125

Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro
 130 135 140

Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg
 145 150 155 160

Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro
 165 170 175

Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg
 180 185 190

Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg
 195 200 205

Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser
 210 215 220

Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala
 225 230 235 240

Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala
 245 250 255

Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp
 260 265 270

Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala
 275 280 285

Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala
 290 295 300
 Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp
 305 310 315 320
 Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln
 325 330 335
 Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln
 340 345 350
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg
 355 360 365
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
 370 375 380
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
 385 390 395 400
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
 405 410 415
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
 420 425 430
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
 435 440 445
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
 450 455 460
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg
 465 470 475 480
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
 485 490 495
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
 500 505 510
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
 515 520 525
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
 530 535 540
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg
 545 550 555 560
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
 565 570 575
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
 580 585 590
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
 595 600 605

Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly
 610 615 620
 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile
 625 630 635 640
 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp
 645 650 655
 Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val
 660 665 670
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala
 675 680 685
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala
 690 695 700
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser
 705 710 715 720
 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu
 725 730 735
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala
 740 745 750
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly
 755 760 765
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly
 770 775 780
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser
 785 790 795 800
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val
 805 810 815
 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr
 820 825 830
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu
 835 840 845
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu
 850 855 860
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp
 865 870 875 880
 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg
 885 890 895
 Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr
 900 905 910
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu
 915 920 925
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser

930 935 940
 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro
 945 950 955 960
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala
 965 970 975
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro
 980 985 990
 Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp
 995 1000 1005
 Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg
 1010 1015 1020
 Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met
 1025 1030 1035 1040
 Glu Gln Arg Glu Phe
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<210> 101

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(861)

<223> RXN03176

<400> 101

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 Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
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ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30

gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc 192
 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60

gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac 240
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80

ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc 288
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95

atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg 336
 Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val

100	105	110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc			384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr			
115	120	125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac			432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn			
130	135	140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa			480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu			
145	150	155	160
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta			528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val			
165	170	175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc			576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly			
180	185	190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc			624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg			
195	200	205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg			672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly			
210	215	220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc			720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly			
225	230	235	240
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc			768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser			
245	250	255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc			816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe			
260	265	270	
aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag			861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu			
275	280	285	

<210> 102

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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Leu	Ala	Val	Ala	Leu	Cys	Thr	Val	Asn	Gly	His	Ile	Tyr	Ser	Ala	Gly
		20						25					30		

Asp	Asp	Asp	Ile	Glu	Phe	Thr	Met	Gln	Ser	Ile	Ser	Lys	Pro	Phe	Ala
		35					40					45			

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95
 Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<210> 103

<211> 861

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(861)

<223> FRXA02879

<400> 103

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 Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
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cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270

aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<210> 104

<211> 287

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 104

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
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Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60

Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser

					245					250					255				
Pro	Arg	Leu	Asn	Pro	Lys	Gly	Asn	Ser	Val	Arg	Gly	Val	Lys	Ile	Phe				
			260					265					270						
Lys	Gln	Leu	Ser	Asp	Asp	Met	Gly	Leu	His	Leu	Met	Ser	Thr	Glu					
		275					280					285							
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<400> 105																			
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gtgggtcggc atccgcccc gtttgcagga gtacttataa atg cac gct ttt cga 115																			
Met His Ala Phe Arg 5																			
1																			
cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca 163																			
Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala																			
10 15 20																			
acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc 211																			
Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr																			
25 30 35																			
ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct 259																			
Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser																			
40 45 50																			
tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag 307																			
Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu																			
55 60 65																			
aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg 355																			
Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg																			
70 75 80 85																			
gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa 403																			
Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln																			
90 95 100																			
tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc 451																			
Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg																			
105 110 115																			
ggg ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt 499																			
Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly																			
120 125 130																			
gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg 547																			
Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu																			
135 140 145																			


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cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg 595
Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr
150 155 160 165

atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg 643
Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu
170 175 180

cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691
Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser
185 190 195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739
Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr
200 205 210

tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787
Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys
215 220 225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835
Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala
230 235 240 245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883
Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln
250 255 260

gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931
Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr
265 270 275

gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979
Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu
280 285 290

att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg 1027
Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met
295 300 305

tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac 1075
Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr
310 315 320 325

ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac 1123
Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn
330 335 340

gat gaa gga taatgaagat ttcatccag att 1155
Asp Glu Gly

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<210> 106

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala

1	5	10	15
Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val	20	25	30
Glu Pro Ala Glu Thr Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro	35	40	45
Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile	50	55	60
Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu	65	70	75
Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile	85	90	95
Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val	100	105	110
Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser	115	120	125
Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly	130	135	140
Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val	145	150	155
Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe	165	170	175
Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser	180	185	190
Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val	195	200	205
Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu	210	215	220
Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu	225	230	235
Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser	245	250	255
Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu	260	265	270
Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr	275	280	285
Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile	290	295	300
Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro	305	310	315
Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu	325	330	335

Glu Gly Thr Glu Asn Asp Glu Gly
340

<210> 107
<211> 1035
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00727

<400> 107
ttattgcacc atggcaggta gtattttgcc catgattgag agtttcaccc gattgcgaat 60

ttcgcagaca cgcctctga aacggctact gcatagcact ttg cgt ttc ccc aaa 115
Leu Arg Phe Pro Lys
1 5

atc ccc aag cgc gct gta gcg gcg acc gtc ggc atc gtg gca acc tca 163
Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly Ile Val Ala Thr Ser
10 15 20

ttc acc ttg gct tct tgt gtc acc aat gag gag cag ggc aac cca gat 211
Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu Gln Gly Asn Pro Asp
25 30 35

ggc tgg gag cag atc gtt cca gat cct gta ccg gag att cag gcg atg 259
Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro Glu Ile Gln Ala Met
40 45 50

gtt ccc gaa gct ctg gct cag cgc ggt gtg ctc acc gcc ggt gcc aac 307
Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu Thr Ala Gly Ala Asn
55 60 65

cca cct ttc cca ccg ttt gag ttt aaa gat tcc gat ggt cag att atc 355
Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser Asp Gly Gln Ile Ile
70 75 80 85

ggt gtg gaa atg gac ctc gtg cgt gca atg gcg ggg gtg atg ggc ttg 403
Gly Val Glu Met Asp Leu Val Arg Ala Met Ala Gly Val Met Gly Leu
90 95 100

gag ttc agc cct cag gag cag gat ttc tcc ctc atc ctt cca tcg gtt 451
Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu Ile Leu Pro Ser Val
105 110 115

caa gct ggc acc ctt gat atc gga gcc tct ggc ttc act gac aac gag 499
Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly Phe Thr Asp Asn Glu
120 125 130

gaa cgc cgc gag aac ttt gat ttc atc gat ttc ctc ttc gca ggt gtg 547
Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe Leu Phe Ala Gly Val
135 140 145

cag tgg gcg cag gca act gat cgt gaa acc cca atc gat ccg gaa aac 595
Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro Ile Asp Pro Glu Asn
150 155 160 165

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gcc tgt ggt ctc acc gtt gct gta cag cgc aca acc gtg gca gag acc 643
Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr Thr Val Ala Glu Thr
170 175 180

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691
Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu
185 190 195

ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739
Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala
200 205 210

ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787
Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser
215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835
Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp
230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883
Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp
250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931
Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly
265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979
Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu
280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa 1032
Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
295 300

aaa 1035

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<210> 108

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

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Leu Arg Phe Pro Lys Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly
1 5 10 15

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Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu
20 25 30

```

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Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro
35 40 45

```

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Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu
50 55 60

```

```

Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser
65 70 75 80

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```

Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala
      85                      90                      95

Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu
      100                      105                      110

Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly
      115                      120                      125

Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe
      130                      135                      140

Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro
      145                      150                      155                      160

Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr
      165                      170                      175

Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu
      180                      185                      190

Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp
      195                      200                      205

Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala
      210                      215                      220

Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile
      225                      230                      235                      240

Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe
      245                      250                      255

Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His
      260                      265                      270

Leu Ile Asp Thr Gly Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile
      275                      280                      285

Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
      290                      295                      300

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<210> 109
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1939)
<223> RXA02139

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<400> 109
tcaggaggat ttttcaatca tgtgcggcct tcttgccata ttgactgcaa atgggaacgc 60

tgaagcattc gttcctgcac tcgagcgggc cttgccatgc atg cgc cac cgt ggt 115
                Met Arg His Arg Gly

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	1	5	
cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc			163
Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp Ala Ala Phe Gly Phe			
	10	15	20
aac cgc ctc tcc atc att gat att gca cac tcc cac caa cca ctg cgt			211
Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser His Gln Pro Leu Arg			
	25	30	35
tgg gga cct gcg gat gaa ccc gac cgc tac gca atg act ttc aac ggt			259
Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala Met Thr Phe Asn Gly			
	40	45	50
gag atc tac aac tac gtt gag ctg cgt aaa gag ctc tcg gat ttg gga			307
Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu Leu Ser Asp Leu Gly			
	55	60	65
tat gcc ttt aat act tct ggc gat ggc gag cca att gtt gtc ggt ttc			355
Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro Ile Val Val Gly Phe			
	70	75	80
cac cac tgg ggc gag tcc gtg gtc gag cat ctc cgc gga atg ttc ggc			403
His His Trp Gly Glu Ser Val Val Glu His Leu Arg Gly Met Phe Gly			
	90	95	100
att gcc att tgg gat aca aag gaa aag tcg ctt ttc ctt gcg cgt gat			451
Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu Phe Leu Ala Arg Asp			
	105	110	115
cag ttc ggc att aag cca ctg ttc tac gca acc acc gag cat ggc acc			499
Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr Thr Glu His Gly Thr			
	120	125	130
gtg ttc tcc tca gag aag aag acc atc ttg gag atg gcc gag gag atg			547
Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu Met Ala Glu Glu Met			
	135	140	145
aat cta gat ctg ggc ctt gat aag cgc acc att gag cac tac gtg gac			595
Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile Glu His Tyr Val Asp			
	150	155	160
ttg cag tac gtg ccc gag cca gat acc ctt cac gcg cag att tcc cgc			643
Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His Ala Gln Ile Ser Arg			
	170	175	180
ttg gag tca ggc tgc acc gca aca gtt cgt ccg ggc ggc aag ctg gaa			691
Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro Gly Gly Lys Leu Glu			
	185	190	195
cag aag cgt tac ttc aag cct cag ttc cca gta cag aag gtc gta aag			739
Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val Gln Lys Val Val Lys			
	200	205	210
ggt aag gag cag gac ctc ttc gat cgc att gcc cag gtg ttg gag gat			787
Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala Gln Val Leu Glu Asp			
	215	220	225
agc gtc gaa aag cat atg cgt gcc gac gtg acc gta ggc tcg ttc ctt			835
Ser Val Glu Lys His Met Arg Ala Asp Val Thr Val Gly Ser Phe Leu			
	230	235	240
			245

ttc ggc ggc att gac tca acc gca att gcg gcg ctt gca aag cgc cac	883
Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala Leu Ala Lys Arg His	
250 255 260	
aac cct gac ctg ctc acc ttc acc acc ggt ttc gag cgt gaa ggc tac	931
Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr	
265 270 275	
tcg gag gtc gat gtg gct gcg gag tcc gcc gct gcg att ggc gct gag	979
Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu	
280 285 290	
cac atc gtg aag att gtc tgc cct gag gaa tac gcc aac gcg att cct	1027
His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro	
295 300 305	
aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc	1075
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val	
310 315 320 325	
ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg	1123
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val	
330 335 340	
ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac	1171
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr	
345 350 355	
aag gag ccg cta tgc ctt gct cca ttt gag aag atc cct tcc cca cta	1219
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu	
360 365 370	
cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag	1267
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys	
375 380 385	
ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac	1315
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr	
390 395 400 405	
tac ggc aac gct cgc tcc ttc aat ttc gag cag atg caa cgc gtt att	1363
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile	
410 415 420	
cca tgg gca aag cgc gaa tgg gac cac cgc gaa gtc act gcg ccg atc	1411
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile	
425 430 435	
tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg	1459
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu	
440 445 450	
gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag	1507
Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys	
455 460 465	
atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag	1555
Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys	
470 475 480 485	

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc 1603
 Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala
 490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt 1651
 Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val
 505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg 1699
 Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met
 520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc 1747
 Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr
 535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg 1795
 Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu
 550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga 1843
 Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg
 570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa 1891
 Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu
 585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt 1939
 Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu
 600 605 610

taagtcttaa agcctaaacc ccc 1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp
1 5 10 15

Ala Ala Phe Gly Phe Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser
20 25 30

His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala
35 40 45

Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu
50 55 60

Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro
65 70 75 80

Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu
85 90 95

Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu
100 105 110

Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr
 115 120 125
 Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu
 130 135 140
 Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile
 145 150 155 160
 Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His
 165 170 175
 Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro
 180 185 190
 Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val
 195 200 205
 Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala
 210 215 220
 Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr
 225 230 235 240
 Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala
 245 250 255
 Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe
 260 265 270
 Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala
 275 280 285
 Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr
 290 295 300
 Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala
 305 310 315 320
 Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys
 325 330 335
 His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly
 340 345 350
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys
 355 360 365
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu
 370 375 380
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr
 385 390 395 400
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln
 405 410 415
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu
 420 425 430

Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala
 435 440 445

Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu
 450 455 460

Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val
 465 470 475 480

Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr
 485 490 495

Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala
 500 505 510

Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly
 515 520 525

Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly
 530 535 540

Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn
 545 550 555 560

Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser
 565 570 575

Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His
 580 585 590

Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser
 595 600 605

Tyr Pro Val Glu Leu
 610

<210> 111

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1261)

<223> RXN00116

<400> 111

cgcggcacgc acgctggggg caagcgtcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgccacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115
 Met Ser Asn Asp Phe
 1 5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
 10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
 25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag	259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln	
40 45 50	
att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg	307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser	
55 60 65	
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Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu	
70 75 80 85	
tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg	403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala	
90 95 100	
att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc	451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile	
105 110 115	
gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg	499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala	
120 125 130	
ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg	547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp	
135 140 145	
gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg	595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg	
150 155 160 165	
atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct	643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser	
170 175 180	
aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg	691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu	
185 190 195	
ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag	739
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln	
200 205 210	
aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg	787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val	
215 220 225	
acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg	835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr	
230 235 240 245	
ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg	883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala	
250 255 260	
aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg	931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val	
265 270 275	

gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag 979
 Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
 280 285 290

ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg 1027
 Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
 295 300 305

ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat 1075
 Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
 310 315 320 325

att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag 1123
 Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
 330 335 340

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag 1171
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
 345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg 1219
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
 360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta 1261
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
 375 380 385

tagtttgaac aggttggttg ggg 1284

<210> 112

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

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 20 25 30

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 35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
 50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
 65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
 85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
 100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
 115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130 135 140
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145 150 155 160
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
 165 170 175
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
 180 185 190
 Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380
 Lys Lys Leu
 385

<210> 113

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 113

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                               Met Thr Gln Arg Ala
                               1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
                               10 15 20

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Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
                               25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
                               40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
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tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
                               70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
                               90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
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Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
                               120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
                               135 140 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
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aag cag ttg gcg 607
Lys Gln Leu Ala

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<210> 114

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

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 Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45
 Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60
 Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80
 Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val
 85 90 95
 Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu
 100 105 110
 Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser
 115 120 125
 Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr
 130 135 140
 Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe
 145 150 155 160
 Ser Lys Lys Ala Leu Lys Gln Leu Ala
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<210> 115

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1207)

<223> RXN00618

<400> 115

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 Met Gln Met Leu Asp
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50

gat	cgt	gag	ttc	cgt	gaa	cgc	atc	gcc	gat	tgg	cac	tct	gct	act	tat	307
Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp	His	Ser	Ala	Thr	Tyr	
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gac	gta	gac	acc	aac	cct	gac	aat	gtt	att	gtc	acc	acc	ggt	tct	tca	355
Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val	Thr	Thr	Gly	Ser	Ser	
	70				75					80					85	
ggt	gga	ttc	gtg	gca	tcg	ttt	atc	gcc	acc	ttg	gat	cac	ggg	gat	tat	403
Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu	Asp	His	Gly	Asp	Tyr	
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Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr	Arg	Asn	Ile	Leu	Glu	
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Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys	Thr	Ala	Glu	Thr	Arg	
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Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu	Pro	His	Lys	Pro	Lys	
	135					140					145					
gct	gtt	att	gtc	acc	agc	cca	gga	aac	cca	acg	ggc	acc	atc	att	gat	595
Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr	Gly	Thr	Ile	Ile	Asp	
	150				155					160					165	
ccg	gaa	gag	cta	gag	cgc	atc	gcc	aag	tgg	tgc	gat	gac	aat	gat	gct	643
Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys	Asp	Asp	Asn	Asp	Ala	
				170					175					180		
gtt	ctt	atc	tct	gat	gag	gac	tac	cac	ggc	atg	agc	ttt	ggt	cgt	ccg	691
Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met	Ser	Phe	Gly	Arg	Pro	
			185					190					195			
ctg	gca	act	gcg	cat	cag	ttt	tcc	aag	aac	gcc	atc	gtg	gtg	ggt	acc	739
Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	Thr	
		200				205						210				
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Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg	Val	Gly	Trp	Ile	Ile	
	215					220					225					
gtt	cca	gat	gag	ctg	gtc	aca	ccg	att	gaa	aac	ctg	cag	gct	tct	ctt	835
Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn	Leu	Gln	Ala	Ser	Leu	
	230				235					240					245	
tcc	ttg	tgt	gct	cct	gcc	atc	ggg	cag	gct	gcg	gga	cgc	gca	gcc	ttc	883
Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala	Gly	Arg	Ala	Ala	Phe	
				250					255					260		
act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	cgc	931
Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	Arg	
			265					270					275			
gag	gcc	cgg	gag	gtg	ttc	gtc	gat	aag	ctc	cct	gaa	atc	ggg	ctt	ggc	979
Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro	Glu	Ile	Gly	Leu	Gly	
		280					285					290				
act	ttc	gcc	gac	ccg	gat	ggc	ggc	ctg	tat	ttg	tgg	gtc	gat	gtt	tct	1027

Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 1217
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 360 365

taggttagtt tcg 1230

<210> 116

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

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Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95

Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110

Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125

Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140

Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160

Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175

Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
180 185 190

Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
195 200 205

Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
210 215 220

Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
225 230 235 240

Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
245 250 255

Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
260 265 270

Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
275 280 285

Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
290 295 300

Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
305 310 315 320

Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
325 330 335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser
340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
355 360 365

Lys

<210> 117
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(634)
<223> FRXA00618

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Met Ser Phe Gly Arg
1 5
ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
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<210> 118
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
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          20             25             30
Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
          35             40             45
Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
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<400> 118

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
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Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 119
 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(385)
 <223> FRXA00627

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 Met Gln Met Leu Asp
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 90 95

<210> 120
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 120
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 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
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 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 85 90 95

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1411)
 <223> RXA02550

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 Val Thr Thr Asp Lys
 1 5
 cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg 163
 Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala
 10 15 20
 gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat 211
 Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp
 25 30 35
 cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg 259
 Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val
 40 45 50
 gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag 307

Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly	His	Asn	Ile	Leu	Lys	
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Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe	Asp	Ala	Pro	Asp	Val	
70					75				80					85		
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Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr	Ser	Gln	Gly	Tyr	Ser	
				90				95					100			
acc	tcc	aaa	ggc	att	att	ccg	gcc	cgg	cga	gca	gtg	gtc	acc	cgc	tac	451
Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala	Val	Val	Thr	Arg	Tyr	
			105				110						115			
gaa	gtt	gtg	ccc	gga	ttc	ccc	cac	ttc	gat	gtt	gat	gat	gtg	ttc	tta	499
Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val	Asp	Asp	Val	Phe	Leu	
	120					125					130					
ggc	aac	ggt	gtc	tca	gaa	cta	atc	acc	atg	acc	acc	caa	gca	ctc	ctc	547
Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr	Thr	Gln	Ala	Leu	Leu	
	135					140					145					
aac	gac	ggc	gat	gaa	gtt	ctt	atc	ccc	gca	ccg	gac	tac	cca	ctg	tgg	595
Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro	Asp	Tyr	Pro	Leu	Trp	
150					155				160					165		
act	gcc	gca	acc	tcc	ctg	gct	ggt	ggt	aag	cct	gtg	cac	tac	ctc	tgt	643
Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro	Val	His	Tyr	Leu	Cys	
				170				175						180		
gat	gag	gaa	gat	gac	tgg	aac	cca	tcc	atc	gaa	gac	atc	aag	tcc	aaa	691
Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu	Asp	Ile	Lys	Ser	Lys	
			185				190						195			
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	gtg	atc	aac	ccc	aac	aac	ccc	739
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile	Asn	Pro	Asn	Asn	Pro	
		200				205						210				
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	ttg	gaa	caa	atc	gtc	gag	att	787
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu	Gln	Ile	Val	Glu	Ile	
	215					220					225					
gca	cgc	gag	cat	gac	ctg	ctg	att	ttg	gcc	gat	gaa	atc	tac	gac	cgc	835
Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp	Glu	Ile	Tyr	Asp	Arg	
230					235				240					245		
att	ctc	tac	gat	gat	gcc	gag	cac	atc	agc	ctg	gca	acc	ctt	gca	cca	883
Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu	Ala	Thr	Leu	Ala	Pro	
				250				255					260			
gat	ctc	ctt	tgc	atc	aca	tac	aac	ggt	cta	tcc	aag	gca	tac	cgc	gtc	931
Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser	Lys	Ala	Tyr	Arg	Val	
			265				270					275				
gca	gga	tac	cga	gct	ggc	tgg	atg	gta	ttg	act	gga	cca	aag	caa	tac	979
Ala	Gly	Tyr	Arg	Ala	Gly	Trp	Met	Val	Leu	Thr	Gly	Pro	Lys	Gln	Tyr	
	280					285					290					
gca	cgt	gga	ttt	att	gag	ggc	ctc	gaa	ctc	ctc	gca	ggc	act	cga	ctc	1027
Ala	Arg	Gly	Phe	Ile	Glu	Gly	Leu	Glu	Leu	Leu	Ala	Gly	Thr	Arg	Leu	

295	300	305	
tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga			1075
Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly			
310	315	320	325
cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa			1123
Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu			
	330	335	340
cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc			1171
Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser			
	345	350	355
tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc			1219
Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro			
	360	365	370
aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc			1267
Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu			
	375	380	385
cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca			1315
Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro			
	390	400	405
cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg			1363
His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu			
	410	415	420
gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag			1411
Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln			
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tagtagttgt taggattcac cac			1434
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<400> 122			
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Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr			
	20	25	30
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	35	40	45
Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly			
	50	55	60
His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe			
	65	70	75
Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr			
	85	90	95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
 100 105 110
 Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
 115 120 125
 Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
 130 135 140
 Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
 145 150 155 160
 Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
 165 170 175
 Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
 180 185 190
 Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
 195 200 205
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
 210 215 220
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
 225 230 235 240
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
 245 250 255
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
 260 265 270
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu

420

425

430

Ser Thr Tyr Lys Gln
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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1678)

<223> RXA02193

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agcaccattg tgatttcctt caacttgtga gaggcagtag atg tct aag acg agc 115
Met Ser Lys Thr Ser
1 5

aac aag tct tca gca gac tca aag aat gac gca aaa gcc gaa gac att 163
Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile
10 15 20

gtg aac ggc gag aac caa atc gcc acg aat gag tcg cag tct tca gac 211
Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp
25 30 35

agc gct gca gtt tcg gaa cgt gtc gtc gaa cca aaa acc acg gtt cag 259
Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln
40 45 50

aaa aag ttc cga atc gaa tcg gat ctg ctt ggt gaa ctt cag atc cca 307
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro
55 60 65

tcc cac gca tat tac ggg gtg cac acc ctt cgt gcg gtg gac aac ttc 355
Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe
70 75 80 85

caa atc tca cga acc acc atc aac cac gtc cca gat ttc att cgc ggc 403
Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly
90 95 100

atg gtc cag gtg aaa aag gcc gca gct tta gca aac cgc cga ctg cac 451
Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His
105 110 115

aca ctt cca gca caa aaa gca gaa gca att gtc tgg gct tgt gat cag 499
Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln
120 125 130

atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc 547
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe
135 140 145

cag ggt ggc gca ggt acc tca ctg aac atg aac acc aac gag gtt gtt 595
Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val

150	155	160	165	
gcc aac ctt gca ctt gag ttc tta ggc cat gaa aag ggc gag tac cac				643
Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His				
	170	175	180	
atc ctg cac ccc atg gat gat gtg aac atg tcc cag tcc acc aac gat				691
Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp				
	185	190	195	
tcc tac cca act ggt ttc cgc ctg ggc att tac gct gga ctg cag acc				739
Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr				
	200	205	210	
ctc atc gct gaa att gat gag ctt cag gtt gcg ttc cgc cac aag ggc				787
Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly				
	215	220	225	
aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat				835
Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp				
	230	235	240	245
gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac				883
Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn				
	250	255	260	
ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc				931
Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala Ala Asn Arg Leu Leu				
	265	270	275	
gag gtc aat ctt ggt gca acc gca atc ggt act ggt gtg aac act cca				979
Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro				
	280	285	290	
gca ggc tac cgc cac cag gtt gtc gct gct ctg tct gag gtc acc gga				1027
Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly				
	295	300	305	
ctg gaa cta aag tcc gca cgt gat ctc atc gag gct acc tct gac acc				1075
Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp Thr				
	310	315	320	325
ggt gca tat gtt cat gcg cac tcc gca atc aag cgt gca gcc atg aaa				1123
Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys				
	330	335	340	
ctg tcc aag atc tgt aac gat cta cgt ctg ctg tct tct ggt cct cgt				1171
Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg				
	345	350	355	
gct ggc ttg aac gaa atc aac ctg cca cca cgc cag gct ggt tcc tcc				1219
Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser				
	360	365	370	
atc atg cca gcc aag gtc aac cca gtg atc cca gaa gtg gtc aac cag				1267
Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln				
	375	380	385	
gtc tgc ttc aag gtc ttc ggt aac gat ctc acc gtc acc atg gct gcg				1315
Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala				
	390	395	400	405

gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa 1363
 Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu
 410 415 420

tcc ctc ttc cag tca ctg cgc atc ctg ggc aat gca gcc aag act ttg 1411
 Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn Ala Ala Lys Thr Leu
 425 430 435

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt 1459
 Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg
 440 445 450

gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc 1507
 Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe
 455 460 465

ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act 1555
 Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr
 470 475 480 485

ggt cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa 1603
 Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu
 490 495 500

aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg 1651
 Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met
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tac 1701

<210> 124

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

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Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro
 35 40 45

Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly
 50 55 60

Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg
 65 70 75 80

Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro
 85 90 95

Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala

100					105					110					
Asn	Arg	Arg	Leu	His	Thr	Leu	Pro	Ala	Gln	Lys	Ala	Glu	Ala	Ile	Val
		115					120					125			
Trp	Ala	Cys	Asp	Gln	Ile	Leu	Ile	Glu	Glu	Arg	Cys	Met	Asp	Gln	Phe
	130					135					140				
Pro	Ile	Asp	Val	Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn
145					150					155					160
Thr	Asn	Glu	Val	Val	Ala	Asn	Leu	Ala	Leu	Glu	Phe	Leu	Gly	His	Glu
				165					170					175	
Lys	Gly	Glu	Tyr	His	Ile	Leu	His	Pro	Met	Asp	Asp	Val	Asn	Met	Ser
			180					185					190		
Gln	Ser	Thr	Asn	Asp	Ser	Tyr	Pro	Thr	Gly	Phe	Arg	Leu	Gly	Ile	Tyr
		195					200					205			
Ala	Gly	Leu	Gln	Thr	Leu	Ile	Ala	Glu	Ile	Asp	Glu	Leu	Gln	Val	Ala
	210					215					220				
Phe	Arg	His	Lys	Gly	Asn	Glu	Phe	Val	Asp	Ile	Ile	Lys	Met	Gly	Arg
225					230					235					240
Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Met	Ser	Leu	Gly	Glu	Glu	Phe	Arg
				245					250					255	
Ala	Phe	Ala	His	Asn	Leu	Ala	Glu	Glu	Gln	Thr	Val	Leu	Arg	Glu	Ala
			260				265						270		
Ala	Asn	Arg	Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr
		275					280					285			
Gly	Val	Asn	Thr	Pro	Ala	Gly	Tyr	Arg	His	Gln	Val	Val	Ala	Ala	Leu
	290					295					300				
Ser	Glu	Val	Thr	Gly	Leu	Glu	Leu	Lys	Ser	Ala	Arg	Asp	Leu	Ile	Glu
305					310					315					320
Ala	Thr	Ser	Asp	Thr	Gly	Ala	Tyr	Val	His	Ala	His	Ser	Ala	Ile	Lys
				325					330					335	
Arg	Ala	Ala	Met	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu
			340					345					350		
Ser	Ser	Gly	Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Pro	Arg
		355					360					365			
Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro
	370					375					380				
Glu	Val	Val	Asn	Gln	Val	Cys	Phe	Lys	Val	Phe	Gly	Asn	Asp	Leu	Thr
385				390						395					400
Val	Thr	Met	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu
				405					410					415	
Pro	Val	Ile	Gly	Glu	Ser	Leu	Phe	Gln	Ser	Leu	Arg	Ile	Leu	Gly	Asn
			420					425					430		

Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn
435 440 445

Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr
450 455 460

Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys
465 470 475 480

Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys
485 490 495

Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn
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<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1075)

<223> RXA02432

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Met Ser Lys Gln His
1 5

tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163
Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys
10 15 20

gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211
Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala
25 30 35

aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259
Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro
40 45 50

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Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu
55 60 65

atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355
Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser
70 75 80 85

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Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly
90 95 100

gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc 451
 Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala
 105 110 115

gta gac acc ttc ctt gat gat ccc cgc cca gtc att ttc acc ggc gcc 499
 Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val Ile Phe Thr Gly Ala
 120 125 130

caa aaa ccc ttc gat cat ccc gaa gcc gac ggc cca aac aac ctt ttc 547
 Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly Pro Asn Asn Leu Phe
 135 140 145

gaa gcc tgc ctc atc gca tcc gac ccc tcc gct cgc gga att ggt gca 595
 Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala Arg Gly Ile Gly Ala
 150 155 160 165

ctc att gtc ttc ggt cac gcc gtc atc cct gct cgc ggc tgc gtt aaa 643
 Leu Ile Val Phe Gly His Ala Val Ile Pro Ala Arg Gly Cys Val Lys
 170 175 180

tgg cac acc tct gat gag ctg gcg ttt gca acc aac ggc cct gaa gaa 691
 Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr Asn Gly Pro Glu Glu
 185 190 195

cca gag cgc ccc gat gcg ctg ccc gta gct aaa ttg gcg gat gtc tct 739
 Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys Leu Ala Asp Val Ser
 200 205 210

gtc gaa atc atc ccc gca tac cct ggt gcc acc ggc gca atg gtg gaa 787
 Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr Gly Ala Met Val Glu
 215 220 225

gct gcc atc gct gcc ggt gct caa gga ctt gta gtg gaa gca atg gga 835
 Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val Val Glu Ala Met Gly
 230 235 240 245

tca ggc aat gtt ggt tcc cgc atg ggt gat gcc cta ggt aaa gca ctt 883
 Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala Leu Gly Lys Ala Leu
 250 255 260

gac gct gga att ccc gtg gtg atg agc act agg gtt cct cgt ggt gaa 931
 Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg Val Pro Arg Gly Glu
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 Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly Ala Thr Leu Ala Ala
 280 285 290

aag ggc gct gtg gga tct cgc tac ttc aga gct ggt cag gca cgt att 1027
 Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala Gly Gln Ala Arg Ile
 295 300 305

ttg ctc gcg att gcc att gcg acg ggc gca cat ccg gtg acg ctt tac 1075
 Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His Pro Val Thr Leu Tyr
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<210> 126

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

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Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala
          35              40              45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala
          50              55              60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe
          65              70              75              80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp
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Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu
          100             105             110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val
          115             120             125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly
          130             135             140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala
          145             150             155             160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala
          165             170             175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr
          180             185             190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys
          195             200             205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr
          210             215             220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val
          225             230             235             240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala
          245             250             255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg
          260             265             270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly
          275             280             285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala
          290             295             300

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Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His
 305 310 315 320

Pro Val Thr Leu Tyr
 325

<210> 127

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN03003

<400> 127

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 Met Thr Ser Arg Thr
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
 55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145

atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595

Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225
 <210> 128
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 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 128
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 20 25 30
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80
 Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
 85 90 95
 Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
 100 105 110
 Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
 115 120 125
 Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
 130 135 140
 Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
 145 150 155 160
 Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
 165 170 175
 Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr
 180 185 190

Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp
 195 200 205

Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser
 210 215 220

Leu
 225

<210> 129

<211> 1206

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1183)

<223> RXN00508

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atcgtatttc tgtccgcggg tgggtggcaca atagttcaac atg aac ttg ctg acc 115
 Met Asn Leu Leu Thr
 1 5

acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163
 Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys
 10 15 20

caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211
 Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala
 25 30 35

tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259
 Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly
 40 45 50

gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307
 Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg
 55 60 65

gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355
 Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu
 70 75 80 85

cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403
 Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile
 90 95 100

tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451
 Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile
 105 110 115

cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcg ggt gtg gat 499
 Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp
 120 125 130

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac 547

Glu	Gln	Glu	Trp	Glu	Gly	Val	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Pro	His		
135						140					145						
att	gag	gtc	acg	ggc	atg	ttc	acg	cac	ttg	gcg	tgc	gcg	gat	gag	cca	595	
Ile	Glu	Val	Thr	Gly	Met	Phe	Thr	His	Leu	Ala	Cys	Ala	Asp	Glu	Pro		
150					155					160					165		
gag	aat	ccg	gaa	act	gat	cgc	caa	att	att	gct	ttt	cga	cgc	gcc	ctt	643	
Glu	Asn	Pro	Glu	Thr	Asp	Arg	Gln	Ile	Ile	Ala	Phe	Arg	Arg	Ala	Leu		
				170					175					180			
gcg	ctc	gcc	cgc	aag	cac	ggg	ctt	gag	tgc	ccg	gtc	aac	cac	gta	tgc	691	
Ala	Leu	Ala	Arg	Lys	His	Gly	Leu	Glu	Cys	Pro	Val	Asn	His	Val	Cys		
			185					190					195				
aac	tca	cct	gca	ttc	ttg	act	cga	tct	gat	tta	cac	atg	gag	atg	gtc	739	
Asn	Ser	Pro	Ala	Phe	Leu	Thr	Arg	Ser	Asp	Leu	His	Met	Glu	Met	Val		
		200					205					210					
cga	ccg	ggt	ttg	gcc	ttt	tat	ggg	ttg	gaa	ccc	gtg	gcg	gga	ctg	gag	787	
Arg	Pro	Gly	Leu	Ala	Phe	Tyr	Gly	Leu	Glu	Pro	Val	Ala	Gly	Leu	Glu		
		215				220					225						
cat	ggt	ttg	aag	ccg	gcg	atg	acg	tgg	gag	gcg	aag	gtg	agc	gtc	gta	835	
His	Gly	Leu	Lys	Pro	Ala	Met	Thr	Trp	Glu	Ala	Lys	Val	Ser	Val	Val		
230						235				240					245		
aag	caa	att	gaa	gct	gga	caa	ggc	act	tcc	tat	ggc	ctg	acc	tgg	cgc	883	
Lys	Gln	Ile	Glu	Ala	Gly	Gln	Gly	Thr	Ser	Tyr	Gly	Leu	Thr	Trp	Arg		
				250					255					260			
gct	gag	gat	cgc	ggc	ttt	gtg	gct	gtg	gtg	cct	gcg	ggc	tat	gcc	gat	931	
Ala	Glu	Asp	Arg	Gly	Phe	Val	Ala	Val	Val	Pro	Ala	Gly	Tyr	Ala	Asp		
			265					270					275				
ggc	atg	ccg	cgg	cat	gcc	cag	ggg	aaa	ttc	tcc	gtc	acg	att	gat	ggc	979	
Gly	Met	Pro	Arg	His	Ala	Gln	Gly	Lys	Phe	Ser	Val	Thr	Ile	Asp	Gly		
		280					285						290				
ctg	gac	tat	ccg	cag	gtt	ggg	cgc	gta	tgc	atg	gat	cag	ttc	gtt	att	1027	
Leu	Asp	Tyr	Pro	Gln	Val	Gly	Arg	Val	Cys	Met	Asp	Gln	Phe	Val	Ile		
		295				300					305						
tct	ttg	ggc	gac	aat	cca	cac	ggc	gtg	gaa	gct	ggg	gcg	aag	gcc	gtg	1075	
Ser	Leu	Gly	Asp	Asn	Pro	His	Gly	Val	Glu	Ala	Gly	Ala	Lys	Ala	Val		
310					315					320				325			
ata	ttc	ggt	gag	aat	ggg	cat	gac	gca	act	gat	ttt	gcg	gag	cgt	tta	1123	
Ile	Phe	Gly	Glu	Asn	Gly	His	Asp	Ala	Thr	Asp	Phe	Ala	Glu	Arg	Leu		
				330				335						340			
gac	acc	att	aac	tat	gag	gta	gtg	tgc	cga	cca	acc	ggc	cga	act	gtc	1171	
Asp	Thr	Ile	Asn	Tyr	Glu	Val	Val	Cys	Arg	Pro	Thr	Gly	Arg	Thr	Val		
			345					350					355				
cgc	gca	tat	gtt	taagtgaata	cggttaagga	gca										1206	
Arg	Ala	Tyr	Val														
			360														

<210> 130

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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Met Asn Leu Leu Thr Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn
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Thr Arg Val Leu Lys Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val
      20              25              30

Val Lys Ala Asn Ala Tyr Asn His Gly Val Glu Lys Val Ala Pro Val
      35              40              45

Ile Ala Ala His Gly Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu
      50              55              60

Ala Met Gln Leu Arg Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp
      65              70              75              80

Ile Trp Thr Pro Glu Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile
      85              90              95

Asp Leu Ala Val Ile Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr
      100             105             110

Asp Ala Glu His Ile Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His
      115             120             125

Arg Ser Gly Val Asp Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu
      130             135             140

Ala Ala Ala Pro His Ile Glu Val Thr Gly Met Phe Thr His Leu Ala
      145             150             155             160

Cys Ala Asp Glu Pro Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala
      165             170             175

Phe Arg Arg Ala Leu Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro
      180             185             190

Val Asn His Val Cys Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu
      195             200             205

His Met Glu Met Val Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro
      210             215             220

Val Ala Gly Leu Glu His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala
      225             230             235             240

Lys Val Ser Val Val Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr
      245             250             255

Gly Leu Thr Trp Arg Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro
      260             265             270

Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser
      275             280             285

Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met
      290             295             300

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Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala
305 310 315 320

Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp
325 330 335

Phe Ala Glu Arg Leu Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro
340 345 350

Thr Gly Arg Thr Val Arg Ala Tyr Val
355 360

<210> 131

<211> 1152

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1129)

<223> RXN00636

<400> 131

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tcgatctggc ccgttcgaac ataaggaata ttctactcc atg atg att gat aca 115
Met Met Ile Asp Thr
1 5

cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg 163
Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg
10 15 20

atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg 211
Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val
25 30 35

aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt 259
Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly
40 45 50

gcc cga ggg atc acc tgc gca acc att ggc gag gcg gaa att ttt gcc 307
Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala
55 60 65

ggc gca ggt ttt acg gac atc ttt att gca tat ccg ctg tat cta acc 355
Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr
70 75 80 85

gat cat gca gtg caa cgc ctg aac gcg atc ccc gga gaa att tcc att 403
Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile
90 95 100

ggc gtg gat tcg gta gag atg gca cag gcg acg gcg ggt ttg cgg gaa 451
Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr Ala Gly Leu Arg Glu
105 110 115

gat atc aag gct ctg att gaa gtg gat tcg gga cat cgt aga agt gga 499
Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly

120	125	130	
gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly 135 140 145			547
agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc ccg Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro 150 155 160 165			595
gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn 170 175 180			643
agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tcg ccg Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro 185 190 195			691
tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr 200 205 210			739
gtg ttt aac gat tcc cag cag atc acc tcg gga gca tgc act gag aag Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys 215 220 225			787
cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser 230 235 240 245			835
gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp 250 255 260			883
aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu 265 270 275			931
gcc cga atc tct gct ttg tcg gag cat cac gca acc att ttc tgg cca Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro 280 285 290			979
gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro 295 300 305			1027
aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg 310 315 320 325			1075
gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg 330 335 340			1123
aac aat tagggaaacc tcttgacctt cac Asn Asn			1152

<210> 132

<211> 343

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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Met Met Ile Asp Thr Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr
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Ala Asn Ile Ser Arg Met Ala Ala His Ala Gly Ala His Glu Ile Ala
      20           25           30

Leu Arg Pro His Val Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met
      35           40           45

Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu
      50           55           60

Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr
      65           70           75           80

Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro
      85           90           95

Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr
      100          105          110

Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly
      115          120          125

His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile
      130          135          140

Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly
      145          150          155          160

His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu
      165          170          175

Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser
      180          185          190

Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met
      195          200          205

Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly
      210          215          220

Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val
      225          230          235          240

Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys
      245          250          255

Ile Leu Ser Thr Asp Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val
      260          265          270

Leu Gly Asn Pro Glu Ala Arg Ile Ser Ala Leu Ser Glu His His Ala
      275          280          285

Thr Ile Phe Trp Pro Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln
      290          295          300

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Leu Asn Ile Val Pro Asn His Ala Cys Asn Val Ile Asn Leu Val Asp
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Glu Val Tyr Val Arg Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val
325 330 335

Val Ala Arg Gly Arg Asn Asn
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<210> 133

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXA02536

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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115
Met Asp Asn Phe Ala
1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
55 60 65

cct gct gac acc gtg cag gcg ggt gaa aaa acg atc tcg cgc gtc aac 355
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
105 110 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
120 125 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu

135	140	145	
gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac			595
Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp			
150	155	160	165
ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca			643
Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala			
	170	175	180
ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca			691
Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro			
	185	190	195
gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc			739
Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser			
	200	205	210
atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag			787
Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu			
	215	220	225
cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att			835
Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile			
	230	235	240
cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act			879
Arg Glu Ala Leu Pro Val Leu			
	250		

<210> 134

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

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	20	25	30
Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe			
	35	40	45
Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val			
	50	55	60
Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr			
	65	70	75
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His			
	85	90	95
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu			
	100	105	110
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp			
	115	120	125

Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
 130 135 140
 Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
 145 150 155 160
 Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
 165 170 175
 Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190
 Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205
 Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220
 Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
 225 230 235 240
 Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 135

<211> 1635

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1612)

<223> RXS00870

<400> 135

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 caacaattca cttcgagag catttaagga atttacacac atg tct gaa cca caa 115
 Met Ser Glu Pro Gln
 1 5

 acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc 163
 Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly
 10 15 20

 aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat 211
 Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn
 25 30 35

 gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc 259
 Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala
 40 45 50

 acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa 307
 Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln
 55 60 65

 gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag 355
 Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu
 70 75 80 85

ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979
Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile	
280 285 290	
gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac	1027
Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp	
295 300 305	
acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac	1075
Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His	
310 315 320 325	

ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat 1123
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr
 330 335 340

gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt 1171
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg
 345 350 355

aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg 1219
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr
 360 365 370

ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc 1267
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile
 375 380 385

ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca 1315
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala
 390 395 400 405

att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc 1363
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe
 410 415 420

acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg 1411
 Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val
 425 430 435

ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac 1459
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His
 440 445 450

tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat 1507
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr
 455 460 465

ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc 1555
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser
 470 475 480 485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca 1603
 Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro
 490 495 500

cag aac gat taattgaagg agagcacagg act 1635
 Gln Asn Asp

<210> 136

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser
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Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly
 20 25 30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala
 35 40 45
 Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser
 50 55 60
 Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn
 65 70 75 80
 Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys
 85 90 95
 Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val
 100 105 110
 Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu
 115 120 125
 Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly
 130 135 140
 Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met
 145 150 155 160
 Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys
 165 170 175
 Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp
 180 185 190
 Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp
 195 200 205
 Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile
 210 215 220
 Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser
 225 230 235 240
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His
 245 250 255
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala
 260 265 270
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser
 275 280 285
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile
 290 295 300
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu
 305 310 315 320
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp
 325 330 335
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile
 340 345 350
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe

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<400> 137
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taaaacttgc aggacaaccc ccataaggac accacaggac atg ctg cgc acc atc 115
Met Leu Arg Thr Ile
1 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
10 15 20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
25 30 35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
40 45 50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile

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      55              60              65
tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
  70              75              80              85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
      90              95              100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
      105              110              115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
      120              125              130

aga agc att tagcggtttta gctcgccaat att 531
Arg Ser Ile
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<210> 138
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

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<400> 138
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Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
      20              25              30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
      35              40              45

Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
      50              55              60

Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
      65              70              75              80

Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
      85              90              95

Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
      100              105              110

Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
      115              120              125

Gly Leu Leu Thr Ser Arg Ser Ile
      130              135

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<210> 139
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA01561

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Tyr	Ala	Gly	Ile	Ala	Ala	Val	Val	Ala	Ala	His	Asp	Ile	Lys	Val	Val	
			185					190					195			


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gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc 739
Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala
      200                      205                      210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg 787
Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu
      215                      220                      225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835
Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His
      230                      235                      240                      245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883
Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg
      250                      255                      260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931
Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala
      265                      270                      275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979
Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp
      280                      285                      290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca 1027
Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr
      295                      300                      305

ctg tgatgtgatt tcaaacgatc aca 1053
Leu
310

<210> 140
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Met Leu Thr Leu Asn Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro
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His Val Arg Arg Thr Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr
      20                      25                      30

Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
      35                      40                      45

Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
      50                      55                      60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
      65                      70                      75                      80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
      85                      90                      95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
      100                      105                      110

Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe

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115					120					125					
Glu	Ala	Ala	Gln	Thr	Phe	Glu	Ser	Glu	Thr	Gly	Ala	Leu	Phe	Cys	His
130						135					140				
Ala	Tyr	Asp	Gln	Pro	Asp	Ile	Ala	Ala	Gly	Ala	Gly	Val	Ile	Gly	Leu
145					150					155					160
Glu	Ile	Val	Glu	Asp	Leu	Pro	Asp	Val	Asp	Thr	Ile	Val	Val	Ala	Val
			165						170					175	
Gly	Gly	Gly	Gly	Leu	Tyr	Ala	Gly	Ile	Ala	Ala	Val	Val	Ala	Ala	His
			180					185					190		
Asp	Ile	Lys	Val	Val	Ala	Val	Glu	Pro	Ser	Lys	Ile	Pro	Thr	Leu	His
		195					200					205			
Asn	Ser	Leu	Ile	Ala	Gly	Gln	Pro	Val	Asp	Val	Asn	Val	Ser	Gly	Ile
		210				215					220				
Ala	Ala	Asp	Ser	Leu	Gly	Ala	Arg	Gln	Ile	Gly	Arg	Glu	Ala	Phe	Asp
225					230					235					240
Ile	Ala	Thr	Ala	His	Pro	Pro	Ile	Gly	Val	Leu	Val	Asp	Asp	Glu	Ala
				245					250					255	
Ile	Ile	Ala	Ala	Arg	Arg	His	Leu	Trp	Asp	Asn	Tyr	Arg	Ile	Pro	Ala
			260					265					270		
Glu	His	Gly	Ala	Ala	Ala	Ala	Leu	Ala	Ser	Leu	Thr	Ser	Gly	Ala	Tyr
		275					280					285			
Lys	Pro	Ala	Ala	Asp	Glu	Lys	Val	Ala	Val	Ile	Val	Cys	Gly	Ala	Asn
		290				295					300				
Thr	Asp	Leu	Thr	Thr	Leu										
305					310										

<210> 141

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXA01850

<400> 141

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				Met	Ala	Ile	Ser	Val	
				1				5	

gtt	gat	cta	ttt	agc	atc	ggg	atc	gga	cca	tca	tcc	tca	cat	acc	gtc	163
Val	Asp	Leu	Phe	Ser	Ile	Gly	Ile	Gly	Pro	Ser	Ser	Ser	His	Thr	Val	
				10				15						20		

ggc ccc atg aga gcc gcc ctc acg tat atc tct gaa ttt ccc agc tcg 211

Gly	Pro	Met	Arg	Ala	Ala	Leu	Thr	Tyr	Ile	Ser	Glu	Phe	Pro	Ser	Ser		
			25					30					35				
cat	gtc	gat	atc	acg	ttg	cac	gga	tcc	ctt	gcc	gcc	acc	ggt	aaa	ggc	259	
His	Val	Asp	Ile	Thr	Leu	His	Gly	Ser	Leu	Ala	Ala	Thr	Gly	Lys	Gly		
		40					45					50					
cac	tgc	act	gac	cgg	gcg	gta	tta	ctg	ggt	ctg	gtg	gga	tgg	gaa	cca	307	
His	Cys	Thr	Asp	Arg	Ala	Val	Leu	Leu	Gly	Leu	Val	Gly	Trp	Glu	Pro		
	55					60					65						
acg	ata	gtt	ccc	att	gat	gct	gca	ccc	tca	ccc	ggc	gcg	ccg	att	cct	355	
Thr	Ile	Val	Pro	Ile	Asp	Ala	Ala	Pro	Ser	Pro	Gly	Ala	Pro	Ile	Pro		
70					75			80						85			
gcg	aaa	ggt	tct	gtg	aac	ggg	cca	aag	gga	acg	gtg	tcg	tat	tcc	ctg	403	
Ala	Lys	Gly	Ser	Val	Asn	Gly	Pro	Lys	Gly	Thr	Val	Ser	Tyr	Ser	Leu		
				90				95						100			
acg	ttt	gat	cct	cat	cct	ctt	cca	gaa	cac	ccc	aat	gcc	gtt	acc	ttt	451	
Thr	Phe	Asp	Pro	His	Pro	Leu	Pro	Glu	His	Pro	Asn	Ala	Val	Thr	Phe		
			105					110					115				
aaa	gga	tca	acc	aca	agg	act	tat	ttg	tcg	gtg	ggt	ggt	ggg	ttc	att	499	
Lys	Gly	Ser	Thr	Thr	Arg	Thr	Tyr	Leu	Ser	Val	Gly	Gly	Gly	Phe	Ile		
		120					125					130					
atg	acg	ttg	gag	gat	ttc	cgg	aag	ctg	gac	gat	atc	gga	tca	ggt	gtg	547	
Met	Thr	Leu	Glu	Asp	Phe	Arg	Lys	Leu	Asp	Asp	Ile	Gly	Ser	Gly	Val		
	135					140					145						
tca	acc	att	cat	cca	gag	gca	gag	gtg	cct	tgt	cct	ttt	cag	aag	agt	595	
Ser	Thr	Ile	His	Pro	Glu	Ala	Glu	Val	Pro	Cys	Pro	Phe	Gln	Lys	Ser		
150					155					160					165		
tcc	caa	tta	ctc	gca	tat	ggt	cgc	gat	ttt	gcg	gag	gtc	atg	aag	gat	643	
Ser	Gln	Leu	Leu	Ala	Tyr	Gly	Arg	Asp	Phe	Ala	Glu	Val	Met	Lys	Asp		
				170				175						180			
aat	gag	cgc	tta	atc	cac	ggg	gat	ctt	ggc	aca	gtg	gat	gcc	cat	ttg	691	
Asn	Glu	Arg	Leu	Ile	His	Gly	Asp	Leu	Gly	Thr	Val	Asp	Ala	His	Leu		
			185					190					195				
gat	cga	gtg	tgg	cag	att	atg	cag	gag	tgc	gtg	gca	caa	ggc	atc	gca	739	
Asp	Arg	Val	Trp	Gln	Ile	Met	Gln	Glu	Cys	Val	Ala	Gln	Gly	Ile	Ala		
		200					205					210					
acg	ccg	ggg	att	tta	ccg	ggt	ggg	ttg	aat	gtg	caa	cgt	cgg	gcg	ccg	787	
Thr	Pro	Gly	Ile	Leu	Pro	Gly	Gly	Leu	Asn	Val	Gln	Arg	Arg	Ala	Pro		
	215					220					225						
cag	gta	cac	gcg	ctg	att	agc	aac	ggg	gat	acg	tgt	gag	ctg	ggt	gct	835	
Gln	Val	His	Ala	Leu	Ile	Ser	Asn	Gly	Asp	Thr	Cys	Glu	Leu	Gly	Ala		
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gat	ctt	gat	gct	gtg	gag	tgg	gtg	aat	ctg	tac	gcc	ttg	gcg	gtg	aat	883	
Asp	Leu	Asp	Ala	Val	Glu	Trp	Val	Asn	Leu	Tyr	Ala	Leu	Ala	Val	Asn		
				250				255						260			
gaa	gaa	aac	gcc	gct	ggt	ggt	cgt	gtg	gtt	act	gct	ccg	act	aat	ggt	931	
Glu	Glu	Asn	Ala	Ala	Gly	Gly	Arg	Val	Val	Thr	Ala	Pro	Thr	Asn	Gly		

265										270										275										
gct	gcg	ggg	att	att	ccg	gcg	gtg	atg	cac	tat	gcg	cgg	gat	ttt	ttg		979													
Ala	Ala	Gly	Ile	Ile	Pro	Ala	Val	Met	His	Tyr	Ala	Arg	Asp	Phe	Leu															
		280						285					290																	
aca	ggt	ttt	ggg	gcg	gag	cag	gcg	cgg	acg	ttt	ttg	tat	acc	gcg	ggt		1027													
Thr	Gly	Phe	Gly	Ala	Glu	Gln	Ala	Arg	Thr	Phe	Leu	Tyr	Thr	Ala	Gly															
	295					300					305																			
gcg	gtg	ggc	atc	atc	att	aag	gaa	aat	gcc	tcg	atc	tct	ggc	gcg	gag		1075													
Ala	Val	Gly	Ile	Ile	Ile	Lys	Glu	Asn	Ala	Ser	Ile	Ser	Gly	Ala	Glu															
310					315				320						325															
gtg	ggg	tgt	cag	ggt	gag	ggt	tca	gcg	tcc	gcg	atg	gcg	gct	gcc			1123													
Val	Gly	Cys	Gln	Gly	Glu	Val	Gly	Ser	Ala	Ser	Ala	Met	Ala	Ala	Ala															
			330					335					340																	
ggg	ttg	tgt	gca	gtc	tta	ggt	ggt	tct	ccg	caa	cag	gtg	gaa	aac	gcc		1171													
Gly	Leu	Cys	Ala	Val	Leu	Gly	Gly	Ser	Pro	Gln	Gln	Val	Glu	Asn	Ala															
			345					350					355																	
gcg	gag	att	gcg	ttg	gag	cac	aat	ttg	gga	ttg	acg	tgc	gat	ccg	gtg		1219													
Ala	Glu	Ile	Ala	Leu	Glu	His	Asn	Leu	Gly	Leu	Thr	Cys	Asp	Pro	Val															
	360					365						370																		
ggc	ggg	tta	gtg	cag	att	ccg	tgt	att	gaa	cgc	aac	gct	att	gct	gcc		1267													
Gly	Gly	Leu	Val	Gln	Ile	Pro	Cys	Ile	Glu	Arg	Asn	Ala	Ile	Ala	Ala															
	375					380					385																			
atg	aag	tcc	atc	aat	gcg	gca	agg	ctt	gcc	cgg	att	ggt	gat	ggc	aac		1315													
Met	Lys	Ser	Ile	Asn	Ala	Ala	Arg	Leu	Ala	Arg	Ile	Gly	Asp	Gly	Asn															
390				395				400							405															
aat	cgc	gtg	agt	ttg	gat	gat	gtg	gtg	gtc	acg	atg	gct	gcc	acc	ggc		1363													
Asn	Arg	Val	Ser	Leu	Asp	Asp	Val	Val	Val	Thr	Met	Ala	Ala	Thr	Gly															
			410					415					420																	
cgg	gac	atg	ctg	acc	aaa	tat	aag	gaa	acg	tcc	ctt	ggt	ggt	ttg	gca		1411													
Arg	Asp	Met	Leu	Thr	Lys	Tyr	Lys	Glu	Thr	Ser	Leu	Gly	Gly	Leu	Ala															
			425					430					435																	
acc	acc	ttg	ggc	ttc	ccg	gtg	tcg	atg	acg	gag	tgt	tagcggtagc					1457													
Thr	Thr	Leu	Gly	Phe	Pro	Val	Ser	Met	Thr	Glu	Cys																			
		440				445																								
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<210> 142

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

Met	Ala	Ile	Ser	Val	Val	Asp	Leu	Phe	Ser	Ile	Gly	Ile	Gly	Pro	Ser
1				5					10					15	

Ser	Ser	His	Thr	Val	Gly	Pro	Met	Arg	Ala	Ala	Leu	Thr	Tyr	Ile	Ser
		20					25					30			

Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala
 35 40 45
 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu
 50 55 60
 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro
 65 70 75 80
 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr
 85 90 95
 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro
 100 105 110
 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val
 115 120 125
 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp
 130 135 140
 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys
 145 150 155 160
 Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala
 165 170 175
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr
 180 185 190
 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val
 195 200 205
 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val
 210 215 220
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr
 225 230 235 240
 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr
 245 250 255
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr
 260 265 270
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr
 275 280 285
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe
 290 295 300
 Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser
 305 310 315 320
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser
 325 330 335
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln
 340 345 350
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu

355	360	365
Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg		
370	375	380
Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg		
385	390	395 400
Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr		
	405	410 415
Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser		
	420	425 430
Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu		
	435	440 445

Cys

<210> 143
 <211> 1425
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1402)
 <223> RXA00580

<400> 143
 ttttatatat gggatatcggc ggtctatgct tgtgggcgta cctgtcccgc gaggtagggtc 60
 ttacgcgcgcg gattcgtctt gtgaaagggtt agctgacctg atg acc gat gcc cac 115
 Met Thr Asp Ala His
 1 5
 caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag 163
 Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu
 10 15 20
 gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta 211
 Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu
 25 30 35
 gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg 259
 Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala
 40 45 50
 cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc 307
 Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg
 55 60 65
 cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca 355
 Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala
 70 75 80 85
 cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag 403
 Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln
 90 95 100

cct cac tct ggc gca cag gct aat gct gct gtg ctg atg act ttg gct	451
Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu Met Thr Leu Ala	
105 110 115	
gag cca ggc gac aag atc atg ggt ctg tct ttg gct cat ggt ggt cac	499
Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His Gly Gly His	
120 125 130	
ttg acc cac gga atg aag ttg aac ttc tcc gga aag ctg tac gag gtt	547
Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu Tyr Glu Val	
135 140 145	
gtt gcg tac ggt gtt gat cct gag acc atg cgt gtt gat atg gat cag	595
Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg Val Asp Met Asp Gln	
150 155 160 165	
gtt cgt gag att gct ctg aag gag cag cca aag gta att atc gct ggc	643
Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys Val Ile Ile Ala Gly	
170 175 180	
tgg tct gca tac cct cgc cac ctt gat ttc gag gct ttc cag tct att	691
Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu Ala Phe Gln Ser Ile	
185 190 195	
gct gcg gaa gtt ggc gcg aag ctg tgg gtc gat atg gct cac ttc gct	739
Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp Met Ala His Phe Ala	
200 205 210	
ggt ctt gtt gct gct ggt ttg cac cca agc cca gtt cct tac tct gat	787
Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro Val Pro Tyr Ser Asp	
215 220 225	
gtt gtt tct tcc act gtc cac aag act ttg ggt gga cct cgt tcc ggc	835
Val Val Ser Ser Thr Val His Lys Thr Leu Gly Gly Pro Arg Ser Gly	
230 235 240 245	
atc att ctg gct aag cag gag tac gcg aag aag ctg aac tct tcc gta	883
Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys Leu Asn Ser Ser Val	
250 255 260	
ttc cca ggt cag cag ggt ggt cct ttg atg cac gca gtt gct gcg aag	931
Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Val Ala Ala Lys	
265 270 275	
gct act tct ttg aag att gct ggc act gag cag ttc cgt gac cgt cag	979
Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln Phe Arg Asp Arg Gln	
280 285 290	
gct cgc acg ttg gag ggt gct cgc att ctt gct gag cgt ctg act gct	1027
Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala Glu Arg Leu Thr Ala	
295 300 305	
tct gat gcg aag gcc gct ggc gtg gat gtc ttg acc ggt ggc act gat	1075
Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu Thr Gly Gly Thr Asp	
310 315 320 325	
gtg cac ttg gtt ttg gct gat ctg cgt aac tcc cag atg gat ggc cag	1123
Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Gln Met Asp Gly Gln	
330 335 340	

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cag gcg gaa gat ctg ctg cac gag gtt ggt atc act gtg aac cgt aac 1171
Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val Asn Arg Asn
      345                      350                      355

gcg gtt cct ttc gat cct cgt cca cca atg gtt act tct ggt ctg cgt 1219
Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val Thr Ser Gly Leu Arg
      360                      365                      370

att ggt act cct gcg ctg gct acc cgt ggt ttc gat att cct gca ttc 1267
Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ile Pro Ala Phe
      375                      380                      385

act gag gtt gca gac atc att ggt act gct ttg gct aat ggt aag tcc 1315
Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Ala Asn Gly Lys Ser
      390                      395                      400                      405

gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat 1363
Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp
      410                      415                      420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc 1412
Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val
      425                      430

tttgagtttt cat 1425

<210> 144
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 144
Met Thr Asp Ala His Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn
  1                      5                      10                      15

Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg
      20                      25                      30

Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg
      35                      40                      45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu
      50                      55                      60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile
      65                      70                      75                      80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu
      85                      90                      95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val
      100                      105                      110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu
      115                      120                      125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly
      130                      135                      140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg

```


145 150 155 160
 Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys
 165 170 175
 Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu
 180 185 190
 Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp
 195 200 205
 Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro
 210 215 220
 Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly
 225 230 235 240
 Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys
 245 250 255
 Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His
 260 265 270
 Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln
 275 280 285
 Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala
 290 295 300
 Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu
 305 310 315 320
 Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser
 325 330 335
 Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile
 340 345 350
 Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val
 355 360 365
 Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe
 370 375 380
 Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu
 385 390 395 400
 Ala Asn Gly Lys Ser Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala
 405 410 415
 Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr
 420 425 430
 Ile Val

<210> 145

<211> 401

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(378)

<223> RXA01821

<400> 145

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cga aac agc caa ggc aaa tgg tgc cca agt acg cga tca cca aaa aat 48
Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
  1             5             10             15

acc agc atc gaa gac aac ggc gat cac gta gtc atc caa gca ggc gaa 96
Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu
          20             25             30

gaa acc aca atc gtg gac cgc gtt atc gtc acc acc ggc agc tgg aca 144
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
          35             40             45

agc gag ctc gtg ccc tcc atc gcg cca ctg ctt gaa gtg cga cgc cta 192
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
          50             55             60

gtg ctc acc tgg ttc ctg ccc aac aat cca gtg gac ttc caa ccg gaa 240
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu
          65             70             75             80

aac ctg cca tgc ttc atc cgt gac cgt gat ggc ttc cac gta ttt gga 288
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly
          85             90             95

gca cca tgc gtc gat ggg tac agc atc aaa att gcc gga ttg gat gag 336
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu
          100             105             110

tgg ggc gtt cca tta agc ctc gat cca ccg atg tgc cct cgg 378
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg
          115             120             125

tgatgtctcg atcccggttc cgg 401

```

<210> 146

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
  1             5             10             15

Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu
          20             25             30

Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
          35             40             45

Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
          50             55             60

Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu

```

65		70		75		80									
Asn	Leu	Pro	Cys	Phe	Ile	Arg	Asp	Arg	Asp	Gly	Phe	His	Val	Phe	Gly
				85					90					95	
Ala	Pro	Cys	Val	Asp	Gly	Tyr	Ser	Ile	Lys	Ile	Ala	Gly	Leu	Asp	Glu
			100					105					110		
Trp	Gly	Val	Pro	Leu	Ser	Leu	Asp	Pro	Pro	Met	Cys	Pro	Arg		
		115					120					125			

<210> 147

<211> 488

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXN02263

<400> 147

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cctgggcaac ccaagtgtat gaaaacgccc tggaaaaagg cgtcggcacc acattgaacc 60
tgtgggaatc acccgcactg gcttgagaga agaaacaaca atg aaa att gcg gta 115
                               Met Lys Ile Ala Val
                               1                               5

atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac 163
Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn
                               10                               15                               20

atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat 211
Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His
                               25                               30                               35

ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac 259
Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr
                               40                               45                               50

cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta 307
His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu
                               55                               60                               65

tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc 355
Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe
                               70                               75                               80                               85

ggg gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg 403
Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu
                               90                               95                               100

gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc 451
Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
                               105                               110                               115

gcg cag atg cgc agc gtt acc cag gtc tagacttccg 488
Ala Gln Met Arg Ser Val Thr Gln Val
                               120                               125

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<400> 148																
Met	Lys	Ile	Ala	Val	Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu	
1				5					10					15		
Trp	His	Leu	Ser	Asn	Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln	
			20					25					30			
Phe	Gly	Ile	Ser	His	Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	
		35					40					45				
Phe	Arg	Met	Ala	Tyr	His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys	
	50					55					60					
Arg	Ala	Arg	Ala	Leu	Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu	
65					70					75					80	
Leu	Phe	His	Asn	Phe	Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala	
				85					90					95		
Pro	Phe	Gln	Arg	Leu	Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His	
			100					105					110			
Glu	Arg	Leu	Thr	Ala	Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val			
		115					120					125				

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<220>
<221> CDS
<222> (101)..(460)
<223> FRXA02263
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<400> 149
cctgggcaac ccaagtgtat gaaaacgccc tggaaaaagg cgctcggcacc acattgaacc 60

tgtgggaatc acccgactg gcttgagaga agaaacaaca atg aaa att gcg gta 115
Met Lys Ile Ala Val
1 5

atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac 163
Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn
10 15 20

atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat 211
Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His
25 30 35

ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac 259
Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr
40 45 50

```

```

cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta 307
His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu
    55                      60                      65

tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc 355
Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe
    70                      75                      80                      85

ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg 403
Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu
                      90                      95                      100

gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc 451
Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
                      105                      110                      115

gcg cag atg 460
Ala Gln Met
    120

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<210> 150

<211> 120

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 150

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Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
    1                      5                      10                      15

Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
    20                      25                      30

Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu
    35                      40                      45

Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
    50                      55                      60

Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
    65                      70                      75                      80

Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
    85                      90                      95

Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
    100                      105                      110

Glu Arg Leu Thr Ala Ala Gln Met
    115                      120

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<210> 151

<211> 1251

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1228)

<223> RXA02176

<400> 151

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gggtgctagg aactgacagc ttcagggtta tagttgttgg gtcagatcgt taacgatccc 60
tggccctttt acttccaagc gcagaaagtt gcccgaagac atg acc gac ttc ccc 115
                                         Met Thr Asp Phe Pro
                                         1           5
acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163
Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly
                        10                        15                        20
cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211
Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala Ile Val Asp Gly Ser
                        25                        30                        35
gca tcc gtc atc ggt acc tca cac cgt cag ccg gca gta aaa aac gtc 259
Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro Ala Val Lys Asn Val
                        40                        45                        50
gtg ggt tca atc cgc gag gga ctc tcc gac ctc ttc tcc ctt cca gaa 307
Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu Phe Ser Leu Pro Glu
                        55                        60                        65
ggc tac gag atc atc ctt tcc cta ggt ggt gcg acc gca ttc tgg gat 355
Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala Thr Ala Phe Trp Asp
                        70                        75                        80                        85
gca gca acc ttc gga ctc att gaa aag aag tcc ggt cac ctt tct ttc 403
Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser Gly His Leu Ser Phe
                        90                        95                        100
ggg gag ttc tcc tcc aag ttc gca aag gct tct aag ctt gct cct tgg 451
Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser Lys Leu Ala Pro Trp
                        105                        110                        115
ctc gac gag cca gag atc gtc acc gca gaa acc ggt gac tct ccg gcc 499
Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr Gly Asp Ser Pro Ala
                        120                        125                        130
cca cag gca ttc gaa ggc gcc gat gtt att gca tgg gca cac aac gaa 547
Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala Trp Ala His Asn Glu
                        135                        140                        145
acc tcc act ggc gcc atg gtt cca gtt ctt cgc ccc gaa ggc tct gaa 595
Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg Pro Glu Gly Ser Glu
                        150                        155                        160                        165
ggc tcc ctg gtt gcc att gac gca acc tcc ggc gct ggt gga ctg cca 643
Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly Ala Gly Gly Leu Pro
                        170                        175                        180
gta gac atc aag aac tcc gat gtt tac tac ttc tcc cca cag aag tgc 691
Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe Ser Pro Gln Lys Cys
                        185                        190                        195
ttc gca tcc gac ggt ggc ctg tgg ctt gca gcg atg agc cca gca gct 739
Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala Met Ser Pro Ala Ala
                        200                        205                        210
ctc gag cgc atc gag aag atc aac gct tcc gat cgc ttc atc cct gag 787

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<210> 152
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 152

Met Thr Asp Phe Pro Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly
1 5 10 15

Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
20 25 30

Ile Val Asp Gly Ser Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro
35 40 45

Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu
50 55 60

Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
 65 70 75 80
 Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
 85 90 95
 Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
 100 105 110
 Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr
 115 120 125
 Gly Asp Ser Pro Ala Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala
 130 135 140
 Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg
 145 150 155 160
 Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly
 165 170 175
 Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe
 180 185 190
 Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
 195 200 205
 Met Ser Pro Ala Ala Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp
 210 215 220
 Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser
 225 230 235 240
 Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met
 245 250 255
 Leu Asp Asn Gln Val Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly
 260 265 270
 Met Val Ala Arg Thr Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala
 275 280 285
 Glu Ala Arg Glu Glu Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg
 290 295 300
 Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala
 305 310 315 320
 Val Ile Ala Lys Ile Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro
 325 330 335
 Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
 340 345 350
 Ile Asp Ser Thr Asp Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile
 355 360 365
 Leu Asp Gly Gly Phe Ala Arg Lys
 370 375

<400> 153
atacatctca cccaattccc cataactaga caattgccca gcaacgactg ataagtctcc 60

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
10 15 20

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
40 45 50

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
70 75 80 85

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
105 110 115

ggt ggt gtt gtt ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc 499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
120 125 130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt 547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
135 140 145

ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
150 155 160 165

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ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct    643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
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gct Ala	ctt Leu	acc Thr	tct Ser	gag Glu	ctg Leu	aat Asn	gtg Val	gat Asp	att Ile	gcg Ala	att Ile	gag Glu	cgt Arg	tct Ser	ggc Gly	691
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cac His	atc Ile	atg Met	ggc Gly	att Ile	tcc Ser	cgc Arg	gac Asp	gag Glu	atc Ile	gat Asp	ctg Leu	gcg Ala	gat Asp	cag Gln	gaa Glu	1363
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<210> 154

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

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Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
 130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
 145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
 165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
 180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
 195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
 210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
 225 230 235 240

Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
 245 250 255

Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala
 260 265 270

Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg
 275 280 285

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
 290 295 300

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
 305 310 315 320

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
 325 330 335

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
 340 345 350

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
 355 360 365

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
 370 375 380

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
 385 390 395 400

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
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Ala

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<220>
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 Val Thr Glu Leu Ile
 1 5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
 Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
 10 15 20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
 Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
 25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
 40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
 Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
 55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
 70 75 80 85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
 Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
 90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
 Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
 105 110 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat 490
 Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
 120 125 130

<210> 156

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
 20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp
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<210> 157

<211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(535)
 <223> FRXA02758

<400> 157
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 Met Gly Tyr Gln Thr
 1 5
 gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag 163
 Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
 10 15 20
 gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 211
 Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
 25 30 35
 ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 259
 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
 40 45 50
 aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 307
 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
 55 60 65
 tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 355
 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
 70 75 80 85
 tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 403
 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
 90 95 100
 gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 451
 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
 105 110 115
 cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 499
 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
 120 125 130
 gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 545
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
 135 140 145
 tttctcgacg ccc 558

<210> 158
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158

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 20 25 30
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 35 40 45
 Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
 50 55 60
 Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
 65 70 75 80
 Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
 85 90 95
 Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
 100 105 110
 Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
 115 120 125
 Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
 130 135 140

Ala
 145

<210> 159
 <211> 205
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (72)..(182)
 <223> FRXA02759

<400> 159
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 aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
 Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
 1 5 10
 att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
 Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
 15 20 25
 gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
 Val Thr Glu Arg Ala Met Arg Gly
 30 35

<210> 160
 <211> 37
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 160

Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val Ile Glu Met
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Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu
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Arg Ala Met Arg Gly
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<210> 161

<211> 1188

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1165)

<223> RXA02501

<400> 161

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 Met Ser Ser Glu Gly
 1 5
 aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163
 Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe
 10 15 20
 ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211
 Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu
 25 30 35
 gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259
 Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly
 40 45 50
 gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307
 Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile Tyr Gly Met Glu Leu
 55 60 65
 aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355
 Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser
 70 75 80 85
 gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403
 Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp
 90 95 100
 gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451
 Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly
 105 110 115
 tcc tcc ctc atc gtt ttc gcc caa gga ctc ttc cgg aag aaa ttc ttc 499
 Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe Arg Lys Lys Phe Phe
 120 125 130

acc atc aaa gaa atc ctc ccc gtg gtg tgg aaa caa gtg aaa ttc aaa 547
 Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys Gln Val Lys Phe Lys
 135 140 145

ctc acc ggc tcc gaa aac gcc gac gac gtc tcc cgc ggc cgc gaa caa 595
 Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser Arg Gly Arg Glu Gln
 150 155 160 165

gcc ctc gaa ttc atc aaa ggc cgc ccc gtc caa gaa cta gtt gac ctc 643
 Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln Glu Leu Val Asp Leu
 170 175 180

tgc gaa gaa atc gtc gac caa cgc atg gcc gac aaa atg tgg ccc ggc 691
 Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp Lys Met Trp Pro Gly
 185 190 195

acc aaa caa ctc gcc gac atg cac atc gcc gcc ggc cac caa gtc tgg 739
 Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala Gly His Gln Val Trp
 200 205 210

ctc gtc tcc gca acc ccc gtc caa ctc gcc caa atc ctg gca caa cgc 787
 Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln Ile Leu Ala Gln Arg
 215 220 225

ctc ggc ttc acc gga gcg atc ggc aca gtc gca gaa gca aaa gat gga 835
 Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala Glu Ala Lys Asp Gly
 230 235 240 245

gta ttc acc ggc cga ctc gtc ggc gac atc ctc cac gga ccc ggc aaa 883
 Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu His Gly Pro Gly Lys
 250 255 260

aga cac gca gtc gca gca ctc gca tcc atc gaa caa ctc gac ctc acc 931
 Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu Gln Leu Asp Leu Thr
 265 270 275

cga tgc acc gcc tac tcc gac tcc atc aac gac ctc ccc atg ctc tcc 979
 Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp Leu Pro Met Leu Ser
 280 285 290

atg gtc ggc acc gcc gtc gca gta aac ccc gac tcc aaa ctc cgc aaa 1027
 Met Val Gly Thr Ala Val Ala Val Asn Pro Asp Ser Lys Leu Arg Lys
 295 300 305

gaa gcc gaa acc cga ggc tgg gac gtc cgc gat ttc cga agc atc cgc 1075
 Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp Phe Arg Ser Ile Arg
 310 315 320 325

aaa gcc acc cgc gaa tac gga atc ccc gcc ctg gtc acc gcc gca ttc 1123
 Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu Val Thr Ala Ala Phe
 330 335 340

agt gtc gcc ggc tgg agt cta cgc cgc cga tgg aga aaa caa 1165
 Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp Arg Lys Gln
 345 350 355

taacgcacag gagccgtttt aag 1188

<210> 162

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

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Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala
          35          40          45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile
          50          55          60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala
 65          70          75          80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro
          85          90          95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn
          100          105          110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe
          115          120          125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys
          130          135          140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser
          145          150          155          160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln
          165          170          175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp
          180          185          190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala
          195          200          205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln
          210          215          220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala
          225          230          235          240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu
          245          250          255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu
          260          265          270

Gln Leu Asp Leu Thr Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp
          275          280          285

Leu Pro Met Leu Ser Met Val Gly Thr Ala Val Ala Val Asn Pro Asp
          290          295          300

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Ser Lys Leu Arg Lys Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp
 305 310 315 320

Phe Arg Ser Ile Arg Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu
 325 330 335

Val Thr Ala Ala Phe Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp
 340 345 350

Arg Lys Gln
 355

<210> 163
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> RXN03105

<400> 163
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 Leu Ile Leu Pro Val
 1 5

cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163
 Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile
 10 15 20

ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211
 Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu
 25 30 35

gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259
 Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe
 40 45 50

ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307
 Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr
 55 60 65

tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355
 Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile
 70 75 80 85

gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403
 Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr
 90 95 100

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451
 Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr
 105 110 115

agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499
 Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys
 120 125 130

acg tat aga aag cta acc ttt tta agt gcg cgg ttt tagggtgaga 545
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe
 135 140 145

atctaacgct gag 558

<210> 164

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu
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His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp
 20 25 30

Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys
 35 40 45

Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser
 50 55 60

Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala
 65 70 75 80

Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys
 85 90 95

Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn
 100 105 110

Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro
 115 120 125

Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg
 130 135 140

Phe
 145

<210> 165

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (62)..(664)

<223> RXS01130

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gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
 Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1 5 10 15

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gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20                      25                      30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35                      40                      45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
      50                      55                      60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
      65                      70                      75                      80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85                      90                      95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100                      105                      110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115                      120                      125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130                      135                      140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145                      150                      155                      160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165                      170                      175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180                      185                      190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
      195                      200

tga 687

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<210> 166

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1                      5                      10                      15

```



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gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
      40                      45                      50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
      55                      60                      65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
      70                      75                      80                      85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
      90                      95                      100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
      105                      110                      115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
      120                      125                      130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
      135                      140                      145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
      150                      155                      160                      165

gcg ctg gct
Ala Leu Ala
804

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<210> 168

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

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Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1                      5                      10                      15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
      20                      25                      30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
      35                      40                      45

Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
      50                      55                      60

Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
      65                      70                      75                      80

Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
      85                      90                      95

```

Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110

His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125

Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140

Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160

Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 169

<211> 1458

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1435)

<223> RXN00969

<400> 169

ctatagtggc taggtaccct ttttgttttg gacacatgta ggggtggccga aacaaagtaa 60

taggacaaca acgctcgacc gcgattatct ttggagaatc atg acc tca gca tct 115
 Met Thr Ser Ala Ser
 1 5

gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
 10 15 20

gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
 25 30 35

acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
 40 45 50

gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
 55 60 65

gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
 70 75 80 85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403
 Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg
 90 95 100

gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451
 Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala
 105 110 115

aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat gca gcg	499
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala	
120 125 130	
gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca	547
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala	
135 140 145	
att cca gtg gtt ggc cca ctg cgt cgc tcc ctg gct ggc gat cag atc	595
Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile	
150 155 160 165	
cag tct gtg atg ggc atc gtt aac ggc acc acc aac ttc atc ttg gac	643
Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp	
170 175 180	
gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca	691
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala	
185 190 195	
act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc	739
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly	
200 205 210	
cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac	787
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His	
215 220 225	
acc cgt gtt acc gcg gat gat gtg tac tgc gaa ggt att agg aac atc	835
Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile	
230 235 240 245	
aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag	883
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys	
250 255 260	
ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct	931
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala	
265 270 275	
att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg	979
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu	
280 285 290	
gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca	1027
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala	
295 300 305	
gct ggt cgc ctg atg ttc tac gga aac ggt gca ggt ggc gcg cca acc	1075
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr	
310 315 320 325	
gcg tct gct gtg ctt ggc gac gtc gtt ggt gcc gca cga aac aag gtg	1123
Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala Ala Arg Asn Lys Val	
330 335 340	
cac ggt ggc cgt gct cca ggt gag tcc acc tac gct aac ctg ccg atc	1171
His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr Ala Asn Leu Pro Ile	
345 350 355	

gct gat ttc ggt gag acc acc act cgt tac cac ctc gac atg gat gtg 1219
Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His Leu Asp Met Asp Val
360 365 370

gaa gat cgc gtg ggg gtt ttg gct gaa ttg gct agc ctg ttc tct gag 1267
Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala Ser Leu Phe Ser Glu
375 380 385

caa gga atc tcc ctg cgt aca atc cga cag gaa gag cgc gat gat gat 1315
Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu Glu Arg Asp Asp Asp
390 395 400 405

gca cgt ctg atc gtg gtc acc cac tct gcg ctg gaa tct gat ctt tcc 1363
Ala Arg Leu Ile Val Val Thr His Ser Ala Leu Glu Ser Asp Leu Ser
410 415 420

cgc acc gtt gaa ctg ctg aag gct aag cct gtt gtt aag gca atc aac 1411
Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val Val Lys Ala Ile Asn
425 430 435

agt gtg atc cgc ctc gaa agg gac taattttact gacatggcaa ttg 1458
Ser Val Ile Arg Leu Glu Arg Asp
440 445

<210> 170

<211> 445

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 170

Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly
1 5 10 15

Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu
20 25 30

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
35 40 45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
130 135 140

Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu
145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr
165 170 175

Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp
180 185 190

Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
195 200 205

Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
210 215 220

Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu
225 230 235 240

Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala
245 250 255

Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys
260 265 270

Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro
275 280 285

Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe
290 295 300

Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
305 310 315 320

Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala
325 330 335

Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr
340 345 350

Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His
355 360 365

Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala
370 375 380

Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu
385 390 395 400

Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu
405 410 415

Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val
420 425 430

Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp
435 440 445

<210> 171

<211> 493

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(493)

<223> FRXA00974

<400> 171

ctatagtggc taggtaccct ttttgttttg gacacatgta ggggtggccga aacaaagtaa 60

taggacaaca	acgctcgacc	gcgattat	tttgagaatc	atg	acc	tca	gca	tct	115
				Met	Thr	Ser	Ala	Ser	
				1				5	

gcc	cca	agc	ttt	aac	ccc	ggc	aag	ggt	ccc	ggc	tca	gca	gtc	gga	att	163
Ala	Pro	Ser	Phe	Asn	Pro	Gly	Lys	Gly	Pro	Gly	Ser	Ala	Val	Gly	Ile	
			10					15						20		

gcc	ctt	tta	gga	ttc	gga	aca	gtc	ggc	act	gag	gtg	atg	cgt	ctg	atg	211
Ala	Leu	Leu	Gly	Phe	Gly	Thr	Val	Gly	Thr	Glu	Val	Met	Arg	Leu	Met	
			25					30					35			

acc	gag	tac	ggt	gat	gaa	ctt	gcg	cac	cg	att	ggt	ggc	cca	ctg	gag	259
Thr	Glu	Tyr	Gly	Asp	Glu	Leu	Ala	His	Arg	Ile	Gly	Gly	Pro	Leu	Glu	
		40					45					50				

gtt	cgt	ggc	att	gct	gtt	tct	gat	atc	tca	aag	cca	cgt	gaa	ggc	gtt	307
Val	Arg	Gly	Ile	Ala	Val	Ser	Asp	Ile	Ser	Lys	Pro	Arg	Glu	Gly	Val	
	55					60					65					

gca	cct	gag	ctg	ctc	act	gag	gac	gct	ttt	gca	ctc	atc	gag	cgc	gag	355
Ala	Pro	Glu	Leu	Leu	Thr	Glu	Asp	Ala	Phe	Ala	Leu	Ile	Glu	Arg	Glu	
	70				75					80					85	

gat	gtt	gac	atc	gtc	gtt	gag	gtt	atc	ggc	ggc	att	gag	tac	cca	cgt	403
Asp	Val	Asp	Ile	Val	Val	Glu	Val	Ile	Gly	Gly	Ile	Glu	Tyr	Pro	Arg	
			90						95					100		

gag	gta	gtt	ctc	gca	gct	ctg	aag	gcc	ggc	aag	tct	gtt	gtt	acc	gcc	451
Glu	Val	Val	Leu	Ala	Ala	Leu	Lys	Ala	Gly	Lys	Ser	Val	Val	Thr	Ala	
			105					110					115			

aat	aag	gct	ctt	gtt	gca	gct	cac	tct	gct	gag	ctt	gct	gat			493
Asn	Lys	Ala	Leu	Val	Ala	Ala	His	Ser	Ala	Glu	Leu	Ala	Asp			
		120					125					130				

<210> 172

<211> 131

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Met	Thr	Ser	Ala	Ser	Ala	Pro	Ser	Phe	Asn	Pro	Gly	Lys	Gly	Pro	Gly	
1				5					10					15		

Ser	Ala	Val	Gly	Ile	Ala	Leu	Leu	Gly	Phe	Gly	Thr	Val	Gly	Thr	Glu	
			20					25					30			

Val	Met	Arg	Leu	Met	Thr	Glu	Tyr	Gly	Asp	Glu	Leu	Ala	His	Arg	Ile	
		35					40					45				

Gly	Gly	Pro	Leu	Glu	Val	Arg	Gly	Ile	Ala	Val	Ser	Asp	Ile	Ser	Lys	
	50					55					60					

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
 65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
 85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
 100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
 115 120 125

Leu Ala Asp
 130

<210> 173

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA00970

<400> 173

gaatctgatac tttccgcac cgttgaactg ctgaaggcta agcctgttgt taaggcaatc 60

aacagtgtga tccgcctega aagggaactaa ttttactgac atg gca att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

aac gtc ggt cgt aag gtt acc gtc acg gta cct gga tct tct gca aac 163
 Asn Val Gly Arg Lys Val Thr Val Thr Val Pro Gly Ser Ser Ala Asn
 10 15 20

ctc gga cct ggc ttt gac act tta ggt ttg gca ctg tcg gta tac gac 211
 Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala Leu Ser Val Tyr Asp
 25 30 35

act gtc gaa gtg gaa att att cca tct ggc ttg gaa gtg gaa gtt ttt 259
 Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu Glu Val Glu Val Phe
 40 45 50

ggc gaa ggc caa ggc gaa gtc cct ctt gat ggc tcc cac ctg gtg gtt 307
 Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly Ser His Leu Val Val
 55 60 65

aaa gct att cgt gct ggc ctg aag gca gct gac gct gaa gtt cct gga 355
 Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp Ala Glu Val Pro Gly
 70 75 80 85

ttg cga gtg gtg tgc cac aac aac att ccg cag tct cgt ggt ctt ggc 403
 Leu Arg Val Val Cys His Asn Asn Ile Pro Gln Ser Arg Gly Leu Gly
 90 95 100

tcc tct gct gca gcg gcg gtt gct ggt gtt gct gca gct aat ggt ttg 451
 Ser Ser Ala Ala Ala Val Ala Gly Val Ala Ala Ala Asn Gly Leu
 105 110 115

gcg gat ttc ccg ctg act caa gag cag att gtt cag ttg tcc tct gcc 499
Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val Gln Leu Ser Ser Ala
120 125 130

ttt gaa ggc cac cca gat aat gct gcg gct tct gtg ctg ggt gga gca 547
Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser Val Leu Gly Gly Ala
135 140 145

gtg gtg tcg tgg aca aat ctg tct atc gac ggc aag agc cag cca cag 595
Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly Lys Ser Gln Pro Gln
150 155 160 165

tat gct gct gta cca ctt gag gtg cag gac aat att cgt gcg act gcg 643
Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn Ile Arg Ala Thr Ala
170 175 180

ctg gtt cct aat ttc cac gca tcc acc gaa gct gtg cgc cga gtc ctt 691
Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala Val Arg Arg Val Leu
185 190 195

ccc act gaa gtc act cac atc gat gcg cga ttt aac gtg tcc cgc gtt 739
Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe Asn Val Ser Arg Val
200 205 210

gca gtg atg atc gtt gcg ttg cag cag cgt cct gat ttg ctg tgg gag 787
Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro Asp Leu Leu Trp Glu
215 220 225

ggt act cgt gac cgt ctg cac cag cct tat cgt gca gaa gtg ttg cct 835
Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg Ala Glu Val Leu Pro
230 235 240 245

att acc tct gag tgg gta aac cgc ctg cgc aac cgt ggc tac gcg gca 883
Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn Arg Gly Tyr Ala Ala
250 255 260

tac ctt tcc ggt gcc ggc cca acc gcc atg gtg ctg tcc act gag cca 931
Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val Leu Ser Thr Glu Pro
265 270 275

att cca gac aag gtt ttg gaa gat gct cgt gag tct ggc att aag gtg 979
Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu Ser Gly Ile Lys Val
280 285 290

ctt gag ctt gag gtt gcg gga cca gtc aag gtt gaa gtt aac caa cct 1027
Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val Glu Val Asn Gln Pro
295 300 305

taggcccaac aaggaaggcc ccc 1050

<210> 174

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Ala Ile Glu Leu Asn Val Gly Arg Lys Val Thr Val Thr Val Pro
1 5 10 15

Gly Ser Ser Ala Asn Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala
 20 25 30
 Leu Ser Val Tyr Asp Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu
 35 40 45
 Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly
 50 55 60
 Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp
 65 70 75 80
 Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln
 85 90 95
 Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Ala
 100 105 110
 Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val
 115 120 125
 Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
 130 135 140
 Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly
 145 150 155 160
 Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn
 165 170 175
 Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala
 180 185 190
 Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe
 195 200 205
 Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro
 210 215 220
 Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg
 225 230 235 240
 Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn
 245 250 255
 Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val
 260 265 270
 Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu
 275 280 285
 Ser Gly Ile Lys Val Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val
 290 295 300
 Glu Val Asn Gln Pro
 305

<210> 175

<211> 1566

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1543)

<223> RXA00330

<400> 175

gcaacacttt aggggtatcgc gtgggcgaag tcaccttttt caacatattt gagacgggtgt 60

gggggagtat tgtgtcaccc cttgggatag gggtatatcc gtg gac tac att tcg 115
 Val Asp Tyr Ile Ser
 1 5

acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg 163
 Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu
 10 15 20

ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct 211
 Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro
 25 30 35

caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac 259
 Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn
 40 45 50

gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat 307
 Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp
 55 60 65

gac atc cca gta gaa gac atc aag gcg atc acc gca cgc gcc tac acc 355
 Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr
 70 75 80 85

tac ccg aag ttc aac agc gaa gac atc gtt cct gtc acc gaa ctc gag 403
 Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro Val Thr Glu Leu Glu
 90 95 100

gac aac att tac ctg ggc cac ctt tcc gaa ggc cca acc gct gca ttc 451
 Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe
 105 110 115

aaa gac atg gcc atg cag ctg ctc ggc gaa ctt ttc gaa tac gag ctt 499
 Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu
 120 125 130

cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat 547
 Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly Ala Thr Ser Gly Asp
 135 140 145

acc ggc tcc tct gcg gaa tac gcc atg cgc ggc cgc gag gga atc cgc 595
 Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg
 150 155 160 165

gta ttc atg ctg acc cca gct ggc cgc atg acc cca ttc cag caa gca 643
 Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr Pro Phe Gln Gln Ala
 170 175 180

cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac 691
 Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp
 185 190 195

gagacgggtgt 60
 gggtatatcc 115
 1 5
 163
 10 15 20
 211
 25 30 35
 259
 40 45 50
 307
 55 60 65
 355
 70 75 80 85
 403
 90 95 100
 451
 105 110 115
 499
 120 125 130
 547
 135 140 145
 595
 150 155 160 165
 643
 170 175 180
 691
 185 190 195

ggc gtt ttc gac gat tgc caa gac gta gtc aag gct gtc tcc gcc gac 739
 Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp
 200 205 210

gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac 787
 Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn
 215 220 225

tgg gca cgc ctt atg gca cag gtt gtg tac tac gtt tcc tca tgg atc 835
 Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile
 230 235 240 245

cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc 883
 Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr
 250 255 260

ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga 931
 Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly
 265 270 275

ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc 979
 Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu
 280 285 290

gac gag ttc ttc cgt acc ggc gac tac cga gtc cgc agc tcc gca gac 1027
 Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val Arg Ser Ser Ala Asp
 295 300 305

acc cac gag acc tcc tca cct tcg atg gat atc tcc cgc gcc tcc aac 1075
 Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile Ser Arg Ala Ser Asn
 310 315 320 325

ttc gag cgt ttc atc ttc gac ctg ctc ggc cgc gac gcc acc cgc gtc 1123
 Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val
 330 335 340

aac gat cta ttt ggt acc cag gtt cgc caa ggc gga ttc tca ctg gct 1171
 Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala
 345 350 355

gat gac gcc aac ttt gag aag gct gca gca gaa tac ggt ttc gcc tcc 1219
 Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser
 360 365 370

gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat 1267
 Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His
 375 380 385

tcc cgc ctc gac gta cta atc gat ccc cac acc gcc gac ggc gtt cac 1315
 Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His
 390 395 400 405

gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta 1363
 Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu
 410 415 420

gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att 1411
 Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile
 425 430 435

ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct 1459
 Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala
 440 445 450
 cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag 1507
 Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln
 455 460 465
 tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt 1553
 Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val Lys
 470 475 480
 tacgccaaagg cct 1566

<210> 176

<211> 481

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 176

Val Asp Tyr Ile Ser Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe
 1 5 10 15
 Ser Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu
 20 25 30
 Pro Ala Thr Tyr Pro Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg
 35 40 45
 Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile
 50 55 60
 Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr
 65 70 75 80
 Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro
 85 90 95
 Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly
 100 105 110
 Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
 115 120 125
 Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly
 130 135 140
 Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
 145 150 155 160
 Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
 165 170 175
 Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe
 180 185 190
 Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
 195 200 205
 Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala

210	215	220
Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr		
225	230	235 240
Val Ser Ser Trp Ile Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser		
	245	250 255
Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile		
	260	265 270
Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn		
	275	280 285
Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val		
	290	295 300
Arg Ser Ser Ala Asp Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile		
	310	315 320
Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg		
	325	330 335
Asp Ala Thr Arg Val Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly		
	340	345 350
Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu		
	355	360 365
Tyr Gly Phe Ala Ser Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr		
	370	375 380
Ile Ala Asp Val His Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr		
	385	390 395 400
Ala Asp Gly Val His Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr		
	405	410 415
Pro Ile Ile Val Leu Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr		
	420	425 430
Ile Val Glu Ala Ile Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala		
	435	440 445
Ala Ile Met Asp Ala Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr		
	450	455 460
Asp Ala Val Lys Gln Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val		
	465	470 475 480

Lys

<210> 177

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 177

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aagtttttagt cttgtccacc cagaacaggc gggtatttttc atg ccc acc ctc gcg 115
 Met Pro Thr Leu Ala
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
 40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
 55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
 90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
 105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
 120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
 135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
 150 155 160 165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
 170 175 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
 185 190 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
 215 220 225

 ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

 aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260

 gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

 aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

 acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

 ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

 gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

 ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

 gag ttc tac atc taataggtat ttacgacaaa tag 1254
 Glu Phe Tyr Ile
 375

<210> 178

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile

370

375

<210> 179

<211> 1210

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA00403

<400> 179

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aagtttttagt	cttgtccacc	cagaacaggc	ggttattttc	atg	ccc	acc	ctc	gcg	115
				Met	Pro	Thr	Leu	Ala	
				1				5	

cct	tca	ggt	caa	ctt	gaa	atc	caa	gcg	atc	ggt	gat	gtc	tcc	acc	gaa	163
Pro	Ser	Gly	Gln	Leu	Glu	Ile	Gln	Ala	Ile	Gly	Asp	Val	Ser	Thr	Glu	
			10						15					20		

gcc	gga	gca	atc	att	aca	aac	gct	gaa	atc	gcc	tat	cac	cgc	tgg	ggt	211
Ala	Gly	Ala	Ile	Ile	Thr	Asn	Ala	Glu	Ile	Ala	Tyr	His	Arg	Trp	Gly	
			25					30					35			

gaa	tac	cgc	gta	gat	aaa	gaa	gga	cgc	agc	aat	gtc	gtt	ctc	atc	gaa	259
Glu	Tyr	Arg	Val	Asp	Lys	Glu	Gly	Arg	Ser	Asn	Val	Val	Leu	Ile	Glu	
		40					45					50				

cac	gcc	ctc	act	gga	gat	tcc	aac	gca	gcc	gat	tgg	tgg	gct	gac	ttg	307
His	Ala	Leu	Thr	Gly	Asp	Ser	Asn	Ala	Ala	Asp	Trp	Trp	Ala	Asp	Leu	
		55				60					65					

ctc	ggt	ccc	ggc	aaa	gcc	atc	aac	act	gat	att	tac	tgc	gtg	atc	tgt	355
Leu	Gly	Pro	Gly	Lys	Ala	Ile	Asn	Thr	Asp	Ile	Tyr	Cys	Val	Ile	Cys	
70					75					80					85	

acc	aac	gtc	atc	ggt	ggt	tgc	aac	ggt	tcc	acc	gga	cct	ggc	tcc	atg	403
Thr	Asn	Val	Ile	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Gly	Ser	Met	
			90					95					100			

cat	cca	gat	gga	aat	ttc	tgg	ggt	aat	cgc	ttc	ccc	gcc	acg	tcc	att	451
His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe	Pro	Ala	Thr	Ser	Ile	
			105					110					115			

cgt	gat	cag	gta	aac	gcc	gaa	aaa	caa	ttc	ctc	gac	gca	ctc	ggc	atc	499
Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu	Asp	Ala	Leu	Gly	Ile	
		120					125					130				

acc	acg	gtc	gcc	gca	gta	ctt	ggt	ggt	tcc	atg	ggt	ggt	gcc	cgc	acc	547
Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met	Gly	Gly	Ala	Arg	Thr	
		135				140					145					

cta	gag	tgg	gcc	gca	atg	tac	cca	gaa	act	gtt	ggc	gca	gct	gct	gtt	595
Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val	Gly	Ala	Ala	Ala	Val	
150					155					160					165	

ctt	gca	gtt	tct	gca	cgc	gcc	agc	gcc	tgg	caa	atc	ggc	att	caa	tcc	643
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Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                170                175                180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                185                190                195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
                200                205                210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
                215                220                225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
230                235                240                245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
                250                255                260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
                265                270                275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
                280                285                290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
295                300                305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
310                315                320                325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
330                335                340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
345                350                355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg 1210
Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
360                365                370

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<210> 180

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

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Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp

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340          345          350
Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
      355          360          365

Pro Ser
  370

<210> 181
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXC01207

<400> 181
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atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
              Val Ser Arg Ile Tyr
              1              5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
              10              15              20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
              25              30              35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
              40              45              50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
              55              60              65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
              70              75              80              85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
              90              95              100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
              105              110              115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
              120              125              130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
              135              140              145

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act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
 150 155 160 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
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agc ctg cgc taaatgggag tcggtttcgc ggg 771
 Ser Leu Arg
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 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 182
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 Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
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 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160
 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
 195 200 205

Gly Val Ser Ala Glu Ser Leu Arg
 210 215

<210> 183
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> RXC00152

<400> 183
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caaatagtagtac tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
 Met Thr Gly Leu Ile
 1 5

ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
 Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
 10 15 20

ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
 Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
 25 30 35

agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
 Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
 40 45 50

gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
 Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
 55 60 65

ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
 Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
 70 75 80 85

gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
 Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro Glu Arg Ala Ile Tyr
 90 95 100

ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
 Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr
 105 110 115

ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
 Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser
 120 125 130

cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
 Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr

135	140	145	
acc aaa tgg ggc ctg cgc atc agc cgt gtg gaa cta aag gca att gat			595
Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp			
150	155	160	165
ccg cca cca tcc atc cag caa tcg atg gaa aag cag atg aag gca gac			643
Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp			
	170	175	180
cgt gaa aag cgc gcc acc att ttg acc gca gaa ggt cag cgc gaa gcc			691
Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu Gly Gln Arg Glu Ala			
	185	190	195
gac atc aaa act gcc gaa ggt gaa aag caa gcc aag atc ctc caa gct			739
Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala Lys Ile Leu Gln Ala			
	200	205	210
gag ggt gaa aag cac gca tcc atc ctg aac gca gaa gca gaa cgc caa			787
Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala Glu Ala Glu Arg Gln			
	215	220	225
gcg atg atc ctg cgc gcc gaa ggt gaa cgc gca gca cgc tac ctc cag			835
Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala Ala Arg Tyr Leu Gln			
	230	235	240
gcg cag ggt gaa gcc cga gca atc caa aag gtc aac gca gca atc aag			883
Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val Asn Ala Ala Ile Lys			
	250	255	260
tct gcc aag ttg acc cca gag gtt ctt gct tat caa tac ctc gaa aag			931
Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr Gln Tyr Leu Glu Lys			
	265	270	275
ctt cct aag atc gca gag ggc aac gcc tcc aag atg tgg gtc atc cca			979
Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys Met Trp Val Ile Pro			
	280	285	290
agc cag ttc tcc gat tct ctg gaa ggt ttt gcg aag cag ttc ggc gca			1027
Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala Lys Gln Phe Gly Ala			
	295	300	305
aag gat gca gaa ggt gtc ttc cgc tac gaa cca aac acc gtg gat gaa			1075
Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro Asn Thr Val Asp Glu			
	310	315	320
gaa acc cgc gac atc gca aac gcc gac aac gtg gaa gac tgg ttc tcc			1123
Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val Glu Asp Trp Phe Ser			
	330	335	340
acc gaa tca gac cct gaa atc gca gca gca gtc gcc gca gca aac gcc			1171
Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val Ala Ala Ala Asn Ala			
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gtg gcc aac aag cca gtc gat cca gaa ccc ggt gag atc ctt tcc aag			1219
Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly Glu Ile Leu Ser Lys			
	360	365	370
aag acc gca cga cgc gtt gaa cct gaa gca gta ttg gag gct ttg caa			1267
Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val Leu Glu Ala Leu Gln			
	375	380	385

aac gga acc act aca caa cct gag gtt gag gca gca cct cct acc gca 1315
 Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala
 390 395 400 405

aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac 1363
 Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala Asn Pro Glu Asp Tyr
 410 415 420

tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg 1416
 Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 425 430

cgg 1419

<210> 184

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

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Val Val Ile Lys Ser Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val
 20 25 30

Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr
 35 40 45

Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg
 50 55 60

Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn
 65 70 75 80

Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro
 85 90 95

Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln
 100 105 110

Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu
 115 120 125

Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu
 130 135 140

Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu
 145 150 155 160

Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys
 165 170 175

Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu
 180 185 190

Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala
 195 200 205

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Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala
 210                               215                      220

Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala
225                               230                      235                      240

Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val
                               245                      250                      255

Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr
                               260                      265                      270

Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys
 275                               280                      285

Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala
 290                               295                      300

Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro
305                               310                      315                      320

Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val
                               325                      330                      335

Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val
 340                               345                      350

Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly
 355                               360                      365

Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val
 370                               375                      380

Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala
385                               390                      395                      400

Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala
                               405                      410                      415

Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 420                               425                      430

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<210> 185

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA00115

<400> 185

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cgtatattgt gacctacacc ccatactgtt aggagttttc atg ctc gac aat agt 115
 Met Leu Asp Asn Ser

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ttt	tac	acc	gca	gag	gtt	cag	ggc	cca	tac	gaa	acc	gct	tcc	att	ggc	163															
Phe	Tyr	Thr	Ala	Glu	Val	Gln	Gly	Pro	Tyr	Glu	Thr	Ala	Ser	Ile	Gly																
				10					15					20																	
cgg	ctc	gaa	ctc	gaa	gaa	ggg	ggg	gtg	att	gag	gat	tgc	tgg	ttg	gct	211															
Arg	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Glu	Asp	Cys	Trp	Leu	Ala																
				25					30					35																	
tac	gct	aca	gct	gga	acg	ctc	aac	gag	gac	aag	tcc	aac	gcc	atc	ctc	259															
Tyr	Ala	Thr	Ala	Gly	Thr	Leu	Asn	Glu	Asp	Lys	Ser	Asn	Ala	Ile	Leu																
				40					45					50																	
att	ccg	acg	tgg	tac	tcc	gga	acc	cat	cag	acc	tgg	ttc	cag	cag	tac	307															
Ile	Pro	Thr	Trp	Tyr	Ser	Gly	Thr	His	Gln	Thr	Trp	Phe	Gln	Gln	Tyr																
				55					60					65																	
atc	ggc	act	gat	cat	gcg	ctg	gat	cca	tca	aag	tat	ttc	atc	atc	tcc	355															
Ile	Gly	Thr	Asp	His	Ala	Leu	Asp	Pro	Ser	Lys	Tyr	Phe	Ile	Ile	Ser																
				70					75					80																	
atc	aac	caa	atc	ggg	aat	ggg	ttg	tcg	gtc	tcc	cct	gcc	aac	acg	gct	403															
Ile	Asn	Gln	Ile	Gly	Asn	Gly	Leu	Ser	Val	Ser	Pro	Ala	Asn	Thr	Ala																
				90					95					100																	
gat	gac	agc	atc	tcg	atg	tcc	aag	ttc	ccg	aat	gtt	cgc	att	ggg	gat	451															
Asp	Asp	Ser	Ile	Ser	Met	Ser	Lys	Phe	Pro	Asn	Val	Arg	Ile	Gly	Asp																
				105					110					115																	
gat	gtc	gtt	gcc	cag	gac	cgg	ctc	ttg	cgc	caa	gag	ttt	ggg	att	acc	499															
Asp	Val	Val	Ala	Gln	Asp	Arg	Leu	Leu	Arg	Gln	Glu	Phe	Gly	Ile	Thr																
				120					125					130																	
gag	ctc	ttt	gcc	gtc	gtt	ggg	ggg	tcg	atg	ggg	gcg	cag	caa	acc	tat	547															
Glu	Leu	Phe	Ala	Val	Val	Gly	Gly	Ser	Met	Gly	Ala	Gln	Gln	Thr	Tyr																
				135					140					145																	
gag	tgg	att	gtt	cgc	ttc	cct	gac	caa	gtt	cat	cga	gca	gct	ccg	atc	595															
Glu	Trp	Ile	Val	Arg	Phe	Pro	Asp	Gln	Val	His	Arg	Ala	Ala	Pro	Ile																
				150					155					160																	
gcg	ggc	act	gcg	aag	aac	act	cct	cat	gat	ttc	atc	ttc	acc	cag	act	643															
Ala	Gly	Thr	Ala	Lys	Asn	Thr	Pro	His	Asp	Phe	Ile	Phe	Thr	Gln	Thr																
				170					175					180																	
ctt	aat	gag	acc	gtt	gag	gcc	gat	cca	ggg	ttc	aat	ggc	ggc	gaa	tac	691															
Leu	Asn	Glu	Thr	Val	Glu	Ala	Asp	Pro	Gly	Phe	Asn	Gly	Gly	Glu	Tyr																
				185					190					195																	
tcc	tcc	cat	gaa	gag	gta	gct	gat	gga	ctt	cgc	cgt	caa	tcg	cat	ctt	739															
Ser	Ser	His	Glu	Glu	Val	Ala	Asp	Gly	Leu	Arg	Arg	Gln	Ser	His	Leu																
				200					205					210																	
tgg	gct	gcc	atg	gga	ttt	tcc	aca	gag	ttc	tgg	aag	cag	gag	gca	tgg	787															
Trp	Ala	Ala	Met	Gly	Phe																										

gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct 883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala
250 255 260

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu
265 270 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979
Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
280 285 290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027
Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075
Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa 1123
Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct 1170
Asn Leu Lys Glu Leu Phe Glu Ser
345

<210> 186

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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20 25 30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly

130	135	140
Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His 145 150 155 160		
Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe 165 170 175		
Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe 180 185 190		
Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg 195 200 205		
Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp 210 215 220		
Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val 225 230 235 240		
Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr 245 250 255		
Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His 260 265 270		
Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr 275 280 285		
Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys 290 295 300		
Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu 305 310 315 320		
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Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser 340 345		

<210> 187

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 187

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	Met Pro Thr Leu Ala	
	1 5	

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa	163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	

	10	15	20	
gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt				211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly				
	25	30	35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa				259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu				
	40	45	50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg				307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu				
	55	60	65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt				355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys				
	70	75	80	85
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg				403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met				
	90	95	100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att				451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile				
	105	110	115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc				499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile				
	120	125	130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc				547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr				
	135	140	145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt				595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val				
	150	155	160	165
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc				643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser				
	170	175	180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac				691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn				
	185	190	195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga				739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg				
	200	205	210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc				787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg				
	215	220	225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc				835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg				
	230	235	240	245
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca				883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala				
	250	255	260	

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag 1254
 Glu Phe Tyr Ile
 375

<210> 188
 <211> 377
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 188
 Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

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Pro  Ala  Thr  Ser  Ile  Arg  Asp  Gln  Val  Asn  Ala  Glu  Lys  Gln  Phe  Leu
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Asp  Ala  Leu  Gly  Ile  Thr  Thr  Val  Ala  Ala  Val  Leu  Gly  Gly  Ser  Met
      130                      135                      140

Gly  Gly  Ala  Arg  Thr  Leu  Glu  Trp  Ala  Ala  Met  Tyr  Pro  Glu  Thr  Val
      145                      150                      155                      160

Gly  Ala  Ala  Ala  Val  Leu  Ala  Val  Ser  Ala  Arg  Ala  Ser  Ala  Trp  Gln
      165                      170                      175

Ile  Gly  Ile  Gln  Ser  Ala  Gln  Ile  Lys  Ala  Ile  Glu  Asn  Asp  His  His
      180                      185                      190

Trp  His  Glu  Gly  Asn  Tyr  Tyr  Glu  Ser  Gly  Cys  Asn  Pro  Ala  Thr  Gly
      195                      200                      205

Leu  Gly  Ala  Ala  Arg  Arg  Ile  Ala  His  Leu  Thr  Tyr  Arg  Gly  Glu  Leu
      210                      215                      220

Glu  Ile  Asp  Glu  Arg  Phe  Gly  Thr  Lys  Ala  Gln  Lys  Asn  Glu  Asn  Pro
      225                      230                      235                      240

Leu  Gly  Pro  Tyr  Arg  Lys  Pro  Asp  Gln  Arg  Phe  Ala  Val  Glu  Ser  Tyr
      245                      250                      255

Leu  Asp  Tyr  Gln  Ala  Asp  Lys  Leu  Val  Gln  Arg  Phe  Asp  Ala  Gly  Ser
      260                      265                      270

Tyr  Val  Leu  Leu  Thr  Asp  Ala  Leu  Asn  Arg  His  Asp  Ile  Gly  Arg  Asp
      275                      280                      285

Arg  Gly  Gly  Leu  Asn  Lys  Ala  Leu  Glu  Ser  Ile  Lys  Val  Pro  Val  Leu
      290                      295                      300

Val  Ala  Gly  Val  Asp  Thr  Asp  Ile  Leu  Tyr  Pro  Tyr  His  Gln  Gln  Glu
      305                      310                      315                      320

His  Leu  Ser  Arg  Asn  Leu  Gly  Asn  Leu  Leu  Ala  Met  Ala  Lys  Ile  Val
      325                      330                      335

Ser  Pro  Val  Gly  His  Asp  Ala  Phe  Leu  Thr  Glu  Ser  Arg  Gln  Met  Asp
      340                      345                      350

Arg  Ile  Val  Arg  Asn  Phe  Phe  Ser  Leu  Ile  Ser  Pro  Asp  Glu  Asp  Asn
      355                      360                      365

Pro  Ser  Thr  Tyr  Ile  Glu  Phe  Tyr  Ile
      370                      375

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<210> 189

<211> 1210

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA00403

<400> 189

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tttttcagac tcgtgagaat gcaaactaga ctagacagag ctgtccatat acactggacg 60

aagtttttagt cttgtccacc cagaacaggc gggtatttttc atg ccc acc ctc gcg 115
                                         Met Pro Thr Leu Ala
                                         1           5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
                10                15                20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
                25                30                35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
                40                45                50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
                55                60                65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
                70                75                80                85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                90                95                100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
                105                110                115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
                120                125                130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
                135                140                145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
                150                155                160                165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                170                175                180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                185                190                195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
                200                205                210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787

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<210> 190
<211> 370
<212> PRT
<213> *Corynebacterium glutamicum*

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser
 370

<210> 191
 <211> 687
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXS03158

<400> 191

caaagctcac cgaaggcacc aacgccaagt tggttgttga caacaccttg gcatcccat 60

acctgcagca gccactaaaa ctcggcgcac acgcaagtcc ttg cac tcc acc acc 115
 Leu His Ser Thr Thr
 1 5

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20

aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35

gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50

aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65

atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80 85

cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
 90 95 100

aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115

gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
 120 125 130

tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145

cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
 His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
 150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
 170 175 180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Gln Ala Leu Asn Asn Leu
 185

<210> 192

<211> 188

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 192

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly
 1 5 10 15

Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
 20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
 145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
 165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
 180 185

<210> 193

<211> 617

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(594)

<223> FRXA00254

<400> 193

cag cca cta aaa ctc ggc gca cac gca gtc ttg cac tcc acc acc aag 48
 Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30
 gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
 35 40 45
 ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192
 Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60
 acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80
 gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95
 ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag 336
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110
 cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384
 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125
 gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140
 ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480
 Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145 150 155 160
 cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc 528
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
 165 170 175
 atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag 576
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
 180 185 190
 cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 617
 Gln Ala Leu Asn Asn Leu
 195

<210> 194

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly

35 40 45
 Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110
 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140
 Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145 150 155 160
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
 165 170 175
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
 180 185 190
 Gln Ala Leu Asn Asn Leu
 195

<210> 195
 <211> 1170
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1147)
 <223> RXA02532

<400> 195
 gatgaatttt taccacccat ctgtacctat taaccctgcg tggcggtccac ccacagtaac 60
 tgtgcaagcg ggacggccag ccagaactcc tgggtgcgccc atg aac cca cct atc 115
 Met Asn Pro Pro Ile
 1 5
 acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163
 Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
 10 15 20
 gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta 211
 Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
 25 30 35
 gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca acg 259
 Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
 40 45 50

tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa	307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys	
55 60 65	
gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc	355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg	
70 75 80 85	
gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg	403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val	
90 95 100	
att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tcg atc gct	451
Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala	
105 110 115	
aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg	499
Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val	
120 125 130	
cgt ggg ctt gga gtt ttg act gtc gtt gac gcg act ttc gca acg cca	547
Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro	
135 140 145	
ctt cgt caa cgt cca ttg gaa ctt ggt gct gat att gtg ctt tac tcg	595
Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser	
150 155 160 165	
gca acc aaa ctt atc ggt gga cac tct gat ctt ctt ctt gga gtc gca	643
Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala	
170 175 180	
gtg tgc aag tct gag cac cat gcg cag ttt ctt gcc act cac cgt cat	691
Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His	
185 190 195	
gat cat ggt tca gtg ccg gga ggt ctt gaa gcg ttt ctt gct ctc cgt	739
Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu Arg	
200 205 210	
gga ttg tat tcc ttg gcg gtg cgt ctt gat cga gca gaa tcc aac gca	787
Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala	
215 220 225	
gca gaa ctt tcg cgg cga ctt aac gcg cat cct tcg gtt acc cgc gtc	835
Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val	
230 235 240 245	
aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga	883
Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg	
250 255 260	
gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca	931
Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala	
265 270 275	
aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc	979
Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr	
280 285 290	

gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac cag 1170
Ala Ser Ile Asp Lys Val Leu Gly
345

<213> Corynebacterium glutamicum

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
 210 215 220
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
 225 230 235 240
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
 245 250 255
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
 260 265 270
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
 275 280 285
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290 295 300
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
 305 310 315 320
 Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
 325 330 335
 Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
 340 345

<210> 197
 <211> 861
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(838)
 <223> RXS03159

<400> 197
 aggggctagt tttacacaaa agtggacagc ttggtctatc attgccagaa gaccggctcct 60
 tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
 Leu Ser Phe Asp Pro
 1 5
 aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20
 gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35
 ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50
 cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65

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ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
120 125 130

gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
135 140 145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
150 155 160 165

gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
170 175 180

ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
185 190 195

agt cct tgc act cca cca cca agt aca tcg aag gac act ccg acg ttg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu
200 205 210

ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc 787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys
215 220 225

tgt tca tgc agg gcg gca tcg gac cga tcc cat cag ttt tcg atg cat 835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His
230 235 240 245

acc tgaccgccccg tggcctcaag acc 861
Thr

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<210> 198

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 198

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Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
1 5 10 15

```

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Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
20 25 30

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Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140
 Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr
 145 150 155 160
 Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu
 165 170 175
 Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys
 180 185 190
 Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys
 195 200 205
 Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys
 210 215 220
 Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
 225 230 235 240
 Gln Phe Ser Met His Thr
 245

<210> 199

<211> 703

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA02768

<400> 199

aggggctagt ttacacaaa agtggacagc ttggtctatc attgccagaa gaccggctct 60

tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115

 Leu Ser Phe Asp Pro
 1 5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
 90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
 Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
 120 125 130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
 135 140 145

gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
 Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
 150 155 160 165

gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
 Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
 170 175 180

aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
 185 190 195

gng cac acg cag 703
 Xaa His Thr Gln
 200

<210> 200

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
 1 5 10 15

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<400> 201
gtgttgctcg cggccaggca gcagtgctgt acctgctga cgcggatggt gacatcgttc 60

ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt    115
                Leu Gly Ala Tyr Gly
                1                      5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att    163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                10                      15                      20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga    211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg

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25										30					35					
ggt	ttg	ggt	gct	gat	ctg	atc	ggt	cga	acc	gtc	ggt	ctg	ctg	gac	atg	259				
Gly	Leu	Gly	Ala	Asp	Leu	Ile	Gly	Arg	Thr	Val	Gly	Leu	Leu	Asp	Met					
		40					45					50								
atc	aac	gtt	gat	cgc	ggg	gcc	cga	tct	tgg	gtg	atg	agc	aca	cgc	ccc	307				
Ile	Asn	Val	Asp	Arg	Gly	Ala	Arg	Ser	Trp	Val	Met	Ser	Thr	Arg	Pro					
		55					60					65								
agc	aga	ttg	acg	cac	ctg	acc	ggc	gat	ttc	ctt	gac	atg	gat	ttg	gat	355				
Ser	Arg	Leu	Thr	His	Leu	Thr	Gly	Asp	Phe	Leu	Asp	Met	Asp	Leu	Asp					
70							75					80			85					
gcg	tgc	gag	gaa	acc	tgg	gga	acg	ggc	gtc	gac	aag	cta	aaa	atc	caa	403				
Ala	Cys	Glu	Glu	Thr	Trp	Gly	Thr	Gly	Val	Asp	Lys	Leu	Lys	Ile	Gln					
				90							95			100						
gtt	gct	ggt	ccc	tgg	act	tta	ggt	gcg	cgc	att	gag	ttg	gcc	aat	ggc	451				
Val	Ala	Gly	Pro	Trp	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Leu	Ala	Asn	Gly					
				105							110			115						
cat	cgc	gtt	ttg	tct	gat	cgc	ggt	gcg	atg	cgt	gat	ctc	acg	cag	gcg	499				
His	Arg	Val	Leu	Ser	Asp	Arg	Gly	Ala	Met	Arg	Asp	Leu	Thr	Gln	Ala					
				120							125			130						
ctg	atc	gcc	ggc	atc	gat	gcg	cat	gca	cgc	aag	gtt	gct	ggg	cga	ttt	547				
Leu	Ile	Ala	Gly	Ile	Asp	Ala	His	Ala	Arg	Lys	Val	Ala	Gly	Arg	Phe					
				135											145					
cgc	gcc	gaa	gtg	cag	gtg	caa	att	gat	gag	ccg	gag	ctg	aaa	tcg	ctt	595				
Arg	Ala	Glu	Val	Gln	Val	Gln	Ile	Asp	Glu	Pro	Glu	Leu	Lys	Ser	Leu					
150							155					160			165					
atc	gac	ggc	tcc	ctc	cct	ggc	act	tcc	acc	ttt	gac	att	att	cct	gcg	643				
Ile	Asp	Gly	Ser	Leu	Pro	Gly	Thr	Ser	Thr	Phe	Asp	Ile	Ile	Pro	Ala					
						170									180					
gtg	aat	gtc	gct	gat	gcc	agt	gaa	cgt	ttg	cag	cag	gtc	ttt	agc	tcg	691				
Val	Asn	Val	Ala	Asp	Ala	Ser	Glu	Arg	Leu	Gln	Gln	Val	Phe	Ser	Ser					
						185									195					
att	gag	ggg	ccg	aca	tat	ctc	aac	ctc	acc	ggc	cag	att	cct	act	tgg	739				
Ile	Glu	Gly	Pro	Thr	Tyr	Leu	Asn	Leu	Thr	Gly	Gln	Ile	Pro	Thr	Trp					
						200									210					
gat	gtg	gct	cgg	ggt	gcg	ggc	gcc	gat	act	gtg	cag	att	tcc	atg	gat	787				
Asp	Val	Ala	Arg	Gly	Ala	Gly	Ala	Asp	Thr	Val	Gln	Ile	Ser	Met	Asp					
						215									225					
caa	gtc	cgt	gga	aat	gaa	cat	ttg	gat	ggt	ttt	ggt	gaa	acc	atc	acc	835				
Gln	Val	Arg	Gly	Asn	Glu	His	Leu	Asp	Gly	Phe	Gly	Glu	Thr	Ile	Thr					
230							235					240			245					
agt	gga	att	cgt	ctt	ggt	ttg	ggc	att	acg	aca	gga	aaa	gat	gtc	gta	883				
Ser	Gly	Ile	Arg	Leu	Gly	Leu	Gly	Ile	Thr	Thr	Gly	Lys	Asp	Val	Val					
						250									260					
gat	gaa	ctg	ctc	gag	cga	ccg	cgg	caa	aag	gcc	gtt	gag	gta	gca	cgc	931				
Asp	Glu	Leu	Leu	Glu	Arg	Pro	Arg	Gln	Lys	Ala	Val	Glu	Val	Ala	Arg					
						265									275					

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ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
      280                      285                      290

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027
Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
      295                      300                      305

gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag 1075
Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
310                      315                      320                      325

gat tca tgc gac ctt taaggcttta ccggcgctgg gtg 1113
Asp Ser Cys Asp Leu
      330

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<210> 202

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1          5          10          15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
      20          25          30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
      35          40          45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
      50          55          60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
      65          70          75          80

Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
      85          90          95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
      100          105          110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
      115          120          125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
      130          135          140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
      145          150          155          160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
      165          170          175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
      180          185          190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly

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195					200					205					
Gln	Ile	Pro	Thr	Trp	Asp	Val	Ala	Arg	Gly	Ala	Gly	Ala	Asp	Thr	Val
210						215					220				
Gln	Ile	Ser	Met	Asp	Gln	Val	Arg	Gly	Asn	Glu	His	Leu	Asp	Gly	Phe
225					230					235					240
Gly	Glu	Thr	Ile	Thr	Ser	Gly	Ile	Arg	Leu	Gly	Leu	Gly	Ile	Thr	Thr
				245					250					255	
Gly	Lys	Asp	Val	Val	Asp	Glu	Leu	Leu	Glu	Arg	Pro	Arg	Gln	Lys	Ala
			260					265					270		
Val	Glu	Val	Ala	Arg	Phe	Phe	Asp	Arg	Leu	Gly	Val	Gly	Arg	Asn	Tyr
		275					280					285			
Leu	Val	Asp	Ala	Val	Asp	Ile	His	Pro	Gly	Glu	Asp	Leu	Val	Gln	Gly
		290				295					300				
Thr	Ile	Thr	Glu	Ala	Ala	Gln	Ala	Tyr	Arg	Met	Ala	Arg	Val	Met	Ser
305					310					315					320
Glu	Met	Leu	Ser	Lys	Asp	Ser	Cys	Asp	Leu						
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<210> 203

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> RXN00402

<400> 203

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Thr	Asp	Glu	Lys	Asp	Gly	Lys	Pro	Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	
1				5				10					15			
gat	gct	gct	tac	cac	gga	ttg	aag	tac	gca	gac	ctt	ggt	gca	cca	gcc	96
Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	
			20				25					30				
ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	ctt	cta	cgc	gac	acc	ggc	tcc	acc	144
Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	
		35				40					45					
ctc	tcc	gca	ttc	aac	gca	tgg	gct	gca	gtc	cag	ggc	atc	gac	acc	ctt	192
Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	
		50				55				60						
tcc	ctg	cgc	ctg	gag	cgc	cac	aac	gaa	aac	gcc	atc	aag	gtt	gca	gaa	240
Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	
		65			70			75							80	
ttc	ctc	aac	aac	cac	gag	aag	gtg	gaa	aag	gtt	aac	ttc	gca	ggc	ctg	288
Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	
				85				90						95		

aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110

acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125

tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140

ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160

cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175

gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190

ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 204

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15

Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30

Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60

Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80

Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95

Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110

Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125

Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile

130 135 140

Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160

Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175

Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190

Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 205

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 205

gta ttg ccc tac ttc gtc act cca gat gct gct tac cac gga ttg aag 48
 Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15

tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30

ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45

gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60

gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80

gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc 288
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95

aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag 336
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110

atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125

cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140


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cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
145          150          155          160

cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
          165          170          175

acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
          180          185          190

tagctttaaa tagactcacc cca 599

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<210> 206

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

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Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1          5          10          15

Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
          20          25          30

Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
          35          40          45

Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
          50          55          60

Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
          65          70          75          80

Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
          85          90          95

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
          100          105          110

Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
          115          120          125

Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
          130          135          140

His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
          145          150          155          160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
          165          170          175

Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
          180          185          190

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<210> 207
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXA00405

<400> 207
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 ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
 Met Pro Lys Tyr Asp
 1 5
 aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
 10 15 20
 ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
 25 30 35
 caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
 40 45 50
 ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
 55 60 65
 acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
 70 75 80 85
 cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
 90 95 100
 ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
 105 110 115
 tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
 Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
 120 125 130
 atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547
 Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
 135 140 145
 gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
 150 155 160 165
 aac cca cag gca gac gtc 613
 Asn Pro Gln Ala Asp Val
 170

<210> 208
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
 1 5 10 15
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
 165 170

<210> 209
 <211> 551
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(528)
 <223> RXA02197

<400> 209
 gcc gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc 48
 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
 1 5 10 15
 ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac 96
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30

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ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
      35              40              45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
      50              55              60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc 240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
      65              70              75              80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
      85              90              95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
      100             105             110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
      115             120             125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
      130             135             140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
      145             150             155             160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
      165             170             175

taacaccttt gagagggaaa act 551

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<210> 210

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
      20              25              30

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Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
      35              40              45

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Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
      50              55              60

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Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
      65              70              75              80

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Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly

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	85		90		95
Gly Ser Val	Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp				
	100		105		110
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro					
	115		120		125
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg					
	130		135		140
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser					
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Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val					
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 <222> (101)..(2599)
 <223> RXN02198

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 Met Ser Thr Ser Val
 1 5
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35
 caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50
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 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65
 cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85
 ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
105 110 115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
120 125 130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac	595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
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Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
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tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag	1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	
cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag	1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
330 335 340	

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc 1171
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
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tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc 1219
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc 1267
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt 1315
 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
 390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc 1363
 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
 410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg 1411
 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
 425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt 1459
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
 440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac 1507
 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
 455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag 1555
 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
 470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag 1603
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
 490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac 1651
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
 505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac 1699
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
 520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat 1747
 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
 535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca 1795
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
 550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac 1843
 Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
 570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att 1891

Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe	Leu	Asn	Glu	Cys	Ile	
			585					590					595			
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Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser	Ser	Lys	Ile	Leu	Pro	
		600					605					610				
atg	aac	cgc	att	gat	gat	cgc	cag	cgc	gaa	gtg	gcg	ttg	gat	atg	gtc	1987
Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Glu	Val	Ala	Leu	Asp	Met	Val	
		615					620					625				
tat	gat	cgc	cgc	acc	gag	gat	tac	gat	ccg	ctg	cag	gaa	ttc	atg	cag	2035
Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu	Gln	Glu	Phe	Met	Gln	
		630				635					640				645	
ctg	ttt	gag	ggc	gtt	tct	gct	gcc	gat	gcc	aag	gat	gct	cgc	gct	gaa	2083
Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys	Asp	Ala	Arg	Ala	Glu	
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cag	ctg	gcc	gct	atg	cct	ttg	ttt	gag	cgT	ttg	gca	cag	cgC	atc	atc	2131
Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu	Ala	Gln	Arg	Ile	Ile	
				665					670					675		
gac	ggc	gat	aag	aat	ggc	ctt	gag	gat	gat	ctg	gaa	gca	ggc	atg	aag	2179
Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu	Glu	Ala	Gly	Met	Lys	
			680					685					690			
gag	aag	tct	cct	att	gcg	atc	atc	aac	gag	gac	ctt	ctc	aac	ggc	atg	2227
Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp	Leu	Leu	Asn	Gly	Met	
						700						705				
aag	acc	gtg	ggt	gag	ctg	ttt	ggt	tcc	gga	cag	atg	cag	ctg	cca	ttc	2275
Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln	Met	Gln	Leu	Pro	Phe	
						715					720				725	
gtg	ctg	caa	tcg	gca	gaa	acc	atg	aaa	act	gcg	gtg	gcc	tat	ttg	gaa	2323
Val	Leu	Gln	Ser	Ala	Glu	Thr	Met	Lys	Thr	Ala	Val	Ala	Tyr	Leu	Glu	
						730									740	
ccg	ttc	atg	gaa	gag	gaa	gca	gaa	gct	acc	gga	tct	gcg	cag	gca	gag	2371
Pro	Phe	Met	Glu	Glu	Glu	Ala	Glu	Ala	Thr	Gly	Ser	Ala	Gln	Ala	Glu	
						745									755	
ggc	aag	ggc	aaa	atc	gtc	gtg	gcc	acc	gtc	aag	ggt	gac	gtg	cac	gat	2419
Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys	Gly	Asp	Val	His	Asp	
							765								770	
atc	ggc	aag	aac	ttg	gtg	gac	atc	att	ttg	tcc	aac	aac	ggt	tac	gac	2467
Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser	Asn	Asn	Gly	Tyr	Asp	
							780								785	
gtg	gtg	aac	ttg	ggc	atc	aag	cag	cca	ctg	tcc	gcc	atg	ttg	gaa	gca	2515
Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser	Ala	Met	Leu	Glu	Ala	
							795				800				805	
gcg	gaa	gaa	cac	aaa	gca	gac	gtc	atc	ggc	atg	tcg	gga	ctt	ctt	gtg	2563
Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met	Ser	Gly	Leu	Leu	Val	
						810									820	
aag	tcc	acc	gtg	gtg	atg	aag	caa	acc	atc	agc	gac					2599
Lys	Ser	Thr	Val	Val	Met	Lys	Gln	Thr	Ile	Ser	Asp					

825

830

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<211> 833

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<213> *Corynebacterium glutamicum*

<400> 212

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 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270

Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln

275					280					285					
Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly
290						295					300				
Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val
305					310					315					320
Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala
				325					330					335	
Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val
			340					345					350		
Ala	Ser	Leu	Tyr	Thr	Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser
		355					360						365		
Met	Ile	Gly	Glu	Arg	Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu
	370					375					380				
Ala	Met	Leu	Ser	Gly	Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln
385					390					395					400
Gln	Thr	Arg	Asp	Gly	Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val
				405					410					415	
Gly	Arg	Asp	Gly	Thr	Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala
			420					425					430		
Thr	Ser	Ser	Thr	Leu	Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val
			435				440					445			
Ile	Arg	Thr	Gly	Leu	Glu	His	Leu	Gly	Gly	Arg	Ser	Ile	Val	Asn	Ser
	450					455					460				
Val	Asn	Phe	Glu	Asp	Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile
465				470						475					480
Met	Lys	Leu	Val	Lys	Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile
				485					490					495	
Asp	Glu	Glu	Gly	Gln	Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala
			500					505					510		
Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys
		515				520						525			
Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu
	530					535					540				
Glu	Thr	Arg	Arg	Asp	Gly	Ile	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Glu	Leu
545					550					555					560
Lys	Lys	Leu	Tyr	Pro	Glu	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile
				565					570					575	
Ser	Phe	Gly	Leu	Asn	Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe
			580					585					590		
Leu	Asn	Glu	Cys	Ile	Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser
		595					600					605			

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
 725 730 735
 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
 740 745 750
 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
 755 760 765
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 770 775 780
 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
 785 790 795 800
 Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
 805 810 815
 Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser
 820 825 830

Asp

<210> 213
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(2578)
 <223> FRXA02198

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											Met	Ser	Thr	Ser	Val	
											1				5	
act	tca	cca	gcc	cac	aac	aac	gca	cat	tcc	tcc	gaa	ttt	ttg	gat	gcg	163
Thr	Ser	Pro	Ala	His	Asn	Asn	Ala	His	Ser	Ser	Glu	Phe	Leu	Asp	Ala	
				10					15					20		
ttg	gca	aac	cat	gtg	ttg	atc	ggc	gac	ggc	gcc	atg	ggc	acc	cag	ctc	211
Leu	Ala	Asn	His	Val	Leu	Ile	Gly	Asp	Gly	Ala	Met	Gly	Thr	Gln	Leu	
				25					30					35		
caa	ggc	ttt	gac	ctg	gac	gtg	gaa	aag	gat	ttc	ctt	gat	ctg	gag	ggg	259
Gln	Gly	Phe	Asp	Leu	Asp	Val	Glu	Lys	Asp	Phe	Leu	Asp	Leu	Glu	Gly	
				40					45					50		
tgt	aat	gag	att	ctc	aac	gac	acc	cgc	cct	gat	gtg	ttg	agg	cag	att	307
Cys	Asn	Glu	Ile	Leu	Asn	Asp	Thr	Arg	Pro	Asp	Val	Leu	Arg	Gln	Ile	
				55					60					65		
cac	cgc	gcc	tac	ttt	gag	gcg	gga	gct	gac	ttg	gtt	gag	acc	aat	act	355
His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu	Val	Glu	Thr	Asn	Thr	
				70					75					80		
ttt	ggc	tgc	aac	ctg	ccg	aac	ttg	gcg	gat	tat	gac	atc	gct	gat	cgt	403
Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr	Asp	Ile	Ala	Asp	Arg	
				90					95					100		
tgc	cgt	gag	ctt	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct	451
Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala	
				105					110					115		
gat	gag	atg	ggg	ccg	ggc	cga	aac	ggc	atg	cgg	cgt	ttc	gtg	gtt	ggc	499
Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly	
				120					125					130		
tcc	ctg	gga	cct	gga	acg	aag	ctt	cca	tcg	ctg	ggc	cat	gca	ccg	tat	547
Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr	
				135					140					145		
gca	gat	ttg	cgt	ggg	cac	tac	aag	gaa	gca	gcg	ctt	ggc	atc	atc	gac	595
Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp	
				150					155					160		
ggc	ggc	ggc	gat	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag	643
Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln	
				170					175					180		
gtc	aag	gct	gcg	gtt	cac	ggc	gtt	caa	gat	gcc	atg	gct	gaa	ctt	gat	691
Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp	
				185					190					195		
aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr	
				200					205					210		
atg	ctc	atg	ggc	tct	gag	atc	ggc	gcc	gcg	ttg	aca	gcg	ctg	cag	cca	787
Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro	
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ctg	ggc	atc	gac	atg	att	ggc	ctg	aac								

230	235	240	245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg				883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca				931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc				979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	280	285	290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca				1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	295	300	305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag				1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	310	315	320	325
cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag				1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	330	335	340	
gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc				1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	345	350	355	
tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc				1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	360	365	370	
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc				1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	375	380	385	
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt				1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	390	395	400	405
gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc				1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	410	415	420	
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg				1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	425	430	435	
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt				1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	440	445	450	
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac				1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	455	460	465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag				1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	470	475	480	485

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Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
490 495 500	
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
505 510 515	
gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac	1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
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tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat	1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp	
535 540 545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca	1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro	
550 555 560 565	
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac	1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
570 575 580	
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att	1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile	
585 590 595	
gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg	1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	
600 605 610	
atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc	1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val	
615 620 625	
tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag	2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln	
630 635 640 645	
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa	2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu	
650 655 660	
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc	2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile	
665 670 675	
gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag	2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys	
680 685 690	
gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg	2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met	
695 700 705	
aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc	2275
Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe	
710 715 720 725	

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Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
              730              735              740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag 2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
              745              750              755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat 2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
              760              765              770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467
Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
              775              780              785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515
Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
              790              795              800              805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg 2563
Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
              810              815              820

aag tcc acc gtg gtg 2578
Lys Ser Thr Val Val
              825

<210> 214
<211> 826
<212> PRT
<213> Corynebacterium glutamicum

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Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
      35              40              45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
      50              55              60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
      65              70              75              80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
      85              90              95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
      100              105              110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
      115              120              125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
      130              135              140

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Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
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 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460


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Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
465                               470               475               480

Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
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Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
                               500                               505               510

Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
                               515                               520               525

Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
                               530                               535               540

Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
545                               550                               555               560

Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
                               565                               570               575

Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
                               580                               585               590

Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
                               595                               600               605

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
                               610                               615               620

Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
625                               630                               635               640

Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
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Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
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Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
                               675                               680               685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
                               690                               695               700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705                               710                               715               720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
                               725                               730               735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
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Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
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Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
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Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser

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																	115
Met Thr Gln Ser Ala																	
1 5																	
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Pro	Glu	Phe	Ile	Ala	Thr	Ala	Asp	Leu	Val	Asp	Ile	Ile	Gly	Asp	Asn		
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25 30 35																	
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Phe	His	Gly	Ile	Ile	Thr	Thr	Val	Lys	Cys	Phe	Gln	Asp	Asn	Ala	Leu		
40 45 50																	
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Leu	Lys	Ser	Ile	Leu	Ser	Glu	Asp	Asn	Pro	Gly	Gly	Val	Leu	Val	Ile		
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Asp	Gly	Asp	Ala	Ser	Val	His	Thr	Ala	Leu	Val	Gly	Asp	Ile	Ile	Ala		
70 75 80 85																	
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Gly	Leu	Gly	Lys	Asp	His	Gly	Trp	Ser	Gly	Val	Ile	Val	Asn	Gly	Ala		
90 95 100																	
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Ile	Arg	Asp	Ser	Ala	Val	Ile	Gly	Thr	Met	Thr	Phe	Gly	Cys	Lys	Ala		
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Leu	Gly	Thr	Asn	Pro	Arg	Lys	Ser	Thr	Lys	Thr	Gly	Ser	Gly	Glu	Arg		
120 125 130																	
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Asp	Val	Val	Val	Ser	Ile	Gly	Gly	Ile	Asp	Phe	Ile	Pro	Gly	His	Tyr		
135 140 145																	

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 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
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<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
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Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
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Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
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Glu Ala Pro Ile Lys Gln
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<210> 217

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<212> DNA

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<222> (101)..(598)

<223> FRXA02906

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Met Thr Gln Ser Ala
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Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
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Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
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Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
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Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
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Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
90 95 100

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Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
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Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
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Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
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<400> 218

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 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
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 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
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<223> RXN00132

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 Met Ala Gln Val Met
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 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
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 Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
 25 30 35

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 Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
 40 45 50

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gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag			403
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu			
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Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg			
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Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu			
	170	175	180
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt			691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly			
	185	190	195
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Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala			
	200	205	210
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Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val			
	215	220	225
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc			835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile			
	230	235	240
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg			883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val			
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Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe			
	265	270	275
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Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn			
	280	285	290
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag			1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu			
	295	300	305

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 185 190 195

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 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

 ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

 cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag 1219
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 360 365 370

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 375 380 385

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 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
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 425 430 435

 gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc 1459
 Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
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 Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
 455 460 465

 cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag 1554
 Pro Phe Lys Pro Glu His Tyr Arg Tyr
 470 475

 gga 1557

<210> 220

<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala

35	40	45
Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile 50 55 60		
Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn 65 70 75 80		
Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser 85 90 95		
Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly 100 105 110		
Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp 115 120 125		
Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr 130 135 140		
Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro 145 150 155 160		
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met 165 170 175		
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala 180 185 190		
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg 195 200 205		
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn 210 215 220		
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr 225 230 235 240		
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met 245 250 255		
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly 260 265 270		
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu 275 280 285		
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val 290 295 300		
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala 305 310 315 320		
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys 325 330 335		
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp 340 345 350		
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys 355 360 365		

Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380

Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro
 385 390 395 400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
 405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 420 425 430

Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu
 435 440 445

Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly
 450 455 460

Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr
 465 470 475

<210> 221

<211> 128

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(105)

<223> FRXA00132

<400> 221

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 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15

gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

tac cgc tac taatgattgt cagcattgag gga 128
 Tyr Arg Tyr
 35

<210> 222

<211> 35

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15

Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

Tyr Arg Tyr
 35

<210> 223
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1396)
 <223> FRXA01371

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 tttcctaatt ttcattttct taaaaggagc tcgccaggac atg gca cag gtt atg 115
 Met Ala Gln Val Met
 1 5
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
 10 15 20
 att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211
 Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
 25 30 35
 gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct 259
 Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
 40 45 50
 atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct 307
 Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala
 55 60 65
 ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355
 Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln
 70 75 80 85
 gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag 403
 Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu
 90 95 100
 cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag 451
 Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu
 105 110 115
 tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca 499
 Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro
 120 125 130
 aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547
 Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
 135 140 145
 ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac 595
 Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn
 150 155 160 165
 gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt 643
 Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu

170								175					180					
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggt	691		
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly			
			185				190						195					
gtc	acc	gag	gaa	acc	acc	acc	ggt	gtg	cac	cgc	ctg	tac	cac	ttc	gct	739		
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala			
			200				205						210					
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	gcg	atg	aac	gtc	aac	gac	gct	gtc	787		
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val			
			215				220						225					
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc	835		
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile			
			230				235						240			245		
gac	ggc	atc	aac	cgc	gcc	act	gac	atg	ctc	atg	ggc	ggc	aag	aac	gtg	883		
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val			
			250				255						260					
ctt	gtc	tgc	ggg	tac	ggc	gat	gtc	ggc	aag	ggc	tgc	gct	gag	gct	ttc	931		
Leu	Val	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys	Gly	Cys	Ala	Glu	Ala	Phe			
			265				270						275					
gac	ggc	cag	ggc	gct	cgc	gtc	aag	gtc	acc	gaa	gct	gac	cca	atc	aac	979		
Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Glu	Ala	Asp	Pro	Ile	Asn			
			280				285						290					
gct	ctt	cag	gct	ctg	atg	gat	ggc	tac	tct	gtg	gtc	acc	gtt	gat	gag	1027		
Ala	Leu	Gln	Ala	Leu	Met	Asp	Gly	Tyr	Ser	Val	Val	Thr	Val	Asp	Glu			
			295				300						305					
gcc	atc	gag	gac	gcc	gac	atc	gtg	atc	acc	gcg	acc	ggc	aac	aag	gac	1075		
Ala	Ile	Glu	Asp	Ala	Asp	Ile	Val	Ile	Thr	Ala	Thr	Gly	Asn	Lys	Asp			
			310				315						320			325		
atc	att	tcc	ttc	gag	cag	atg	ctc	aag	atg	aag	gat	cac	gct	ctg	ctg	1123		
Ile	Ile	Ser	Phe	Glu	Gln	Met	Leu	Lys	Met	Lys	Asp	His	Ala	Leu	Leu			
			330				335						340					
ggc	aac	atc	ggg	cac	ttt	gat	aat	gag	atc	gat	atg	cat	tcc	ctg	ttg	1171		
Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp	Met	His	Ser	Leu	Leu			
			345				350						355					
cac	cgc	gac	gac	gtc	acc	cgc	acc	acg	atc	aag	cca	cag	gtc	gac	gag	1219		
His	Arg	Asp	Asp	Val	Thr	Arg	Thr	Thr	Ile	Lys	Pro	Gln	Val	Asp	Glu			
			360				365						370					
ttc	acc	ttc	tcc	acc	ggg	cgc	tcc	atc	atc	gtc	ctg	tcc	gaa	ggg	cgc	1267		
Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val	Leu	Ser	Glu	Gly	Arg			
			375				380						385					
ctg	ttg	aac	ctt	ggc	aac	gcc	acc	gga	cac	cca	tca	ttt	gtc	atg	tcc	1315		
Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His	Pro	Ser	Phe	Val	Met	Ser			
			390				395						400			405		
aac	tct	ttc	gcc	gat	cag	acc												

gaa gga cag tac gag aac gag gtc tac cgt ctg
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 425 430

1396

<210> 224

<211> 432

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 224

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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190

Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205

Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220

Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240

Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255

Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly

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260										265					270				
Cys	Ala	Glu	Ala	Phe	Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Glu				
		275					280					285							
Ala	Asp	Pro	Ile	Asn	Ala	Leu	Gln	Ala	Leu	Met	Asp	Gly	Tyr	Ser	Val				
		290				295						300							
Val	Thr	Val	Asp	Glu	Ala	Ile	Glu	Asp	Ala	Asp	Ile	Val	Ile	Thr	Ala				
305					310				315						320				
Thr	Gly	Asn	Lys	Asp	Ile	Ile	Ser	Phe	Glu	Gln	Met	Leu	Lys	Met	Lys				
				325					330					335					
Asp	His	Ala	Leu	Leu	Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp				
			340					345					350						
Met	His	Ser	Leu	Leu	His	Arg	Asp	Asp	Val	Thr	Arg	Thr	Thr	Ile	Lys				
		355					360					365							
Pro	Gln	Val	Asp	Glu	Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val				
		370				375					380								
Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His	Pro				
385					390					395					400				
Ser	Phe	Val	Met	Ser	Asn	Ser	Phe	Ala	Asp	Gln	Thr	Ile	Ala	Gln	Ile				
				405					410					415					
Glu	Leu	Phe	Gln	Asn	Glu	Gly	Gln	Tyr	Glu	Asn	Glu	Val	Tyr	Arg	Leu				
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<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2335)

<223> RXN02085

<400> 225

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				Met	Thr	Ser	Asn	Phe		
				1				5		

tct	tcc	act	gtc	gct	ggt	ctt	cct	cgc	atc	gga	gcg	aag	cgt	gaa	ctg		163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu		
			10					15					20				

aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggt	cgc	gaa		211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu		
		25						30					35				

ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259
 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
 40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
 55 60 65

atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
 70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
 90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
 105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
 120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
 135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
 Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
 150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
 Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
 170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly
 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979

Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg			
		280					285					290						
acc	gac	ctg	tgt	gct	gct	ctt	gct	tcc	ctg	aag	cgc	ctg	gca	gct	cgc		1027	
Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg			
		295				300				305								
ggc	cca	atc	gca	gtg	tct	acc	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac		1075	
Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr			
		310			315					320					325			
acc	ctc	gag	gct	gag	aac	att	gag	cct	gag	gtc	cgc	gac	tgg	ctt	gcc		1123	
Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala			
				330					335					340				
ttc	ggc	tcg	gag	aag	atc	acc	gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta		1171	
Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu			
			345					350					355					
gcc	ggc	aac	atc	gac	gcg	gct	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att		1219	
Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile			
		360				365						370						
gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc		1267	
Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu			
		375				380					385							
cct	ggc	cgt	agc	cgt	gga	tcc	ttc	gac	act	cgt	gtt	acg	ctg	cag	gag		1315	
Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu			
		390			395				400					405				
aag	tca	ctg	gag	ctt	cca	gct	ctg	cca	acc	acc	acc	att	ggc	tct	ttc		1363	
Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe			
				410					415					420				
cca	cag	acc	cca	tcc	att	cgt	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa		1411	
Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu			
			425					430					435					
tcc	atc	act	ttg	gag	cag	tac	gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat		1459	
Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp			
		440					445					450						
ctg	gtc	atc	gcc	aag	cag	gaa	gaa	ctt	ggc	ctt	gat	gtg	ttg	gtt	cac		1507	
Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	Asp	Val	Leu	Val	His			
		455				460					465							
ggc	gag	cca	gag	cgc	aac	gac	atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc		1555	
Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	Phe	Ser	Glu	Leu	Leu			
		470			475					480				485				
gac	ggc	ttc	ctc	tca	acc	gcc	aac	ggc	tgg	gtc	caa	agc	tac	ggc	tcc		1603	
Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser			
				490				495						500				
cgc	tgt	gtt	cgt	cct	cca	gtg	ttg	ttc	gga	aac	gtt	tcc	cgc	cca	gcg		1651	
Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn	Val	Ser	Arg	Pro	Ala			
			505				510						515					
cca	atg	act	gtc	aag	tgg	ttc	cag	tac	gca	cag	agc	ctg	acc	cag	aag		1699	
Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	Ser	Leu	Thr	Gln	Lys			

520	525	530	
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser 535 540 545			1747
ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala 550 555 560 565			1795
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys 570 575 580			1843
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg 585 590 595			1891
gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg 600 605 610			1939
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met 615 620 625			1987
tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp 630 635 640 645			2035
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu 650 655 660			2083
gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val 665 670 675			2131
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly 680 685 690			2179
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val 695 700 705			2227
aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala 710 715 720 725			2275
tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile 730 735 740			2323
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<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
      35           40           45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
      50           55           60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
      65           70           75           80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
      85           90           95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
      100          105          110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
      115          120          125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
      130          135          140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
      145          150          155          160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
      165          170          175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
      180          185          190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
      195          200          205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
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Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
      225          230          235          240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
      245          250          255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
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Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
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Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
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 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
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 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
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 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
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 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
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 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser

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Asp Met Gln Val Leu	Ala Ala Leu Lys Ser Ser	Gly Phe Glu Leu Gly	
	660	665	670
Val Gly Pro Gly Val	Trp Asp Ile His Ser Pro Arg	Val Pro Ser Ala	
	675	680	685
Gln Lys Val Asp Gly	Leu Leu Glu Ala Ala Leu	Gln Ser Val Asp Pro	
	690	695	700
Arg Gln Leu Trp Val	Asn Pro Asp Cys Gly Leu Lys	Thr Arg Gly Trp	
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Pro Glu Val Glu Ala	Ser Leu Lys Val Leu Val Glu	Ser Ala Lys Gln	
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Ala Arg Glu Lys Ile	Gly Ala Thr Ile		
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<211> 1923

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 227

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	1 5	

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Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
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ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
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gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
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gcc	ggc	aac	atc	gac	gcg	gct	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att		1219	
Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile			
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gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc		1267	
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Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu			
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Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp			
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Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	Asp	Val	Leu	Val	His			
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Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	Ser	Leu	Thr	Gln	Lys			
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cat	gtc	aag	gga	atg	ctc	acc	ggt	cca	gtc	acc	atc	ctt	gca	tgg	tcc		1747	
His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr	Ile	Leu	Ala	Trp	Ser			
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Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr	Ala	Asp	Gln	Val	Ala			
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Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile	Glu	Ala	Gly	Ala	Lys			

570 575 580
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 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
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 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
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 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
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 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
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 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
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 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
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 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
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 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
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 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
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 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
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Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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<212> DNA

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<220>

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<223> FRXA02086

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Met Ser Leu Arg Phe
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Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
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Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
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Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
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cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
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ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
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Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
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Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

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Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala

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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
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Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
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Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
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Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
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<223> RXN02648

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Ile	Arg	Thr	Thr	His	Val	Gly	Ser	Leu	Pro	Arg	Thr	Pro	Glu	Leu	Leu	
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gat	gca	aac	atc	aag	cgt	tct	aac	ggc	gag	att	ggg	gag	gag	gaa	ttc	211
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Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val	
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Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn	Tyr	Ser	Phe	Thr	Arg	
											70				75	
ctg	ggc	gga	ctg	acc	atg	acc	gat	acc	gac	cgt	tgg	gca	agc	cag	gaa	403
Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu	
											90				95	
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp	
											105				110	
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser	
											120				125	
ggc	atc	ttc	acc	ggc	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly	
											135				140	
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu	
											150				155	
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala	
											170				175	
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
											185				190	
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
											200				205	
tac	aag	atc	atc	acc	gat	gca	ggc	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag 835
 Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys
 230 235 240 245

 gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

 gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

 tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

 ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

 tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

 cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

 gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

 aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

 ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

 gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

 aacgagggtt gct 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
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Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
385 390 395 400

Phe

<210> 233

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(525)

<223> FRXA02648

<400> 233

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro	
1 5 10 15	
agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc	96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile	
20 25 30	
aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc	144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile	
35 40 45	
tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt	192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly	
50 55 60	
gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc	240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe	
65 70 75 80	
gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa	288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu	
85 90 95	
aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac	336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His	
100 105 110	
tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt	384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val	
115 120 125	
cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac	432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp	
130 135 140	
tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg	480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu	
145 150 155 160	

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

taagctagac aacgaggggtt gct 548

<210> 234

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 235

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 235

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gagtttgata cttttctttcg acttttagat tggattttca atg agc cag aac cgc 115

	Met	Ser	Gln	Asn	Arg	
	1				5	
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt						163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu						
			10		15	20
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc						211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe			25		30	35
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt						259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val			40		45	50
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc						307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr			55		60	65
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc						355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg			70		75	80
						85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa						403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu			90		95	100
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat						451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp			105		110	115
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct						499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser			120		125	130
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga						547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly			135		140	145
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg						595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu			150		155	160
						165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca						643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala			170		175	180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac						691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp			185		190	195
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa						739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu			200		205	210
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca						784
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala			215		220	225

<210> 236

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
 225

<210> 237

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 237

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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac 408

<210> 238

<211> 95

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 238

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
 1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85 90 95

<210> 239

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 239

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca	gtg agt aaa att tcg	115
	Val Ser Lys Ile Ser	
	1 5	

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg	163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val	
10 15 20	

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc	211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg	
25 30 35	

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg	259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro	
40 45 50	

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg	307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala	
55 60 65	

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg	355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	

aga aac gat ctg ccg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	

gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	

185	190	195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly 200 205 210			739
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp 215 220 225			787
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu 230 235 240 245			835
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val 250 255 260			883
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala 265 270 275			931
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp 280 285 290			979
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu 295 300 305			1027
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val 310 315 320 325			1075
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala 330 335 340			1123
att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn 345 350 355			1171
gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala 360 365 370			1219
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser 375 380 385			1267
ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg 390 395 400 405			1315
tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu 410 415 420			1363
cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr 425 430 435			1411

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ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc 1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
      440                      445                      450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
      455                      460                      465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470                      475                      480                      485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
      490                      495                      500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat 1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
      505                      510                      515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
      520                      525                      530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
      535                      540                      545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550                      555                      560                      565

gtt gcg tac tgatggagct gttcttcccg cgc 1827
Val Ala Tyr

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<210> 240

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

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Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
      20                      25                      30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
      35                      40                      45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
      50                      55                      60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
      65                      70                      75                      80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
      85                      90                      95

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Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
 530 535 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 241

<211> 1344

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1321)

<223> RXA02240

<400> 241

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aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115
 Val Ala Gln Pro Thr
 1 5

gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
 10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
 25 30 35

aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly
 40 45 50

atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc 307

Ile	Val	His	Val	Val	Gly	Glu	Val	Arg	Thr	Ser	Ala	Tyr	Val	Glu	Ile		
	55					60					65						
cct	caa	tta	gtc	cgc	aac	aag	ctc	atc	gaa	atc	gga	ttc	aac	tcc	tct	355	
Pro	Gln	Leu	Val	Arg	Asn	Lys	Leu	Ile	Glu	Ile	Gly	Phe	Asn	Ser	Ser		
	70				75				80					85			
gag	gtt	gga	ttc	gac	gga	cgc	acc	tgt	ggc	gtc	tca	gta	tcc	atc	ggc	403	
Glu	Val	Gly	Phe	Asp	Gly	Arg	Thr	Cys	Gly	Val	Ser	Val	Ser	Ile	Gly		
				90				95						100			
gag	cag	tcc	cag	gaa	atc	gct	gac	ggc	gtg	gat	aac	tcc	gac	gaa	gcc	451	
Glu	Gln	Ser	Gln	Glu	Ile	Ala	Asp	Gly	Val	Asp	Asn	Ser	Asp	Glu	Ala		
			105					110					115				
cgc	acc	aac	ggc	gac	gtt	gaa	gaa	gac	gac	cgc	gca	ggc	gct	ggc	gac	499	
Arg	Thr	Asn	Gly	Asp	Val	Glu	Glu	Asp	Asp	Arg	Ala	Gly	Ala	Gly	Asp		
		120					125					130					
cag	ggc	ctg	atg	ttc	ggc	tac	gcc	acc	aac	gaa	acc	gaa	gag	tac	atg	547	
Gln	Gly	Leu	Met	Phe	Gly	Tyr	Ala	Thr	Asn	Glu	Thr	Glu	Glu	Tyr	Met		
	135					140					145						
cct	ctt	cct	atc	gcg	ttg	gcg	cac	cga	ctg	tca	cgt	cgt	ctg	acc	cag	595	
Pro	Leu	Pro	Ile	Ala	Leu	Ala	His	Arg	Leu	Ser	Arg	Arg	Leu	Thr	Gln		
	150				155					160					165		
gtt	cgt	aaa	gag	ggc	atc	gtt	cct	cac	ctg	cgt	cca	gac	gga	aaa	acc	643	
Val	Arg	Lys	Glu	Gly	Ile	Val	Pro	His	Leu	Arg	Pro	Asp	Gly	Lys	Thr		
				170					175					180			
cag	gtc	acc	ttc	gca	tac	gat	gcg	caa	gac	cgc	cct	agc	cac	ctg	gat	691	
Gln	Val	Thr	Phe	Ala	Tyr	Asp	Ala	Gln	Asp	Arg	Pro	Ser	His	Leu	Asp		
			185					190					195				
acc	gtt	gtc	atc	tcc	acc	cag	cac	gac	cca	gaa	gtt	gac	cgt	gca	tgg	739	
Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu	Val	Asp	Arg	Ala	Trp		
		200					205					210					
ttg	gaa	acc	caa	ctg	cgc	gaa	cac	gtc	att	gat	tgg	gta	atc	aaa	gac	787	
Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp	Trp	Val	Ile	Lys	Asp		
	215					220					225						
gca	ggc	att	gag	gat	ctg	gca	acc	ggc	gag	atc	acc	gtg	ttg	atc	aac	835	
Ala	Gly	Ile	Glu	Asp	Leu	Ala	Thr	Gly	Glu	Ile	Thr	Val	Leu	Ile	Asn		
	230				235					240				245			
cct	tca	ggc	tcc	ttc	att	ctg	ggc	ggc	ccc	atg	ggc	gat	gag	ggc	ctg	883	
Pro	Ser	Gly	Ser	Phe	Ile	Leu	Gly	Gly	Pro	Met	Gly	Asp	Ala	Gly	Leu		
				250					255					260			
acc	ggc	cgc	aag	atc	atc	gtg	gat	acc	tac	ggc	ggc	atg	gct	cgc	cat	931	
Thr	Gly	Arg	Lys	Ile	Ile	Val	Asp	Thr	Tyr	Gly	Gly	Met	Ala	Arg	His		
			265					270					275				
ggc	ggc	gga	gca	ttc	tcc	ggc	aag	gat	cca	agc	aag	gtg	gac	cgc	tct	979	
Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser	Lys	Val	Asp	Arg	Ser		
		280					285					290					
gct	gca	tac	gcc	atg	cgt	tgg	gta	gca	aag	aac	atc	gtg	gca	gca	ggc	1027	
Ala	Ala	Tyr	Ala	Met	Arg	Trp	Val	Ala	Lys	Asn	Ile	Val	Ala	Ala	Gly		

295	300	305	
ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca			1075
Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala			
310	315	320	325
aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc			1123
Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly			
	330	335	340
ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg			1171
Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu			
	345	350	355
cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac			1219
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr			
	360	365	370
gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt			1267
Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu			
	375	380	385
cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag			1315
Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys			
390	395	400	405
ttg gcc taaaaatctg atgtagtatc ttc			1344
Leu Ala			

<210> 242

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr			
1	5	10	15
Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu			
	20	25	30
Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr			
	35	40	45
Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser			
	50	55	60
Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile			
	65	70	75
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val			
	85	90	95
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp			
	100	105	110
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg			
	115	120	125

Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu
 130 135 140
 Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser
 145 150 155 160
 Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg
 165 170 175
 Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg
 180 185 190
 Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu
 195 200 205
 Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp
 210 215 220
 Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile
 225 230 235 240
 Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met
 245 250 255
 Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
 260 265 270
 Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser
 275 280 285
 Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn
 290 295 300
 Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr
 305 310 315 320
 Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp
 325 330 335
 Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu
 340 345 350
 Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu
 355 360 365
 Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg
 370 375 380
 Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu
 385 390 395 400
 Arg Ala Ala Leu Lys Leu Ala
 405

<210> 243

<211> 669

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(646)

<223> RXA00780

<400> 243

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tcacgctggt agacttgccg gcatgctctc gacaataaaa atg atc cgt gaa gat 115
                                         Met Ile Arg Glu Asp
                                         1 5

ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
                        10 15 20

aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
                        25 30 35

gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
                        40 45 50

gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
                        55 60 65

acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
                        70 75 80 85

ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
                        90 95 100

acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
                        105 110 115

tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
                        120 125 130

acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
                        135 140 145

gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
                        150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643
Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr
                        170 175 180

att taagaacagt tagcgcccta cct 669
Ile

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<210> 244

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala
 1 5 10 15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile
 20 25 30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly
 35 40 45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu
 50 55 60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly
 65 70 75 80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met
 85 90 95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys
 100 105 110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys
 115 120 125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn
 130 135 140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile
 145 150 155 160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val
 165 170 175

Asp Pro Asp Tyr Tyr Ile
 180

<210> 245

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00779

<400> 245

cagaggccac ttcaagtaga tgtttcgtaa ttgtttacag cgtttacgca agcgggtcgac 60

caacaaaaac agcacttcaa tgattggagc accaccgcgac atg ggc aat gtg tac 115
 Met Gly Asn Val Tyr
 1 5

aac aac atc acc gaa acc atc ggc cac acc cca ctg gta aag ctg aac 163
 Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro Leu Val Lys Leu Asn

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc 1027
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile
 295 300 305

cgc gac taattcttag cgactgttaa cca 1056
 Arg Asp
 310

<210> 246

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro
 1 5 10 15

Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu
 20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
 35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro
 50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
 65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro
 85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala
 100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp
 115 120 125

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg
 130 135 140

Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala
 145 150 155 160

Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala
 165 170 175

Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys
 180 185 190

Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser

195					200					205					
Pro	Leu	Leu	Thr	Ala	Gly	Lys	Ala	Gly	Pro	His	Lys	Ile	Gln	Gly	Ile
210						215					220				
Gly	Ala	Asn	Phe	Ile	Pro	Glu	Val	Leu	Asp	Arg	Lys	Val	Leu	Asp	Asp
225					230					235					240
Val	Leu	Thr	Val	Ser	Asn	Glu	Asp	Ala	Ile	Ala	Phe	Ser	Arg	Lys	Leu
				245					250					255	
Ala	Thr	Glu	Glu	Gly	Ile	Leu	Gly	Gly	Ile	Ser	Thr	Gly	Ala	Asn	Ile
			260					265					270		
Lys	Ala	Ala	Leu	Asp	Leu	Ala	Ala	Lys	Pro	Glu	Asn	Ala	Gly	Lys	Thr
	275						280					285			
Ile	Val	Thr	Val	Val	Thr	Asp	Phe	Gly	Glu	Arg	Tyr	Val	Ser	Thr	Val
	290					295					300				
Leu	Tyr	Glu	Asp	Ile	Arg	Asp									
305					310										

<210> 247

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> RXN00402

<400> 247

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Thr	Asp	Glu	Lys	Asp	Gly	Lys	Pro	Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	
1				5					10				15			

gat	gct	gct	tac	cac	gga	ttg	aag	tac	gca	gac	ctt	ggt	gca	cca	gcc	96
Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	
			20					25					30			

ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	ctt	cta	cgc	gac	acc	ggc	tcc	acc	144
Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	
		35					40					45				

ctc	tcc	gca	ttc	aac	gca	tgg	gct	gca	gtc	cag	ggc	atc	gac	acc	ctt	192
Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	
	50					55					60					

tcc	ctg	cgc	ctg	gag	cgc	cac	aac	gaa	aac	gcc	atc	aag	gtt	gca	gaa	240
Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	
65					70				75					80		

ttc	ctc	aac	aac	cac	gag	aag	gtg	gaa	aag	gtt	aac	ttc	gca	ggc	ctg	288
Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	
				85					90					95		

aag	gat	tcc	cct	tgg	tac	gca	acc	aag	gaa	aag	ctt	ggc	ctg	aag	tac	336
Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr	

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      100              105              110
acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
      115              120              125

tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
      130              135              140

ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
      145              150              155              160

cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
      165              170              175

gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
      180              185              190

ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623
Leu Glu Gly Gly Phe Ala Ala Ile
      195              200

<210> 248
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 248
Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
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Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
      20              25              30

Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
      35              40              45

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
      50              55              60

Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
      65              70              75              80

Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
      85              90              95

Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
      100              105              110

Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
      115              120              125

Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
      130              135              140

Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser

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145 150 155 160

Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175

Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190

Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 249

<211> 599

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 249

gta ttg ccc tac ttc gtc act cca gat gct gct tac cac gga ttg aag 48
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
1 5 10 15

tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96
Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30

ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45

gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
50 55 60

gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
65 70 75 80

gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc 288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95

aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag 336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
100 105 110

atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
115 120 125

cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
130 135 140

cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala


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145              150              155              160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
              165              170              175

acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
              180              185              190

tagctttaaa tagactcacc cca 599

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<210> 250

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

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Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
              20              25              30

Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
              35              40              45

Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
  50              55              60

Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
  65              70              75              80

Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
              85              90              95

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
  100             105             110

Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
  115             120             125

Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
  130             135             140

His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
  145             150             155             160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
              165              170              175

Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
  180             185             190

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<211> 613

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(613)

<223> RXS00405

<400> 251

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ggagaagaat ttcctaataa aaactcttaa ggacctocaa atg cca aag tac gac 115
 Met Pro Lys Tyr Asp
 1 5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
 10 15 20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
 25 30 35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
 40 45 50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
 55 60 65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
 70 75 80 85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
 90 95 100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
 105 110 115

tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
 Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
 120 125 130

atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547
 Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
 135 140 145

gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
 150 155 160 165

aac cca cag gca gac gtc 613
 Asn Pro Gln Ala Asp Val
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<210> 252

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

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Arg  Ser  Ile  His  Ala  Gly  Gln  Ser  Val  Asp  Ala  Gln  Thr  Ser  Ala  Arg
          20          25          30

Asn  Leu  Pro  Ile  Tyr  Gln  Ser  Thr  Ala  Phe  Val  Phe  Asp  Ser  Ala  Glu
          35          40          45

His  Ala  Lys  Gln  Arg  Phe  Ala  Leu  Glu  Asp  Leu  Gly  Pro  Val  Tyr  Ser
          50          55          60

Arg  Leu  Thr  Asn  Pro  Thr  Val  Glu  Ala  Leu  Glu  Asn  Arg  Ile  Ala  Ser
          65          70          75          80

Leu  Glu  Gly  Gly  Val  His  Ala  Val  Ala  Phe  Ser  Ser  Gly  Gln  Ala  Ala
          85          90          95

Thr  Thr  Asn  Ala  Ile  Leu  Asn  Leu  Ala  Gly  Ala  Gly  Asp  His  Ile  Val
          100          105          110

Thr  Ser  Pro  Arg  Leu  Tyr  Gly  Gly  Thr  Glu  Thr  Leu  Phe  Leu  Ile  Thr
          115          120          125

Leu  Asn  Arg  Leu  Gly  Ile  Asp  Val  Ser  Phe  Val  Glu  Asn  Pro  Asp  Asp
          130          135          140

Pro  Glu  Ser  Trp  Gln  Ala  Ala  Val  Gln  Pro  Asn  Thr  Lys  Ala  Phe  Phe
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Gly  Glu  Thr  Phe  Ala  Asn  Pro  Gln  Ala  Asp  Val
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<211> 1812

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1789)

<223> RXC00164

<400> 253

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ggccagcctg ccgcaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115
                               Val Gly Arg Ile Pro
                               1          5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
          10          15          20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211

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Ala	Tyr	Ala	Ser	Val	Leu	Val	Pro	Gln	Val	Leu	Gly	Arg	Ile	Val	Asp	259
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Leu	Val	Ser	Asp	Gly	Ala	Gln	Met	Arg	Asp	Phe	Val	Glu	Leu	Ser	Val	
			25				30				35					
			40				45				50					
att	ctc	att	gcg	gtg	gca	att	gcc	ggc	gcg	gtg	ctc	agt	gcg	tgc	ggg	307
Ile	Leu	Ile	Ala	Val	Ala	Ile	Ala	Gly	Ala	Val	Leu	Ser	Ala	Cys	Gly	
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Phe	Tyr	Val	Val	Ser	Arg	Ile	Ser	Glu	Lys	Ile	Ile	Ala	Asn	Leu	Arg	
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			85													
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Glu	Asp	Met	Val	Gly	Thr	Ala	Leu	Gly	Leu	Pro	Thr	His	Gln	Val	Glu	
			90				95				100					
gat	gcg	ggc	tct	ggc	gat	ttg	gtg	agc	cgc	tcc	acc	gat	gat	gtc	tcc	451
Asp	Ala	Gly	Ser	Gly	Asp	Leu	Val	Ser	Arg	Ser	Thr	Asp	Asp	Val	Ser	
			105				110				115					
gag	cta	tcc	gca	gcg	gtg	aca	gag	acc	gtc	ccg	att	tta	agt	tcc	tca	499
Glu	Leu	Ser	Ala	Ala	Val	Thr	Glu	Thr	Val	Pro	Ile	Leu	Ser	Ser	Ser	
			120				125				130					
ctg	ttt	acc	att	gcc	gcg	acg	atc	att	gcg	ctg	ttt	tct	ttg	gac	tgg	547
Leu	Phe	Thr	Ile	Ala	Ala	Thr	Ile	Ile	Ala	Leu	Phe	Ser	Leu	Asp	Trp	
			135				140				145					
caa	ttt	gtg	ctc	att	cct	gtc	gtg	gtg	gcg	ccg	gtg	tac	tac	ttc	gcg	595
Gln	Phe	Val	Leu	Ile	Pro	Val	Val	Val	Ala	Pro	Val	Tyr	Tyr	Phe	Ala	
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			165													
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Ser	Lys	His	Tyr	Leu	Ser	Lys	Ala	Pro	Asp	Arg	Tyr	Ala	Ala	Glu	Arg	
			170				175				180					
gcg	gcg	atg	gcg	gag	cgt	gcg	cga	aag	gta	ctt	gag	gct	att	cgc	ggg	691
Ala	Ala	Met	Ala	Glu	Arg	Ala	Arg	Lys	Val	Leu	Glu	Ala	Ile	Arg	Gly	
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cgt	gca	act	gtg	cgg	gcg	tat	tcc	atg	gaa	gat	gcc	atg	cat	aat	cag	739
Arg	Ala	Thr	Val	Arg	Ala	Tyr	Ser	Met	Glu	Asp	Ala	Met	His	Asn	Gln	
			200				205				210					
att	gat	cag	gcg	tcg	tgg	tct	gtg	gtg	gtc	aag	ggt	att	cgt	gcg	cgc	787
Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys	Gly	Ile	Arg	Ala	Arg	
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acc	acc	atg	ttg	att	ttg	aac	atg	tgg	atg	ctg	ttt	gcg	gaa	ttc	ctc	835
Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu	Phe	Ala	Glu	Phe	Leu	
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			245													
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Met	Leu	Ala														

265							270							275							
ctg	cgt	ggc	ccg	atg	aat	atg	ttc	atg	cgc	gtg	ctc	gac	acc	att	caa	979					
Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val	Leu	Asp	Thr	Ile	Gln						
280							285							290							
tcc	ggc	tat	gcg	tcg	ctg	gcg	cgc	atc	gtg	gga	gtt	gtt	gcg	gat	ccg	1027					
Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly	Val	Val	Ala	Asp	Pro						
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ccg	att	cct	gtg	ccc	gac	agc	ggc	gtg	aaa	gca	cct	cag	ggc	aaa	gtg	1075					
Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala	Pro	Gln	Gly	Lys	Val						
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Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp	Ser	Trp	Ala	Val	Lys						
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gac	atc	gac	atc	acg	atc	aat	tcc	ggc	gaa	act	gtc	gcg	ctc	gtg	ggc	1171					
Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr	Val	Ala	Leu	Val	Gly						
345							350							355							
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Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala	Leu	Leu	Ala	Gly	Leu						
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cgg	gtg	cca	gat	caa	ggg	caa	gtg	ctt	gtc	gac	gac	ttc	ccc	gtc	tct	1267					
Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp	Asp	Phe	Pro	Val	Ser						
375							380							385							
cac	ctc	tct	gac	cgc	gag	cgt	atc	gcc	cgc	ttg	gcc	atg	gtc	agc	cag	1315					
His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu	Ala	Met	Val	Ser	Gln						
390							395							400							405
gag	gtt	cat	gtt	ttc	tcc	ggc	acg	ctg	cgc	cag	gat	ctc	acc	ttg	gct	1363					
Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln	Asp	Leu	Thr	Leu	Ala						
410							415							420							
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Lys	Pro	Asp	Ala	Ser	Asp	Glu	Glu	Leu	Ala	His	Ala	Leu	Gly	Gln	Val						
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Asn	Ala	Leu	Asp	Trp	Leu	Glu	Ser	Leu	Pro	Glu	Gly	Leu	Asp	Thr	Val						
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Val	Gly	Ala	Arg	Gly	Ile	Gln	Leu	Glu	Pro	Val	Val	Ala	Gln	Gln	Leu						
455							460							465							
gcg	ttg	gcc	cgg	gtg	ttg	ttg	ctc	aat	ccg	gcg	atc	gtc	atc	atg	gat	1555					
Ala	Leu	Ala	Arg	Val	Leu	Leu	Leu	Asn	Pro	Ala	Ile	Val	Ile	Met	Asp						
470							475							480							485
gaa	gcc	acg	gca	gaa	gca	gga	tcg	gcg	ggt	gcc	agc	gca	ctg	gaa	gag	1603					
Glu	Ala	Thr	Ala	Glu	Ala	Gly	Ser	Ala	Gly	Ala	Ser	Ala	Leu	Glu	Glu						
490							495							500							
gct	gca	gat	gca	gtg	agc	aag	aac	cgt	tcc	gca	ttg	gtg	gtg	gcg	cac	1651					
Ala	Ala	Asp	Ala	Val	Ser	Lys	Asn	Arg	Ser	Ala	Leu	Val	Val	Ala	His						
505							510							51							

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag 1699
 Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530

 ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg 1747
 Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545

 ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga 1789
 Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
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<211> 563

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 254

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 Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

 Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60

 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80

 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95

 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110

 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125

 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140

 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160

 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175

 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190

 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205

Ala	Met	His	Asn	Gln	Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys
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Gly	Ile	Arg	Ala	Arg	Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu
225					230					235					240
Phe	Ala	Glu	Phe	Leu	Met	Leu	Ala	Val	Ala	Leu	Val	Ile	Gly	Tyr	Lys
				245					250					255	
Leu	Val	Ile	Asp	Asn	Ala	Leu	Thr	Ile	Gly	Ala	Val	Thr	Gly	Ala	Val
			260					265					270		
Leu	Met	Ile	Ile	Arg	Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val
		275					280					285			
Leu	Asp	Thr	Ile	Gln	Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly
	290					295					300				
Val	Val	Ala	Asp	Pro	Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala
305					310					315					320
Pro	Gln	Gly	Lys	Val	Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp
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Ser	Trp	Ala	Val	Lys	Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr
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Val	Ala	Leu	Val	Gly	Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala
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Leu	Leu	Ala	Gly	Leu	Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp
	370					375					380				
Asp	Phe	Pro	Val	Ser	His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu
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Ala	Met	Val	Ser	Gln	Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln
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Asp	Leu	Thr	Leu	Ala	Lys	Pro	Asp	Ala	Ser	Asp	Glu	Glu	Leu	Ala	His
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	450					455					460				
Val	Ala	Gln	Gln	Leu	Ala	Leu	Ala	Arg	Val	Leu	Leu	Leu	Asn	Pro	Ala
465					470					475					480
Ile	Val	Ile	Met	Asp	Glu	Ala	Thr	Ala	Glu	Ala	Gly	Ser	Ala	Gly	Ala
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Ser	Ala	Leu	Glu	Glu	Ala	Ala	Asp	Ala	Val	Ser	Lys	Asn	Arg	Ser	Ala
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Leu	Val	Val	Ala	His	Arg	Leu	Asp	Gln	Ala	Ser	Arg	Ala	Asp	Gln	Ile
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Val Gly Gly Leu Val																5
1																
gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg																163
Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala																
10 15 20																
ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg																211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp																
25 30 35																
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg																259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu																
40 45 50																
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Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile																
55 60 65																
gaa acg gcg ggg cgc ggc gac gtg att tcg cgt atc gcg gat gat tcg																355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser																
70 75 80 85																
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag																403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln																
90 95 100																
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Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp																
105 110 115																
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc																499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr																
120 125 130																
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag																547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu																
135 140 145																

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Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tcg ctg atc cgc atg gtg ggc gtt att aac gcg	931
Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala	
265 270 275	
gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct	979
Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala	
280 285 290	
tta acg ctt ttc gac gtc tcc cac cac tat cac act gca ccc gtc atc	1027
Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile	
295 300 305	
aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg	1075
Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val	
310 315 320 325	
ggt gcg acc ggc gct ggt aaa agc acg ctc gcc ctc att gcg gca ggc	1123
Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly	
330 335 340	
ctg ctc agc cca act tcc ggg cag gtg gct ctc ggc gga tcg agt ttt	1171
Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe	
345 350 355	
tct aac gtc gaa ccg gaa gca ttg cgc cag aag atc gcg atg gtc agc	1219
Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser	
360 365 370	
caa gaa atc cac tgc ttc cga gga tct gtt tta gat aat ctt cgt atc	1267
Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile	
375 380 385	

gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat 1315
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp
 390 395 400 405

 att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc 1363
 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile
 410 415 420

 gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg 1411
 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met
 425 430 435

 gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat 1459
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp
 440 445 450

 gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat 1507
 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp
 455 460 465

 gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac 1555
 Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His
 470 475 480 485

 cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc 1603
 Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser
 490 495 500

 gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc 1651
 Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly
 505 510 515

 ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca 1700
 Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg
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 cccaagacca cgc 1713

<210> 256

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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Val Val Val Phe Ala Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser
 20 25 30

Leu Gly Thr Trp Trp Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro
 35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu
 50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg
 65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val

85																90				95			
Pro	Leu	Met	Val	Gln	Ala	Gly	Phe	Thr	Val	Val	Ile	Ser	Ala	Phe	Gly								
			100				105						110										
Met	Ala	Ala	Val	Asp	Trp	Arg	Leu	Gly	Leu	Val	Gly	Leu	Val	Ala	Ile								
			115				120						125										
Pro	Leu	Tyr	Trp	Thr	Thr	Leu	Arg	Val	Tyr	Leu	Pro	Arg	Ser	Gly	Pro								
			130				135						140										
Leu	Tyr	Thr	Arg	Glu	Arg	Glu	Ala	Phe	Gly	Val	Arg	Thr	Gln	Arg	Leu								
145				150						155			160										
Val	Gly	Ala	Val	Glu	Gly	Ala	Glu	Thr	Leu	Arg	Ala	Phe	Arg	Ala	Glu								
			165						170			175											
Asp	Thr	Glu	Leu	Lys	Arg	Ile	Asp	Ala	Ala	Ser	Gly	Glu	Ala	Arg	Asp								
			180			185						190											
Ile	Ser	Ile	Ser	Val	Phe	Arg	Phe	Leu	Thr	Trp	Ala	Phe	Ser	Arg	Asn								
			195			200						205											
Asn	Arg	Ala	Glu	Cys	Ile	Thr	Leu	Val	Leu	Ile	Leu	Gly	Thr	Gly	Phe								
			210			215						220											
Tyr	Leu	Val	Asn	Ile	Asp	Leu	Val	Thr	Val	Gly	Ala	Val	Ser	Thr	Ala								
225				230						235			240										
Ala	Leu	Ile	Phe	His	Arg	Leu	Phe	Gly	Pro	Ile	Gly	Thr	Leu	Val	Gly								
			245						250			255											
Met	Phe	Ser	Asp	Ile	Gln	Ser	Ala	Ser	Ala	Ser	Leu	Ile	Arg	Met	Val								
			260			265						270											
Gly	Val	Ile	Asn	Ala	Ala	Ser	Asn	Gln	Val	Ser	Gly	Thr	Ser	Pro	Ala								
			275			280						285											
Ser	Ala	Ser	Thr	Ala	Leu	Thr	Leu	Phe	Asp	Val	Ser	His	His	Tyr	His								
			290			295						300											
Thr	Ala	Pro	Val	Ile	Lys	Asn	Ala	Ser	Val	Gln	Leu	Glu	Pro	Gly	Glu								
305				310						315			320										
His	Ile	Ala	Ile	Val	Gly	Ala	Thr	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ala								
			325						330			335											
Leu	Ile	Ala	Ala	Gly	Leu	Leu	Ser	Pro	Thr	Ser	Gly	Gln	Val	Ala	Leu								
			340			345						350											
Gly	Gly	Ser	Ser	Phe	Ser	Asn	Val	Glu	Pro	Glu	Ala	Leu	Arg	Gln	Lys								
			355			360						365											
Ile	Ala	Met	Val	Ser	Gln	Glu	Ile	His	Cys	Phe	Arg	Gly	Ser	Val	Leu								
			370			375						380											
Asp	Asn	Leu	Arg	Ile	Ala	Arg	Pro	Glu	Ala	Thr	Asp	Ala	Asp	Ile	His								
385				390						395			400										
Ala	Val	Leu	Ala	Asp	Ile	Gly	Asp	Ser	Trp	Leu	Glu	Arg	Leu	Pro	Gln								
			405						410			415											

Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile
 485 490 495
 Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu
 500 505 510
 Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser
 515 520 525
 Ala Arg
 530

<210> 257

<211> 1392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1369)

<223> RXA02646

<400> 257

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catgagtgaa acatacgtgt ctgagaaaag tccaggagtg atg gct agc gga gcg 115
 Met Ala Ser Gly Ala
 1 5

gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163
 Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser
 10 15 20

tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211
 Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu
 25 30 35

gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259
 Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val
 40 45 50

cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307
 Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr
 55 60 65

caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355
 Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His

70	75				80				85				
gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc	403												
Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg													
	90				95				100				
atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg	451												
Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met													
	105				110				115				
gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc	499												
Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe													
	120				125				130				
gac gaa gca tgc gct gca gcg cat gaa gat gca gag cgc acc ggc gca	547												
Asp Glu Ala Ser Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala													
	135				140				145				
acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc	595												
Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly													
	150				155				160				
acc gtg gct gct gag atc ttg tgc cag ctg act tcc atg ggc aag agt	643												
Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser													
	170				175				180				
gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt	691												
Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly													
	185				190				195				
gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt	739												
Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly													
	200				205				210				
atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt	787												
Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly													
	215				220				225				
gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca	835												
Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala													
	230				235				240				
gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag	883												
Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln													
	250				255				260				
ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag	931												
Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu													
	265				270				275				
atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc	979												
Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly													
	280				285				290				
gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct	1027												
Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser													
	295				300				305				
gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat	1075												
Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr													
	310				315				320				
									325				

gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac 1123
 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr
 330 335 340

ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg 1171
 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu
 345 350 355

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc 1219
 Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu
 360 365 370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg 1267
 Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu
 375 380 385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg 1315
 Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser
 390 395 400 405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac 1363
 Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr
 410 415 420

ttg acc taaacatagc tgaaggccac ctc 1392
 Leu Thr

<210> 258

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala
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Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys
 20 25 30

Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu
 35 40 45

Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser
 50 55 60

Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala
 65 70 75 80

Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu
 85 90 95

Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys
 100 105 110

Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val
 115 120 125

Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala

130	135	140
Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr 145	150	155 160
Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr 165	170	175
Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly 180	185	190
Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg 195	200	205
Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala 210	215	220
Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe 225	230	235 240
Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile 245	250	255
Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly 260	265	270
Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile 275	280	285
Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser 290	295	300
Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn 305	310	315 320
Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg 325	330	335
Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln 340	345	350
Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr 355	360	365
Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu 370	375	380
Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu 385	390	395 400
Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr 405	410	415
Pro Glu Tyr Glu Tyr Leu Thr 420		

<210> 259

<211> 966

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(943)

<223> RXA00766

<400> 259

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ctacggcgggg tccatccggc aacaaaaccc caacctacca atg gtt ttt tgg gac 115
                               Met Val Phe Trp Asp
                               1                               5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile
                               10                               15                               20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys
                               25                               30                               35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp
                               40                               45                               50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn
                               55                               60                               65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser
                               70                               75                               80                               85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp
                               90                               95                               100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg
                               105                               110                               115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg
                               120                               125                               130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val
                               135                               140                               145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr
                               150                               155                               160                               165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg
                               170                               175                               180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys
                               185                               190                               195

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gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787
Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu
215 220 225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835
Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu
230 235 240 245

gtg	tcc	tcc	gtc	cgc	gga	cca	gtt	cgg	gtg	acc	agg	ctc	gat	gga	cac	883
Val	Ser	Ser	Val	Arg	Gly	Pro	Val	Arg	Val	Thr	Arg	Leu	Asp	Gly	His	
				250					255					260		

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931
Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr
265 270 275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966
Lys Ala Leu Gly
280

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Val Phe Trp Asp Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe
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Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His
20 25 30

Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro
35 40 45

Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp
50 55 60

Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser
65 70 75 80

Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr
85 90 95

Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val
100 105 110

Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile
115 120 125

Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala
130 135 140

Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met
145 150 155 160

Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe
 165 170 175

Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser
 180 185 190

Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu
 195 200 205

Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly
 210 215 220

Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala
 225 230 235 240

Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr
 245 250 255

Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile
 260 265 270

Lys Ala Leu Ile Thr Lys Ala Leu Gly
 275 280

<210> 261

<211> 1224

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1201)

<223> RXN01690

<400> 261

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 Met Thr Ser Leu Glu
 1 5

ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163
 Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys
 10 15 20

gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211
 Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met
 25 30 35

gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259
 Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu
 40 45 50

gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307
 Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His
 55 60 65

tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355
 Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp
 70 75 80 85

gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag	403
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln	
90 95 100	
cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt	451
Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe	
105 110 115	
att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct	499
Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro	
120 125 130	
gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc	547
Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser	
135 140 145	
acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg	595
Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu	
150 155 160 165	
gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct	643
Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro	
170 175 180	
gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga	691
Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly	
185 190 195	
act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc	739
Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala	
200 205 210	
cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat	787
Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp	
215 220 225	
gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg	835
Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly	
230 235 240 245	
ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt	883
Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu	
250 255 260	
tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta	931
Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val	
265 270 275	
gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc	979
Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr	
280 285 290	
gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct	1027
Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala	
295 300 305	
tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct	1075
Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala	
310 315 320 325	

cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg 1123
 His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac 1171
 Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga 1221
 Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

ccc 1224

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<211> 367

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
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Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln

BGI-121CP
 1123
 1171
 1221
 1224
 262
 367
 PRT
 Corynebacterium glutamicum
 262
 1
 5
 10
 15
 20
 25
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 35
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 45
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 200
 205

210	215	220
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly		
225	230	235 240
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu		
	245	250 255
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys		
	260	265 270
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg		
	275	280 285
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met		
	290	295 300
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly		
305	310	315 320
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val		
	325	330 335
Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln		
	340	345 350
Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly		
	355	360 365

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1053)
 <223> FRXA01690

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Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe	
1 5 10 15	
ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg	96
Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp	
20 25 30	
cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc	144
His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala	
35 40 45	
acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc	192
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala	
50 55 60	
tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac	240
Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn	
65 70 75 80	

gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg 288
 Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 85 90 95

cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat 336
 Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 100 105 110

cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc 384
 Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 115 120 125

cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat 432
 Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 130 135 140

gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc 480
 Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 145 150 155 160

ggt gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc 528
 Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 165 170 175

gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg 576
 Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 180 185 190

gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag 624
 Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 195 200 205

gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt 672
 Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
 210 215 220

ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta 720
 Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
 225 230 235 240

gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag 768
 Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 245 250 255

tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga 816
 Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 260 265 270

aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg 864
 Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 275 280 285

acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc 912
 Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 290 295 300

acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc 960
 Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 305 310 315 320

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa 1008

taaatcaacc ggttttaaga ccc 1076

<210> 264
<211> 351
<212> PRT
<213> Corynebacterium glutamicum

<400> 264															
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Phe	Thr	Asp	His 20	Met	Val	Thr	Ile	Asp 25	Trp	Asn	Glu	Ser	Glu 30	Gly	Trp
His	Asn	Ala 35	Gln	Leu	Val	Pro	Tyr 40	Ala	Pro	Ile	Pro	Met 45	Asp	Pro	Ala
Thr	Thr 50	Val	Phe	His	Tyr	Gly 55	Gln	Ala	Ile	Phe	Glu 60	Gly	Ile	Lys	Ala
Tyr 65	Arg	His	Ser	Asp 70	Glu	Thr	Ile	Lys	Thr	Phe 75	Arg	Pro	Asp	Glu	Asn 80
Ala	Glu	Arg	Met	Gln 85	Arg	Ser	Ala	Ala	Arg 90	Met	Ala	Met	Pro	Gln 95	Leu
Pro	Thr	Glu	Asp 100	Phe	Ile	Lys	Ala 105	Leu	Glu	Leu	Leu	Val 110	Asp	Ala	Asp
Gln	Asp	Trp 115	Val	Pro	Glu	Tyr	Gly 120	Gly	Glu	Ala	Ser	Leu 125	Tyr	Leu	Arg
Pro	Phe 130	Met	Ile	Ser	Thr	Glu 135	Ile	Gly	Leu	Gly	Val 140	Ser	Pro	Ala	Asp
Ala 145	Tyr	Lys	Phe	Leu 150	Val	Ile	Ala	Ser	Pro	Val 155	Gly	Ala	Tyr	Phe	Thr 160
Gly	Gly	Ile	Lys 165	Pro	Val	Ser	Val	Trp	Leu 170	Ser	Glu	Asp	Tyr	Val 175	Arg
Ala	Ala	Pro	Gly 180	Gly	Thr	Gly	Asp 185	Ala	Lys	Phe	Ala	Gly	Asn 190	Tyr	Ala
Ala	Ser	Leu 195	Leu	Ala	Gln	Ser	Gln 200	Ala	Ala	Glu	Lys	Gly 205	Cys	Asp	Gln
Val 210	Val	Trp	Leu	Asp	Ala	Ile 215	Glu	His	Lys	Tyr	Ile 220	Glu	Glu	Met	Gly
Gly 225	Met	Asn	Leu	Gly 230	Phe	Ile	Tyr	Arg	Asn 235	Gly	Asp	Gln	Val	Lys	Leu 240

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 245 250 255

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 260 265 270

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 275 280 285

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 290 295 300

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 305 310 315 320

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 325 330 335

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 340 345 350

<210> 265
 <211> 1782
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1759)
 <223> RXN01026

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tatagtgaga tttacagatt tttaaaggac ggtgagttcc atg acc agc ccc gtg 115
 Met Thr Ser Pro Val
 1 5

gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg 163
 Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp
 10 15 20

cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc 211
 Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu
 25 30 35

tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt 259
 Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe
 40 45 50

gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac 307
 Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His
 55 60 65

ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc 355
 Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys Thr Gly
 70 75 80 85

tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta tct act 403
 Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val Ser Thr

90										95										100									
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggt	451													
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly														
			105					110					115																
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499													
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala														
			120					125					130																
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggg	gac	tcc	cac	acc	tcc	acc	547													
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr														
			135					140					145																
cac	ggg	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggg	acc	tca	gag	gtt	595													
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val														
150						155					160		165																
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643													
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr														
			170					175						180															
atg	gcc	att	gaa	gtt	act	ggg	gaa	ctg	cag	cca	ggg	gtt	tcc	tcc	aag	691													
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys														
			185					190					195																
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739													
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln														
			200					205					210																
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787													
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met														
			215		220						225																		
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835													
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg														
230						235					240		245																
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883													
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly														
			250					255						260															
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931													
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr														
			265					270					275																
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979													
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val														
			280		285						290																		
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac	1027													
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn														
			295		300						305																		
cca	ggc	cag	ggc	ctg	cca	ctg	ggc	gaa	tcc	gta	cca	agc	cca	gaa	gac	1075													
Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro	Glu	Asp														
310						315		320						325															
ttc	acc	aac	gac	aac	gac	aag	gca	gca	gcc	gaa	aag	gca	ctg	cag	tac	1123													
Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu	Lys	Ala	Leu	Gln	Tyr														
			330					335						340															

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atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc 1171
Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr
      345                      350                      355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc 1219
Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile
      360                      365                      370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg 1267
Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met
      375                      380                      385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc 1315
Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu
390                      395                      400                      405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca 1363
Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala
      410                      415                      420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc 1411
Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly
      425                      430                      435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga 1459
Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly
      440                      445                      450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc 1507
Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr
      455                      460                      465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga 1555
Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg
470                      475                      480                      485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc 1603
Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys
      490                      495                      500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca 1651
Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser
      505                      510                      515

agc gcg tca ccc gga ccg gct tgc aag acg gac tgt ttt cca act ggc 1699
Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly
      520                      525                      530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg 1747
Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr
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gct ccg ttc tgc tagcaggccc tgactttggc acc 1782
Ala Pro Phe Ser
550

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<210> 266

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

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Met Thr Ser Pro Val Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu
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Ala Glu Lys Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly
      20           25           30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr
      35           40           45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg
      50           55           60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu
      65           70           75           80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg
      85           90           95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg
      100           105           110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly
      115           120           125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp
      130           135           140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile
      145           150           155           160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu
      165           170           175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro
      180           185           190

Gly Val Ser Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly
      195           200           205

Thr Gly Gly Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile
      210           215           220

Arg Lys Met Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile
      225           230           235           240

Glu Ala Gly Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe
      245           250           255

Asp Tyr Val Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp
      260           265           270

Glu Ala Val Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr
      275           280           285

Phe Asp Lys Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile
      290           295           300

Thr Trp Gly Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val

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305          310          315          320
Pro Ser Pro Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu
          325          330          335
Lys Ala Leu Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp
          340          345          350
Ile Lys Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile
          355          360          365
Glu Asp Leu Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala
          370          375          380
Asp Gly Met Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln
385          390          395          400
Glu Ala Glu Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala
          405          410          415
Glu Trp Arg Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp
          420          425          430
Gln Leu Lys Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe
          435          440          445
Glu Gly Arg Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala
          450          455          460
Val Ala Ala Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr
465          470          475          480
Leu Arg Lys Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala
          485          490          495
Leu Ala Phe His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser
          500          505          510
Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp
          515          520          525
Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro
          530          535          540
Thr Pro Thr Arg Thr Ala Pro Phe Ser
545          550

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<210> 267

<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1602)

<223> FRXA01026

<400> 267

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gtg tgg cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac 48
Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp

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ctc	ctc	tac	atc	gac	ctg	cag	ctg	ctg	cat	gaa	gtg	acc	tca	cca	cag	96
Leu	Leu	Tyr	Ile	Asp	Leu	Gln	Leu	Leu	His	Glu	Val	Thr	Ser	Pro	Gln	
20				25				30								
gca	ttt	gac	ggc	ctg	cgc	atg	acc	ggc	cgt	aaa	ctg	cgc	cac	cca	gaa	144
Ala	Phe	Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	Leu	Arg	His	Pro	Glu	
35				40				45								
ctg	cac	ctg	gcc	acc	gaa	gac	cac	aac	gtg	cca	acc	gaa	ggc	atc	aag	192
Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	
50				55				60								
act	ggc	tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	240
Thr	Gly	Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	
65				70				75				80				
tct	act	ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	288
Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	
85				90				95								
atg	ggc	gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	336
Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	
100				105				110								
ggc	gca	acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	384
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	
115				120				125								
tcc	acc	cac	ggt	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggt	acc	tca	432
Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	
130				135				140								
gag	gtt	gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	480
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	
145				150				155				160				
aag	acc	atg	gcc	att	gaa	gtt	act	ggt	gaa	ctg	cag	cca	ggt	gtt	tcc	528
Lys	Thr	Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	
165				170				175								
tcc	aag	gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	576
Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	
180				185				190								
gga	cag	ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	624
Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	
195				200				205								
tcc	atg	gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	672
Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	
210				215				220								
gca	cgt	gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	720
Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	
225				230				235				240				
gaa	ggc	cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	768
Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	
245				250				255								

gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag 816
 Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys
 260 265 270

gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc 864
 Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly
 275 280 285

acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca 912
 Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro
 290 295 300

gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg 960
 Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu
 305 310 315 320

cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc 1008
 Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile
 325 330 335

gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg 1056
 Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu
 340 345 350

cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg 1104
 Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365

cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa 1152
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt 1200
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag 1248
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc 1296
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc 1344
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag 1392
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc 1440
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct 1488
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca 1536
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca 1584
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525

aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc 1625
 Arg Thr Ala Pro Phe Ser
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<210> 268

<211> 534

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 268

Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp
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Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln
 20 25 30

Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu
 35 40 45

Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys
 50 55 60

Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val
 65 70 75 80

Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro
 85 90 95

Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu
 100 105 110

Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr
 115 120 125

Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser
 130 135 140

Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe
 145 150 155 160

Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser
 165 170 175

Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly
 180 185 190

Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met
 195 200 205

Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly
 210 215 220

Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val
 225 230 235 240
 Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val
 245 250 255
 Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys
 260 265 270
 Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly
 275 280 285
 Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro
 290 295 300
 Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu
 305 310 315 320
 Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile
 325 330 335
 Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu
 340 345 350
 Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525
 Arg Thr Ala Pro Phe Ser
 530

<210> 269
 <211> 1143
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(1120)
 <223> RXN01127

<400> 269
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 cactagtgaag gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
 25 30 35
 ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259
 Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp
 40 45 50
 ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307
 Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly
 55 60 65
 gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355
 Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu
 70 75 80 85
 aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403
 Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys
 90 95 100
 ctg tac gac ggc gtg gag tcc cca ctg cgt aac cca ggc aag att gat 451
 Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn Pro Gly Lys Ile Asp
 105 110 115
 ttc gtt gtg gtc cgc gaa ggt acc gaa ggc gcc tac act ggc aac ggt 499
 Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala Tyr Thr Gly Asn Gly
 120 125 130
 gga gca atc cgc gtg gga acc cct cac gag att gcc aat gaa acc tcc 547
 Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile Ala Asn Glu Thr Ser
 135 140 145
 gtg aac act cgc tac ggc gct gag cgc gtt att cgc tac gca ttc gag 595
 Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile Arg Tyr Ala Phe Glu
 150 155 160 165
 ctg gca cag agc cgc cgc aag aag ctc acc ctc gtg cac aag acc aac 643
 Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu Val His Lys Thr Asn
 170 175 180

gtc ctg gtt cac ggt ggt ggc ctg tgg cag cgc acc gta gat gag gtt 691
 Val Leu Val His Gly Gly Gly Leu Trp Gln Arg Thr Val Asp Glu Val
 185 190 195

 gca aag gaa tac cca gag gta gcc gtc gat tac aac cac atc gat gca 739
 Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr Asn His Ile Asp Ala
 200 205 210

 gca acc atc tat ctg gtc act gat cct tcc cgc ttc gat gtg att gtt 787
 Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg Phe Asp Val Ile Val
 215 220 225

 acc gat aac ctc ttc ggc gac atc ctc acc gat gag gca ggc gca gtc 835
 Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp Glu Ala Gly Ala Val
 230 235 240 245

 tct ggc gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc 883
 Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly
 250 255 260

 acc aac cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc 931
 Thr Asn Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile
 265 270 275

 gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala
 280 285 290

 atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa 1027
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu
 295 300 305

 aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att 1075
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile
 310 315 320 325

 tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc 1120
 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
 330 335 340

 taaatttcaa cgccgacccc ctt 1143

<210> 270

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
 1 5 10 15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
 20 25 30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
 65 70 75 80
 Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95
 Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn
 100 105 110
 Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
 115 120 125
 Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile
 130 135 140
 Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile
 145 150 155 160
 Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu
 165 170 175
 Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Leu Trp Gln Arg
 180 185 190
 Thr Val Asp Glu Val Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr
 195 200 205
 Asn His Ile Asp Ala Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg
 210 215 220
 Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp
 225 230 235 240
 Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
 245 250 255
 Ile Asp Ala Thr Gly Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
 260 265 270
 Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
 275 280 285
 Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
 290 295 300
 Ala Val Arg Ile Glu Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp
 305 310 315 320
 Asn Ser Gln Pro Ile Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys
 325 330 335
 Ala Leu Gln Ser
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<210> 271

<211> 403

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> FRXA01132

<400> 271

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cactagtgaag gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
 Met Lys Leu Ala Val
 1 5

att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20

gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
 25 30 35

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259
 Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp
 40 45 50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307
 Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly
 55 60 65

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355
 Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu
 70 75 80 85

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403
 Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys
 90 95 100

<210> 272

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
 1 5 10 15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
 20 25 30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
 65 70 75 80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95

Leu Arg Pro Ser Lys

100

<210> 273

<211> 1494

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00536

<400> 273

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tcgtggaccc	acccaaaact	ttttaagaag	gttgaacaca	atg	tct	cct	aac	gat	115
				Met	Ser	Pro	Asn	Asp	
				1				5	

gca	ttc	atc	tcc	gca	cct	gcc	aag	atc	gaa	acc	cca	gtt	ggg	cct	cgc	163
Ala	Phe	Ile	Ser	Ala	Pro	Ala	Lys	Ile	Glu	Thr	Pro	Val	Gly	Pro	Arg	
			10					15					20			

aac	gaa	ggc	cag	cca	gca	tgg	aat	aag	cag	cgt	ggc	tcc	tca	atg	cca	211
Asn	Glu	Gly	Gln	Pro	Ala	Trp	Asn	Lys	Gln	Arg	Gly	Ser	Ser	Met	Pro	
			25					30				35				

gtt	aac	cgc	tac	atg	cct	ttc	gag	gtt	gag	gta	gaa	gat	att	tct	ctg	259
Val	Asn	Arg	Tyr	Met	Pro	Phe	Glu	Val	Glu	Val	Glu	Asp	Ile	Ser	Leu	
			40				45					50				

cgc	gac	cgc	act	tgg	cca	gat	aaa	aaa	atc	acc	gtt	gca	cct	cag	tgg	307
Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	Val	Ala	Pro	Gln	Trp	
	55					60					65					

tgt	gct	gtt	gac	ctg	cgt	gac	ggc	aac	cag	gct	ctg	att	gat	cgc	atg	355
Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	Leu	Ile	Asp	Pro	Met	
70					75				80						85	

tct	cct	gag	cgt	aag	cgc	cgc	atg	ttt	gag	ctg	ctg	gtt	cag	atg	ggc	403
Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	Leu	Val	Gln	Met	Gly	
				90					95				100			

ttc	aaa	gaa	atc	gag	gtc	ggc	ttc	cct	tca	gct	tcc	cag	act	gat	ttt	451
Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	Ser	Gln	Thr	Asp	Phe	
			105					110					115			

gat	ttc	gtt	cgt	gag	atc	atc	gaa	aag	ggc	atg	atc	cct	gac	gat	gtc	499
Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	Ile	Pro	Asp	Asp	Val	
		120					125					130				

acc	att	cag	gtt	ctg	gtt	cag	gct	cgt	gag	cac	ctg	att	cgc	cgt	act	547
Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	Leu	Ile	Arg	Arg	Thr	
	135					140					145					

ttt	gaa	gct	tgc	gaa	ggc	gca	aaa	aac	gtt	atc	gtg	cac	ttc	tac	aac	595
Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	Val	His	Phe	Tyr	Asn	
150					155					160					165	

tcc	acc	tcc	atc	ctg	cag	cgc	aac	gtg	gtg	ttc	cgc	atg	gac	aag	gtg	643
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Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931
Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu	
265 270 275	
tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag	979
Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu	
280 285 290	
ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc	1027
Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly	
295 300 305	
aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac	1075
Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn	
310 315 320 325	
atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc	1123
Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg	
330 335 340	
cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag	1171
Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu	
345 350 355	
cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc	1219
Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser	
360 365 370	
cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt	1267
His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val	
375 380 385	
cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac	1315
Gln Pro Gly Ala Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp	
390 395 400 405	
acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg	1363
Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg	

410	415	420	
tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg			1411
Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly			
425	430	435	
cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg			1459
Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser			
440	445	450	
ctc cat gca ggt tgagttctcc accgttgtcc aga			1494
Leu His Ala Gly			
455			

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val			
35	40	45	
Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr			
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Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala			
65	70	75	80
Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu			
85	90	95	
Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala			
100	105	110	
Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met			
115	120	125	
Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His			
130	135	140	
Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile			
145	150	155	160
Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe			
165	170	175	
Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu			
180	185	190	
Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp			
195	200	205	
Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys			

210	215	220
Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn		
225	230	235 240
Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn		
	245	250 255
Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg		
	260	265 270
Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly		
	275	280 285
Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu		
	290	295 300
Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val		
305	310	315 320
Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp		
	325	330 335
Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln		
	340	345 350
Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr		
	355	360 365
Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala		
	370	375 380
Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp		
385	390	395 400
Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg		
	405	410 415
Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu		
	420	425 430
Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg		
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Ser Ala Asp Pro Ser Leu His Ala Gly		
450	455	

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<211> 1333

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> FRXA00536

<400> 275

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gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163								
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg									
10 15 20									
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211								
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro									
25 30 35									
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259								
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu									
40 45 50									
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307								
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp									
55 60 65									
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355								
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met									
70 75 80 85									
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403								
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly									
90 95 100									
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451								
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe									
105 110 115									
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499								
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val									
120 125 130									
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547								
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr									
135 140 145									
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595								
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn									
150 155 160 165									
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643								
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val									
170 175 180									
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691								
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile									
185 190 195									
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739								
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu									
200 205 210									
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787								
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala									
215 220 225									
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835								

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Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn
230                               235                               240                               245

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc      883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
                               250                               255                               260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg      931
Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
                               265                               270                               275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag      979
Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
                               280                               285                               290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc      1027
Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
                               295                               300                               305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac      1075
Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
310                               315                               320                               325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc      1123
Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
                               330                               335                               340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag      1171
Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
                               345                               350                               355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc      1219
Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
                               360                               365                               370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt      1267
His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
                               375                               380                               385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac      1315
Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
390                               395                               400                               405

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Thr Glu Trp Glu Val Pro
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<210> 276
<211> 411
<212> PRT
<213> Corynebacterium glutamicum

<400> 276
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Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
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Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

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35					40					45					
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Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala
	65					70					75				80
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu
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Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala
			100					105					110		
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met
		115					120					125			
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His
	130					135					140				
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile
	145					150					155				160
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe
				165					170					175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu
			180					185					190		
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp
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Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys
	210					215					220				
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn
	225					230					235				240
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn
				245					250					255	
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg
			260					265					270		
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly
		275					280					285			
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu
	290					295					300				
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val
	305					310					315				320
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp
				325					330					335	
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln
			340					345					350		
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr
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Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
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Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro
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<210> 277

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

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Met Glu Lys Phe Thr
1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163
Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr
10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211
Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly
25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259
Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe
40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307
Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly
55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355
Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu
70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403
Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile
90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451
Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu
105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499
Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly
120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp
 135 140 145
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met
 150 155 160 165
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile
 170 175 180
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala
 185 190 195
 taagtttcag tctgatagcg aaa 714

<210> 278

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

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 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
 20 25 30
 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln
 35 40 45
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser
 50 55 60
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His
 65 70 75 80
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser
 85 90 95
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu
 100 105 110
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met
 115 120 125
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile
 130 135 140
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile
 145 150 155 160
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg
 165 170 175
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys
 180 185 190
 Pro Arg Thr Asn Ala

gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala
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<210> 279
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(913)
<223> RXN01929
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										Met		Pro		Met		Ser		Gly
										1						5		
att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta		163																
Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val																		
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		15																
		20																
aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg		211																
Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala																		
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		30																
		35																
cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc		259																
Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser																		
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		45																
		50																
gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg		307																
Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu																		
		55																
		60																
		65																
gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt		355																
Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg																		
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		75																
		80																
		85																
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Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro																		
		90																
		95																
		100																
aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg		451																
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala																		
		105																
		110																
		115																
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Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg																		
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		125																
		130																
cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc		547																
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr																		
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		140																
		145																
ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc		595																
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly																		
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		155																
		160																
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gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg		643																

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
170 175 180

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Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
250 255 260

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Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
265 270

aag 936

<210> 280
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<212> PRT
<213> Corynebacterium glutamicum

<400> 280
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

130 135 140
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
 145 150 155 160
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
 165 170 175
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
 180 185 190
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
 195 200 205
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
 210 215 220
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
 225 230 235 240
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
 245 250 255
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265 270

 <210> 281
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(907)
 <223> FRXA01929

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 Met Ser Gly Ile Asp
 1 5

 gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc 163
 Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly
 10 15 20

 cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att 211
 Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile
 25 30 35

 ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc 259
 Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala
 40 45 50

 aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag 307
 Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu
 55 60 65

 atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt 355

Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu
 70 75 80 85

gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag 403
 Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln
 90 95 100

gcg gtg gag tcc gcg atc ccg gtc atg cgt gaa acg ggt gcg gct gcg 451
 Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala
 105 110 115

gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att 499
 Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile
 120 125 130

gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag 547
 Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln
 135 140 145

tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt 595
 Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser
 150 155 160 165

tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg 643
 Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala
 170 175 180

ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt 691
 Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val
 185 190 195

acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc 739
 Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly
 200 205 210

aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc 787
 Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg
 215 220 225

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
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<210> 282

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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 20 25 30
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 283

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXN01420

<400> 283

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gcggaatgcg ctgctcatcc acacgtggaa tcctgattgg gtg acg ctg ggt gga 115
 Val Thr Leu Gly Gly
 1 5

ttg aat gta cca tcg tgg tcg ctg ggc gcg gaa atg ctg ttc tac ctg 163
 Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu Met Leu Phe Tyr Leu
 10 15 20

acg ttc ccg ctg ttt att ccg tta gtg cgc aaa gtg aag ggc gtg ggc 211
 Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys Val Lys Gly Val Gly
 25 30 35

aac tgg tgg gca ttt ggc atc acc ttt gcc gtg agc ctg gcg ctg att 259
 Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val Ser Leu Ala Leu Ile
 40 45 50

aca gtg att cac ttt tat gcg gac gga cca aag ggg att gag aac ttc 307
 Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys Gly Ile Glu Asn Phe
 55 60 65

ttt gtt cct cgc ctg tgg gac acc aat gtg tca ccg gtc gcg gaa gtt 355
 Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser Pro Val Ala Glu Val
 70 75 80 85

cac gcc gat cca gtg tgg ttt atg cag gaa gaa att ccc gtg ctg gaa 403
 His Ala Asp Pro Val Trp Phe Met Gln Glu Glu Ile Pro Val Leu Glu
 90 95 100

tct tac tgg ctg tct tac tac ttc ccg ctg acc aga ctc atc gag ttc 451
 Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr Arg Leu Ile Glu Phe
 105 110 115

tac ctc ggt gtg ttt ggc gcg aag ctg gtt gct gaa ggc atg ttt aaa 499
 Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala Glu Gly Met Phe Lys
 120 125 130

aac acc aac atc acc atc ccg ctg atc gca ctg gct gtt tct ttt gtt 547
 Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu Ala Val Ser Phe Val
 135 140 145

gct act tgg ttt gtg cca ctg gca ttc aag atg tct gtc atc atg tcc 595
 Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met Ser Val Ile Met Ser
 150 155 160 165

ctg cca atg gct ttt gtt gtg gca acg ctt gcg gtg aga gac att gaa 643
 Leu Pro Met Ala Phe Val Val Ala Thr Leu Ala Val Arg Asp Ile Glu
 170 175 180

ggc aag agt ggg gaa atc gcc tcg cct cgc gca gtt ttg ttg ggt aat 691
 Gly Lys Ser Gly Glu Ile Ala Ser Pro Arg Ala Val Leu Leu Gly Asn
 185 190 195

att tcc ttt gcc ttc tac atg gtg caa ttc ccc gtc atg gtg ttt gtg 739
 Ile Ser Phe Ala Phe Tyr Met Val Gln Phe Pro Val Met Val Phe Val
 200 205 210

cag cgc tat ttc att gct ggc aaa gaa tac ggc ttc ctt ggc tgg gca 787
 Gln Arg Tyr Phe Ile Ala Gly Lys Glu Tyr Gly Phe Leu Gly Trp Ala
 215 220 225

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ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg      835
Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val
230                      235                      240                      245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag      883
Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys
                      250                      255                      260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg      931
Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu
                      265                      270                      275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act      979
Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr
                      280                      285                      290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct      1027
Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala
                      295                      300                      305

acc gga atc aaa tct tagggaagga aaacatatgg cta                        1065
Thr Gly Ile Lys Ser
310

<210> 284
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 284
Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu
  1                      5                      10                      15

Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys
                      20                      25                      30

Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val
  35                      40                      45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys
  50                      55                      60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser
  65                      70                      75                      80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu
                      85                      90                      95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr
  100                      105                      110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala
  115                      120                      125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu
  130                      135                      140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met
  145                      150                      155                      160

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Ser Val Ile Met Ser Leu Pro Met Ala Phe Val Val Ala Thr Leu Ala
 165 170 175

Val Arg Asp Ile Glu Gly Lys Ser Gly Glu Ile Ala Ser Pro Arg Ala
 180 185 190

Val Leu Leu Gly Asn Ile Ser Phe Ala Phe Tyr Met Val Gln Phe Pro
 195 200 205

Val Met Val Phe Val Gln Arg Tyr Phe Ile Ala Gly Lys Glu Tyr Gly
 210 215 220

Phe Leu Gly Trp Ala Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val
 225 230 235 240

Ile Leu Ala Trp Val Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys
 245 250 255

Ala Thr Ala Arg Lys Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile
 260 265 270

Leu Val Arg Asp Leu Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro
 275 280 285

Leu Lys Val Glu Thr Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala
 290 295 300

Pro Ala Lys Val Ala Thr Gly Ile Lys Ser
 305 310

<210> 285

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 285

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cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser	Ala	Glu	Lys	Ala	Lys	Glu	Ala	Gly	Phe	Glu	Val	Lys	Thr	Thr	Ala	
55						60					65					
gag	gct	gca	gct	tgg	gct	gac	gtc	atc	atg	ctc	ctg	gct	cca	gac	acc	355
Glu	Ala	Ala	Ala	Trp	Ala	Asp	Val	Ile	Met	Leu	Leu	Ala	Pro	Asp	Thr	
70					75					80					85	
tcc	cag	gca	gaa	atc	ttc	acc	aac	gac	atc	gag	cca	aac	ctg	aac	gca	403
Ser	Gln	Ala	Glu	Ile	Phe	Thr	Asn	Asp	Ile	Glu	Pro	Asn	Leu	Asn	Ala	
				90					95					100		
ggc	gac	gca	ctg	ctg	ttc	ggc	cac	ggc	ctg	aac	att	cac	ttc	gac	ctg	451
Gly	Asp	Ala	Leu	Leu	Phe	Gly	His	Gly	Leu	Asn	Ile	His	Phe	Asp	Leu	
			105					110					115			
atc	aag	cca	gct	gac	gac	atc	atc	gtt	ggc	atg	gtt	gcg	cca	aag	ggc	499
Ile	Lys	Pro	Ala	Asp	Asp	Ile	Ile	Val	Gly	Met	Val	Ala	Pro	Lys	Gly	
		120					125					130				
cca	ggc	cac	ttg	gtt	cgc	cgt	cag	ttc	gtt	gat	ggc	aag	ggc	gtt	cct	547
Pro	Gly	His	Leu	Val	Arg	Arg	Gln	Phe	Val	Asp	Gly	Lys	Gly	Val	Pro	
	135					140					145					
tgc	ctc	atc	gca	gtc	gac	cag	gac	cca	acc	gga	acc	gca	cag	gct	ctg	595
Cys	Leu	Ile	Ala	Val	Asp	Gln	Asp	Pro	Thr	Gly	Thr	Ala	Gln	Ala	Leu	
150					155					160					165	
acc	ctg	tcc	tac	gca	gca	gca	atc	ggt	ggc	gca	cgc	gca	ggc	gtt	atc	643
Thr	Leu	Ser	Tyr	Ala	Ala	Ala	Ile	Gly	Gly	Ala	Arg	Ala	Gly	Val	Ile	
				170					175					180		
cca	acc	acc	ttc	gaa	gct	gag	acc	gtc	acc	gac	ctc	ttc	ggc	gag	cag	691
Pro	Thr	Thr	Phe	Glu	Ala	Glu	Thr	Val	Thr	Asp	Leu	Phe	Gly	Glu	Gln	
			185					190					195			
gct	gtt	ctc	tgc	ggc	ggc	acc	gag	gaa	ctg	gtc	aag	gtt	ggc	ttc	gag	739
Ala	Val	Leu	Cys	Gly	Gly	Thr	Glu	Glu	Leu	Val	Lys	Val	Gly	Phe	Glu	
		200					205					210				
gtt	ctc	acc	gaa	gct	ggc	tac	gag	cca	gag	atg	gca	tac	ttc	gag	gtt	787
Val	Leu	Thr	Glu	Ala	Gly	Tyr	Glu	Pro	Glu	Met	Ala	Tyr	Phe	Glu	Val	
	215					220					225					
ctt	cac	gag	ctc	aag	ctc	atc	gtt	gac	ctc	atg	ttc	gaa	ggc	ggc	atc	835
Leu	His	Glu	Leu	Lys	Leu	Ile	Val	Asp	Leu	Met	Phe	Glu	Gly	Gly	Ile	
230					235					240					245	
agc	aac	atg	aac	tac	tct	gtt	tct	gac	acc	gct	gag	ttc	ggc	ggc	tac	883
Ser	Asn	Met	Asn	Tyr	Ser	Val	Ser	Asp	Thr	Ala	Glu	Phe	Gly	Gly	Tyr	
				250					255					260		
ctc	tcc	ggc	cca	cgc	gtc	atc	gat	gca	gac	acc	aag	tcc	cgc	atg	aag	931
Leu	Ser	Gly	Pro	Arg												

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      295              300              305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc 1075
Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310              315              320              325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac 1124
Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
      330              335

ccctttgacg gct 1137

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<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 286
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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
      20              25              30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
      35              40              45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
      50              55              60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
      65              70              75              80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
      85              90              95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
      100              105              110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
      115              120              125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
      130              135              140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
      145              150              155              160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
      165              170              175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
      180              185              190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
      195              200              205

Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
      210              215              220

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Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300

Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320

Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335

Thr Ala

<210> 287

<211> 556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> FRXA01145

<400> 287

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cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307
 Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145

tgc ctc atc 556
 Cys Leu Ile
 150

<210> 288
 <211> 152
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 288
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 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
 145 150

<210> 289
 <211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02375

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aagcgttcga ttacgggata atctcccaac gccaaacccaa atg gcg ccg gtg aca 115
 Met Ala Pro Val Thr
 1 5

ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
 Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
 10 15 20

ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
 Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
 25 30 35

gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
 Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
 40 45 50

aaa att ggt tcc tcc tca ttg act aac gat gag gac gga cac acc gtc 307
 Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
 55 60 65

gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
 Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
 70 75 80 85

gaa gct ggc tcc gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
 Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala
 90 95 100

gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
 Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
 105 110 115

aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
 Lys Gln Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
 120 125 130

gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
 Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
 135 140 145

acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
 Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
 150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643
 Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu
 170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691
 Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg

	185	190	195	
ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg				739
Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu				
	200	205	210	
ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc				787
Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr				
	215	220	225	
gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc				835
Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val				
	230	235	240	245
att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag				883
Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys				
	250	255		260
gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg				931
Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu				
	265	270		275
acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc				979
Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly				
	280	285	290	
act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg				1027
Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp				
	295	300	305	
gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc				1075
Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly				
	310	315	320	325
gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc				1123
Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly				
	330	335		340
att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc				1171
Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile				
	345	350		355
ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat				1219
Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp				
	360	365	370	
tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca				1267
Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro				
	375	380	385	
gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac				1315
Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr				
	390	395	400	405
gcc agc cgc gcg taaagcgcg gacctgctggt ggc				1350
Ala Ser Arg Ala				

<210> 290

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Met Ala Pro Val Thr Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala
 1          5          10          15

Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser
          20          25          30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala
          35          40          45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu
          50          55          60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala
          65          70          75          80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser
          85          90          95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro
          100          105          110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Val Gly Gln Val His
          115          120          125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile
          130          135          140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala
          145          150          155          160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val
          165          170          175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe
          180          185          190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala
          195          200          205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn
          210          215          220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn
          225          230          235          240

Asp Leu Lys Gly Val Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly
          245          250          255

Gly Met Ala Ser Lys Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly
          260          265          270

Val Pro Val Leu Leu Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu
          275          280          285

Asp Ala Gln Val Gly Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser
          290          295          300

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Ala Trp Lys Phe Trp Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile
 305 310 315 320

Arg Leu Asp Asp Gly Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser
 325 330 335

Leu Leu Ala Val Gly Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly
 340 345 350

Glu Ile Val Glu Ile Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly
 355 360 365

Glu Val Ser Tyr Asp Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln
 370 375 380

Thr Gln Asp Leu Pro Asp Gly Met Gln Arg Pro Val Val His Ala Asp
 385 390 395 400

Tyr Leu Ser Asn Tyr Ala Ser Arg Ala
 405

<210> 291
 <211> 1419
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> RXN02382

<400> 291
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cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
 Met Ser Ser Thr Thr
 1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
 10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val
 40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
 55 60 65

ggg cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
 70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala

	90	95	100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa				451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu				
	105	110	115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc				499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly				
	120	125	130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg				547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu				
	135	140	145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct				595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala				
	150	155	160	165
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag				643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu				
	170	175	180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc				691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr				
	185	190	195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg				739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val				
	200	205	210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt				787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly				
	215	220	225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac				835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr				
	230	235	240	245
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac				883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn				
	250	255	260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt				931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu				
	265	270	275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg				979
Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala				
	280	285	290	
ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa				1027
Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu				
	295	300	305	
gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat				1075
Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp				
	310	315	320	325
tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg				1123
Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val				
	330	335	340	

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gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa 1171
Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu
      345                      350                      355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc 1219
Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg
      360                      365                      370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat 1267
Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp
      375                      380                      385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa 1315
Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys
      390                      395                      400                      405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag 1363
Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys
      410                      415                      420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca 1416
Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro
      425                      430

agc 1419

<210> 292
<211> 432
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
  1                      5                      10                      15

Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
      20                      25                      30

Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
      35                      40                      45

Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
      50                      55                      60

Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
      65                      70                      75                      80

Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
      85                      90                      95

Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
      100                      105                      110

Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
      115                      120                      125

Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
      130                      135                      140

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Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg
 195 200 205
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn
 210 215 220
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly
 225 230 235 240
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile
 245 250 255
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala
 260 265 270
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu
 275 280 285
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg
 290 295 300
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr
 305 310 315 320
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala
 325 330 335
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser
 340 345 350
 Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln
 355 360 365
 Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser
 370 375 380
 Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly
 385 390 395 400
 Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu
 405 410 415
 Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro
 420 425 430

<210> 293

<211> 724

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> FRXA02378

<400> 293

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gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgatc 60

cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
              Met Ser Ser Thr Thr
              1                      5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
              10                      15                      20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
              25                      30                      35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Asp Glu Leu Val
              40                      45                      50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
              55                      60                      65

ggg cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
              70                      75                      80                      85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala
              90                      95                      100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu
              105                      110                      115

aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly
              120                      125                      130

atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu
              135                      140                      145

gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala
              150                      155                      160                      165

gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu
              170                      175                      180

cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro
              185                      190                      195

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gcg gat ccg tcc aag att tgatcacccg acgcg
 Ala Asp Pro Ser Lys Ile
 200

724

<210> 294
 <211> 203
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 294
 Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
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 Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile
 195 200

<210> 295
 <211> 623
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(600)
 <223> FRXA02382

<400> 295

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ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac atc gat gcc 48
Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
  1           5           10           15

gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc 96
Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
          20           25           30

cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc 144
Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
          35           40           45

gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa 192
Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
          50           55           60

gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt 240
Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
          65           70           75           80

gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac 288
Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
          85           90           95

ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct 336
Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
          100          105          110

ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc 384
Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
          115          120          125

acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca 432
Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
          130          135          140

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480
Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
          145          150          155          160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528
Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
          165          170          175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576
Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
          180          185          190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623
Gln Gly Thr Gly Gln Ile Arg Pro
          195          200

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<210> 296

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

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Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
 1              5              10              15

Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
      20              25              30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
      35              40              45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
      50              55              60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
      65              70              75              80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
      85              90              95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
      100              105              110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
      115              120              125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
      130              135              140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
      145              150              155              160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
      165              170              175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
      180              185              190

Gln Gly Thr Gly Gln Ile Arg Pro
      195              200

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<210> 297

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXA02499

<400> 297

cctggtcatg acgttcgggc cgctggcaat cgtcatgtaa tttgtcgttt tgggcccccg 60

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ctgctgcaaa acaggggtgg ttagtggcag tgtgggaacc atg aca aca att gct      115
                               Met Thr Thr Ile Ala
                               1              5

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gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc      163
Val Ile Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile
      10              15              20

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gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa	211
Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu	
25 30 35	
gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg	259
Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr	
40 45 50	
gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg	307
Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val	
55 60 65	
aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg	355
Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu	
70 75 80 85	
gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc	403
Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile	
90 95 100	
agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg	451
Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val	
105 110 115	
cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act	499
Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr	
120 125 130	
gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag	547
Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys	
135 140 145	
gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac	595
Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp	
150 155 160 165	
atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc	643
Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe	
170 175 180	
ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc	691
Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro	
185 190 195	
cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca	739
Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala	
200 205 210	
acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc	787
Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly	
215 220 225	
gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa	835
Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu	
230 235 240 245	
gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc	883
Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala	
250 255 260	
gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tatttccccg	930

Asp Arg Ser Glu Glu Leu Gly Lys Arg
265 270

tta

933

<210> 298

<211> 270

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 298

Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu
1 5 10 15

Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val
20 25 30

Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly
35 40 45

Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val
50 55 60

Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu
65 70 75 80

Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser
85 90 95

Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala
100 105 110

Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly
115 120 125

Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln
130 135 140

Leu Glu Gln Val Lys Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu
145 150 155 160

Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser
165 170 175

Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val
180 185 190

Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser
195 200 205

Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser
210 215 220

Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala
225 230 235 240

Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala
245 250 255

Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg

270

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<222> (101)..(1273)  
<223> RXS02157
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1 5

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
25 30 35

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
 55 60 65

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
90 95 100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
105 110 115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
120 125 130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
135 140 145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643

Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	Met	Val	Glu	Thr	Asn	
				170					175					180		
cca	acg	gat	gtg	gct	gct	atc	ttc	ctc	gag	cca	atc	cag	ggc	gaa	acg	691
Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	Ile	Gln	Gly	Glu	Thr	
			185					190					195			
ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739
Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	Ala	Val	Arg	Glu	Leu	
		200					205					210				
tgc	gat	gag	tac	ggc	atc	ttg	atg	atc	acc	gat	gaa	gtc	cag	act	ggc	787
Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp	Glu	Val	Gln	Thr	Gly	
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gtt	ggc	cgt	acc	ggc	gat	ttc	ttt	gca	cat	cag	cac	gat	ggc	gtt	gtt	835
Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln	His	Asp	Gly	Val	Val	
230					235					240					245	
ccc	gat	gtg	gtg	acc	atg	gcc	aag	gga	ctt	ggc	ggc	ggc	ctt	ccc	atc	883
Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly	Gly	Gly	Leu	Pro	Ile	
				250					255					260		
ggc	gct	tgt	ttg	gcc	act	ggc	cgt	gca	gct	gaa	ttg	atg	acc	cca	ggc	931
Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu	Leu	Met	Thr	Pro	Gly	
			265					270					275			
aag	cac	ggc	acc	act	ttc	ggc	ggc	aac	cca	gtt	gct	tgt	gca	gct	gcc	979
Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	
		280					285					290				
aag	gca	gtg	ctg	tct	gtt	gtc	gat	gac	gct	ttc	tgc	gca	gaa	gtt	gcc	1027
Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe	Cys	Ala	Glu	Val	Ala	
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cgc	aag	ggc	gag	ctg	ttc	aag	gaa	ctt	ctt	gcc	aag	gtt	gac	ggc	gtt	1075
Arg	Lys	Gly	Glu	Leu	Phe	Lys	Glu	Leu	Leu	Ala	Lys	Val	Asp	Gly	Val	
310					315					320					325	
gta	gac	gtc	cgt	ggc	agg	ggc	ttg	atg	ttg	ggc	gtg	gtg	ctg	gag	cgc	1123
Val	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly	Val	Val	Leu	Glu	Arg	
				330					335					340		
gac	gtc	gca	aag	caa	gct	gtt	ctt	gat	ggc	ttt	aag	cac	ggc	gtt	att	1171
Asp	Val	Ala	Lys	Gln	Ala	Val	Leu	Asp	Gly	Phe	Lys	His	Gly	Val	Ile	
			345					350					355			
ttg	aat	gca	ccg	gcg	gac	aac	att	atc	cgt	ttg	acc	ccg	ccg	ctg	gtg	1219
Leu	Asn	Ala	Pro	Ala	Asp	Asn	Ile	Ile	Arg	Leu	Thr	Pro	Pro	Leu	Val	
		360					365					370				
atc	acc	gac	gaa	gaa	atc	gca	gac	gca	gtc	aag	gct	att	gcc	gag	aca	1267
Ile	Thr	Asp	Glu	Glu	Ile	Ala	Asp	Ala	Val	Lys	Ala	Ile	Ala	Glu	Thr	
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Ile	Ala															
390																

<210> 300

<211> 391

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 300

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Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
          20          25          30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
          35          40          45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50          55          60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65          70          75          80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
          85          90          95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
          100          105          110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
          115          120          125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
          130          135          140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
          145          150          155          160

Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
          165          170          175

Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
          180          185          190

Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
          195          200          205

Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
          210          215          220

Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
          225          230          235          240

His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
          245          250          255

Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
          260          265          270

Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
          275          280          285

Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
          290          295          300

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Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
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 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
 370 375 380
 Ala Ile Ala Glu Thr Ile Ala
 385 390

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 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(1246)
 <223> RXS02262

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 Met Thr Ala Thr Tyr
 1 5
 acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20
 atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35
 gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
 40 45 50
 aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65
 ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
 70 75 80 85
 ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
 90 95 100

gga Gly	tcc Ser	aac Asn	gcg Ala 105	gaa Glu	aac Asn	aag Lys	gcc Ala	tca Ser 110	ggc Gly	ttg Leu	cct Pro	cgc Arg	tcg Ser 115	atc Ile	cac His	451
acc Thr	ttc Phe	gtc Val 120	ctc Leu	aac Asn	gac Asp	acg Thr	gtc Val 125	acc Thr	ggg Gly	gca Ala	ccg Pro	aag Lys 130	gcc Ala	atc Ile	atg Met	499
tcc Ser 135	gcg Ala	aac Asn	ctg Leu	ctg Leu	tcc Ser	gcc Ala 140	tac Tyr	cgc Arg	acc Thr	ggc Gly 145	gcg Ala	gtt Val	ccc Pro	ggc Gly	gtg Val	547
ggc Gly 150	gtg Val	aag Lys	cac His	tta Leu	gcg Ala 155	gtc Val	gcc Ala	gac Asp	gcg Ala	aca Thr 160	acc Thr	ttg Leu	gct Ala	gtc Val	gtc Val 165	595
gga Gly	cct Pro	ggg Gly	gtc Val	atg Met 170	gcg Ala	aaa Lys	acc Thr	atc Ile	acc Thr 175	gaa Glu	gcg Ala	tgc Cys	atc Ile	gca Ala 180	gag Glu	643
cgc Arg	cca Pro	gga Gly	atc Ile 185	acc Thr	acc Thr	atc Ile	aag Lys	atc Ile 190	aag Lys	gga Gly	cgc Arg	agc Ser	gaa Glu 195	cgc Arg	ggc Gly	691
atc Ile	aac Asn	gcc Ala 200	ttt Phe	gca Ala	aca Thr	tgg Trp	gcg Ala 205	ttg Leu	gaa Glu	aaa Lys	ttc Phe	ccc Pro 210	gag Glu	atc Ile	gaa Glu	739
gtg Val 215	gtc Val	gcc Ala	gtc Val	gga Gly	tct Ser	gaa Glu 220	gaa Glu	gac Asp	gtg Val	gtc Val	aaa Lys 225	gac Asp	gcc Ala	gac Asp	atc Ile	787
gtc Val 230	atc Ile	gcc Ala	gcc Ala	acc Thr	acc Thr	acg Thr 235	gac Asp	gcc Ala	gcc Ala	ggc Gly 240	tcc Ser	tcc Ser	gcc Ala	ttc Phe	cca Pro 245	835
tac Tyr	ttc Phe	aaa Lys	aaa Lys	gaa Glu 250	tgg Trp	ctc Leu	aag Lys	ccg Pro	ggc Gly 255	gca Ala	ttg Leu	ctg Leu	ctg Leu	ctt Leu 260	cca Pro	883
gcc Ala	gcc Ala	ggg Gly	cgc Arg 265	ttc Phe	gac Asp	gac Asp	gct Ala	tat Tyr 270	ttg Leu	ctt Leu	gac Asp	gac Asp	gcc Ala 275	cgc Arg	ctc Leu	931
gtt Val	gtt Val	gac Asp 280	tac Tyr	atg Met	ggg Gly	ctc Leu	tac Tyr 285	gaa Glu	gcc Ala	tgg Trp	gca Ala	gaa Glu 290	gaa Glu	tac Tyr	ggc Gly	979
cca Pro	cag Gln 295	gcc Ala	tac Tyr	caa Gln	cta Leu	ctc Leu 300	ggc Gly	att Ile	cca Pro	gga Gly	acc Thr 305	cac His	tgg Trp	tac Tyr	gac Asp	1027
ctg Leu 310	gcg Ala	ctg Leu	caa Gln	gga Gly	aaa Lys 315	ctc Leu	gac Asp	ctt Leu	gca Ala	aag Lys 320	att Ile	tcc Ser	cag Gln	att Ile	ggc Gly 325	1075
gat Asp	atc Ile	tgc Cys	tcc Ser	ggc Gly 330	aag Lys	cta Leu	ccc Pro	gga Gly 335	cgc Arg	acc Thr	aac Asn	gat Asp	gag Glu	gaa Glu 340	atc Ile	1123
atc	ctc	tat	tcc	gtc	ggc	ggc	atg	cca	gta	gaa	gac	gtc	gcc	tgg	gca	1171

Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
 345 350 355

acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg 1219
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
 360 365 370

aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg 1266
 Asn Leu Trp Glu Ser Pro Ala Leu Ala

375 380

aaa 1269

<210> 302

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

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 20 25 30

Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
 35 40 45

Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60

Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80

Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95

Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110

Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125

Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140

Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160

Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
 165 170 175

Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190

Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205

Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220

Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
 370 375 380

<210> 303

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1468)

<223> RXS02970

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 Leu Ala Leu Lys Gly
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
 135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
 150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys Glu Arg Ala Leu Lys
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027

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<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380

Leu Thr Phe Ala Gly Ala Leu Phe
450 455

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

cgc gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115

[illegible]

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 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
 135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
 150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219

Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
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ttc aag gaa cgc ggc 1330
 Phe Lys Glu Arg Gly
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<210> 306

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
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Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys
 195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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<210> 307

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3556)

<223> RXN00023

<400> 307

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 Met Thr Ser Met Asn
 1 5

 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
 10 15 20

cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
170 175 180	
aag gtc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag gcc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931

Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	Ala	Gln	Phe	Gly	Arg		
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gag	cgc	gtc	aac	aca	ggc	ggg	gcg	ggc	gtt	aag	gtt	cgc	ctg	gtc	aag	979	
Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys		
		280					285					290					
ggt	gct	aat	ttg	cct	atg	gag	cac	gtc	cac	gcg	cag	atc	acc	ggc	tgg	1027	
Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala	Gln	Ile	Thr	Gly	Trp		
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cca	gtt	gcc	aca	gaa	cct	tcc	aaa	caa	gcc	acc	gat	gcc	aat	tac	aag	1075	
Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	Asp	Ala	Asn	Tyr	Lys		
310					315				320						325		
cgc	gtc	ctc	tat	tgg	acg	atg	cgc	aaa	gaa	aac	atg	gag	ggc	ctg	cgc	1123	
Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn	Met	Glu	Gly	Leu	Arg		
			330					335						340			
ctg	ggc	gtt	gcc	ggc	cac	aac	ctt	ttc	gac	ata	gca	ttc	gca	cat	ttg	1171	
Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile	Ala	Phe	Ala	His	Leu		
			345					350					355				
ctc	tct	gtg	gag	cgt	ggg	gta	gcg	gac	cgt	gtg	gag	ttc	gaa	atg	ctg	1219	
Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	Glu	Phe	Glu	Met	Leu		
		360					365					370					
cag	ggc	atg	gcg	tcc	gat	cag	gcg	cgc	gcc	gtc	agc	gtt	gac	gtc	ggt	1267	
Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	Ser	Val	Asp	Val	Gly		
	375					380					385						
gag	ctg	ctg	ctt	tac	gta	cca	gcc	gtg	cgc	cca	caa	gaa	ttc	gac	gtg	1315	
Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	Gln	Glu	Phe	Asp	Val		
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gcc	att	tct	tac	ctc	gtg	cgc	cgc	ctc	gag	gaa	aac	gcc	gcg	agc	gaa	1363	
Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu	Asn	Ala	Ala	Ser	Glu		
				410				415						420			
aac	ttc	atg	tcc	gcc	atc	ttc	gac	ctc	gac	gcc	gac	aac	ccg	tcc	ttc	1411	
Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	Asp	Asn	Pro	Ser	Phe		
			425					430					435				
aag	cga	gag	gag	agc	cgc	ttc	cgc	gcc	tcc	ata	tct	gac	ctc	gcc	acg	1459	
Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr		
		440				445						450					
ctc	atc	gac	gtg	ccc	gcg	ccc	ggc	ccc	aac	cac	aca	caa	gac	cgc	agc	1507	
Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His	Thr	Gln	Asp	Arg	Ser		
	455					460					465						
aaa	gag	acg	ctt	ctc	gac	gcc	ccc	ctc	gtc	cca	ttt	atc	aac	gag	ccc	1555	
Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro	Phe	Ile	Asn	Glu	Pro		
470					475				480						485		
gac	acc	aac	cca	gcg	ctc	atc	caa	aac	caa	cag	tgg	gcc	aca	aaa	gcc	1603	
Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln	Trp	Ala	Thr	Lys	Ala		
			490					495					500				
gtc	gcc	acc	gca	gca	gag	ccc	ggt	tgg	ttg	gaa	aaa	caa	aca	aag	ccg	1651	
Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu	Lys	Gln	Thr	Lys	Pro		

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Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln	
760 765 770	
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc	2467
Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro	
775 780 785	
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac	2515
Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His	
790 795 800 805	
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc	2563
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro	
810 815 820	
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa	2611
Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu	
825 830 835	
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca	2659
Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro	
840 845 850	
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc	2707
Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe	
855 860 865	
caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac	2755
Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Glu Leu Gln Ser Leu Asp	
870 875 880 885	
gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc	2803
Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala	
890 895 900	
tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc	2851
Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe	
905 910 915	
gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga	2899
Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly	
920 925 930	
ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac	2947
Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His	
935 940 945	
cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc	2995
His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro	
950 955 960 965	
gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca	3043
Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr	
970 975 980	
gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat	3091
Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp	
985 990 995	


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gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga 3139
Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg
      1000                1005                1010

ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca 3187
Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala
      1015                1020                1025

gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt 3235
Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val
      1030                1035                1040                1045

tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa 3283
Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu
      1050                1055                1060

aca gtc gat gat tgc gta ttt att tcc aac gtg ttg cgc ggc gaa tac 3331
Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr
      1065                1070                1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac 3379
Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp
      1080                1085                1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac 3427
Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp
      1095                1100                1105

gat gca gta act gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa 3475
Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys
      1110                1115                1120                1125

gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg 3523
Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala
      1130                1135                1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcggtttt gcgcatgggt 3576
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cgc 3579

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<211> 1152

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

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Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
      20              25              30

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Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
      35              40              45

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Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
      50              55              60

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Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
 65 70 75 80
 Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
 85 90 95
 Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
 100 105 110
 Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro

385		390		395		400
Gln Glu Phe Asp Val	Ala Ile Ser Tyr	Leu Val Arg Arg	Leu Glu Glu			
	405		410		415	
Asn Ala Ala Ser Glu	Asn Phe Met	Ser Ala Ile Phe Asp	Leu Asp Ala			
	420	425	430			
Asp Asn Pro Ser Phe	Lys Arg Glu Glu	Ser Arg Phe Arg	Ala Ser Ile			
	435	440	445			
Ser Asp Leu Ala Thr	Leu Ile Asp Val	Pro Ala Pro Gly	Pro Asn His			
	450	455	460			
Thr Gln Asp Arg Ser	Lys Glu Thr Leu	Leu Asp Ala Pro	Leu Val Pro			
465	470	475	480			
Phe Ile Asn Glu Pro	Asp Thr Asn Pro	Ala Leu Ile Gln	Asn Gln Gln			
	485	490	495			
Trp Ala Thr Lys Ala	Val Ala Thr Ala	Ala Glu Pro Gly	Trp Leu Glu			
	500	505	510			
Lys Gln Thr Lys Pro	Glu Val Leu Glu	Gly Asp Val Asp	Lys Leu			
	515	520	525			
Ile Asn Asp Val Arg	Asp Ala Ala Glu	Ala Trp Ala Ala	Arg Pro Ala			
	530	535	540			
Arg Glu Arg Ala Glu	Ile Leu Tyr Lys	Thr Ala Glu Ile	Leu Arg Val			
545	550	555	560			
Arg Arg Gly His Leu	Ile Ser Val Thr	Ala Ala Glu Val	Gly Lys Ala			
	565	570	575			
Val Glu Gln Thr Asp	Pro Glu Ile Ser	Glu Ala Ile Asp	Phe Ala Arg			
	580	585	590			
Tyr Tyr Ala His Leu	Ala Leu Glu Leu	Asp Asp Val Asp	Asn Ala Glu			
	595	600	605			
Phe Thr Pro Asp Arg	Val Val Val Val	Thr Pro Pro Trp	Asn Phe Pro			
	610	615	620			
Ile Ala Ile Pro Ala	Gly Ser Thr Phe	Ala Ala Leu Ala	Ala Gly Ala			
625	630	635	640			
Gly Val Ile His Lys	Pro Ser Lys Pro	Ser Gln His Cys	Ser Ala Ala			
	645	650	655			
Val Val Glu Ala Leu	Trp Glu Ala Gly	Val Pro Arg Glu	Val Leu His			
	660	665	670			
Cys Ile Tyr Pro Ala	Asn Arg Asp Val	Gly Cys Ala Leu	Ile Ser His			
	675	680	685			
Glu His Val Asp Arg	Val Ile Leu Thr	Gly Ser Ser Glu	Thr Ala Ala			
	690	695	700			
Met Phe Ser Ser Trp	Arg Pro Glu Leu	Thr Ile Asn Gly	Glu Thr Ser			
705	710	715	720			

Gly Lys Asn Ala Ile Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala
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 Val Ala Asp Leu Val Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys
 740 745 750
 Ser Ala Ala Ser Leu Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu
 755 760 765
 Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
 805 810 815
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
 820 825 830
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
 835 840 845
 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
 865 870 875 880
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
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 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
 900 905 910
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
 915 920 925
 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
 930 935 940
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
 965 970 975
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005
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 Arg Ala Leu Leu Ala Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu
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Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala
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Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val
 1060 1065 1070

Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu
 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu
 1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu
 1105 1110 1115 1120

Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe
 1125 1130 1135

Gly Asn Pro Val Ala Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
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<210> 309

<211> 476

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (1)..(453)

<223> FRXA00023

<400> 309

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gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca gcc cgt cgc gcc 96
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
 20 25 30

ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt tca gag caa gtc 144
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45

cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat 192
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60

tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80

agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336

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Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
      100                      105                      110

gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384
Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
      115                      120                      125

tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag 432
Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu
      130                      135                      140

ttg gcg gag gaa ctt aaa cgt tgatcggtttt gcgcatgggt cgc 476
Leu Ala Glu Glu Leu Lys Arg
145                      150

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<210> 310

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<212> PRT

<213> Corynebacterium glutamicum

<400> 310

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His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser
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Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
      20              25              30

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Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
      35              40              45

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Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
      50              55              60

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Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
      65              70              75              80

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Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
      85              90              95

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Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
      100                      105                      110

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Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
      115                      120                      125

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Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu
      130                      135                      140

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Leu Ala Glu Glu Leu Lys Arg
145                      150

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<211> 3124

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(3124)

<223> FRXA02284

<400> 311

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gaaacggcac ccacaccgct gatcttgaag gagaaccacc atg acg tcg atg aat 115
                                   Met Thr Ser Met Asn
                                   1           5

ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
              10              15              20

cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp
              25              30              35

gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc 259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe
              40              45              50

acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg 307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala
              55              60              65

gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg 355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met
              70              75              80              85

tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg 403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg
              90              95              100

gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag 451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln
              105              110              115

atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag 499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys
              120              125              130

gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg 547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu
              135              140              145

cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat 595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp
              150              155              160              165

gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn 643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa
              170              175              180

nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac 691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp
              185              190              195

acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc 739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro
              200              205              210

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gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931
Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	
gag cgc gtc aac aca ggc ggg gcg gcc gtt aag gtt cgc ctg gtc aag	979
Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys	
280 285 290	
ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc gcc tgg	1027
Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp	
295 300 305	
cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag	1075
Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys	
310 315 320 325	
cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag gcc ctg cgc	1123
Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg	
330 335 340	
ctg gcc gtt gcc gcc cac aac ctt ttc gac ata gca ttc gca cat ttg	1171
Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu	
345 350 355	
ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg	1219
Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu	
360 365 370	
cag gcc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt	1267
Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly	
375 380 385	
gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg	1315
Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val	
390 395 400 405	
gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa	1363
Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu	
410 415 420	
aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc	1411
Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe	
425 430 435	
aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg	1459
Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr	
440 445 450	
ctc atc gac gtg ccc gcg ccc gcc ccc aac cac aca caa gac cgc agc	1507

Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His	Thr	Gln	Asp	Arg	Ser	
455						460					465					
aaa	gag	acg	ctt	ctc	gac	gcc	ccc	ctc	gtc	cca	ttt	atc	aac	gag	ccc	1555
Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro	Phe	Ile	Asn	Glu	Pro	
470					475				480					485		
gac	acc	aac	cca	gcg	ctc	atc	caa	aac	caa	cag	tgg	gcc	aca	aaa	gcc	1603
Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln	Trp	Ala	Thr	Lys	Ala	
				490				495						500		
gtc	gcc	acc	gca	gca	gag	ccc	ggg	tgg	ttg	gaa	aaa	caa	aca	aag	ccg	1651
Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu	Lys	Gln	Thr	Lys	Pro	
			505				510					515				
gag	gtg	ttg	gaa	gag	ggg	gac	gtc	gac	aag	cta	att	aac	gat	gtg	cgc	1699
Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu	Ile	Asn	Asp	Val	Arg	
		520					525					530				
gac	gct	gct	gaa	gcg	tgg	gca	gcg	cgc	cca	gcc	cgt	gaa	cgc	gct	gag	1747
Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala	Arg	Glu	Arg	Ala	Glu	
	535					540				545						
att	ttg	tac	aag	acc	gcc	gag	att	ttg	cgc	gtg	cga	cgc	gga	cac	ctg	1795
Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val	Arg	Arg	Gly	His	Leu	
550					555				560						565	
atc	tca	gtg	acg	gcc	gcg	gag	gtg	ggc	aaa	gct	gtg	gaa	caa	acc	gac	1843
Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala	Val	Glu	Gln	Thr	Asp	
				570				575						580		
ccg	gaa	atc	tct	gaa	gcc	att	gat	ttc	gcc	cgc	tac	tac	gcg	cat	ttg	1891
Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg	Tyr	Tyr	Ala	His	Leu	
			585					590					595			
gcc	ctg	gaa	ttg	gac	gac	gta	gac	aat	gcg	gaa	ttc	acc	cca	gat	cgc	1939
Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu	Phe	Thr	Pro	Asp	Arg	
		600					605					610				
gtc	gtt	gtg	gtg	acc	ccg	ccc	tgg	aat	ttc	ccc	atc	gcg	atc	ccc	gct	1987
Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro	Ile	Ala	Ile	Pro	Ala	
	615					620				625						
gga	tcg	act	ttc	gca	gca	ctc	gcg	gcg	ggc	gct	ggc	gtg	atc	cac	aaa	2035
Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala	Gly	Val	Ile	His	Lys	
630				635					640					645		
ccc	tca	aag	cct	agc	caa	cat	tgc	tcc	gct	gca	gtg	gtc	gaa	gcc	ctc	2083
Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala	Val	Val	Glu	Ala	Leu	
				650				655					660			
tgg	gaa	gcc	ggc	gtt	ccc	cgc	gag	gtt	ctg	cat	tgc	att	tac	cca	gct	2131
Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His	Cys	Ile	Tyr	Pro	Ala	
			665				670					675				
aat	cgc	gat	gtt	gga	tgt	gcg	ttg	atc	agc	cat	gaa	cac	gtc	gac	cgc	2179
Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His	Glu	His	Val	Asp	Arg	
		680					685				690					
gtc	att	ttg	acc	ggc	tcc	tcc	gag	acc	gcc	gcg	atg	ttc	tcc	tcc	tgg	2227
Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala	Met	Phe	Ser	Ser	Trp	

695	700	705	
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc			2275
Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile			
710	715	720	725
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg			2323
Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val			
	730	735	740
aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc			2371
Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu			
	745	750	755
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag			2419
Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln			
	760	765	770
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc			2467
Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro			
	775	780	785
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac			2515
Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His			
	790	795	800
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc			2563
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro			
	810	815	820
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa			2611
Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu			
	825	830	835
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca			2659
Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro			
	840	845	850
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc			2707
Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe			
	855	860	865
caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac			2755
Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp			
	870	875	880
gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc			2803
Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala			
	890	895	900
tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc			2851
Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe			
	905	910	915
gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga			2899
Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly			
	920	925	930
ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac			2947
Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His			
	935	940	945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc 2995
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
 950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca 3043
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
 970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat 3091
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
 985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca 3124
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 1000 1005

<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met Thr Ser Met Asn Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln
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Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
 20 25 30

Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
 35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
 50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
 65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
 85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
 100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125

Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140

Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160

Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175

Glu Tyr Val Ser Xaa Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190

Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro

195					200					205					
Leu	Tyr	Ile	Glu	Pro	Ala	Arg	Ala	Pro	Lys	Gly	Thr	Lys	Phe	Ile	Asn
210						215					220				
Leu	Asp	Met	Glu	Glu	Tyr	Arg	Asp	Leu	Arg	Leu	Thr	Met	Glu	Val	Phe
225					230					235					240
Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile
				245					250					255	
Val	Leu	Gln	Ala	Tyr	Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu
			260					265					270		
Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys
		275					280					285			
Val	Arg	Leu	Val	Lys	Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala
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Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr
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Asp	Ala	Asn	Tyr	Lys	Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn
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Met	Glu	Gly	Leu	Arg	Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile
			340					345					350		
Ala	Phe	Ala	His	Leu	Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val
		355					360					365			
Glu	Phe	Glu	Met	Leu	Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val
	370					375					380				
Ser	Val	Asp	Val	Gly	Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro
385					390					395					400
Gln	Glu	Phe	Asp	Val	Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu
				405					410					415	
Asn	Ala	Ala	Ser	Glu	Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala
			420					425					430		
Asp	Asn	Pro	Ser	Phe	Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile
		435					440					445			
Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
	450					455					460				
Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
465					470					475					480
Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
				485					490					495	
Trp	Ala	Thr	Lys	Ala	Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu
			500					505					510		
Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
	515						520					525			

Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala
 530 535 540
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val
 545 550 555 560
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala
 565 570 575
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg
 580 585 590
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu
 595 600 605
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro
 610 615 620
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala
 625 630 635 640
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala
 645 650 655
 Val Val Glu Ala Leu Trp Glu Ala Gly Val Pro Arg Glu Val Leu His
 660 665 670
 Cys Ile Tyr Pro Ala Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His
 675 680 685
 Glu His Val Asp Arg Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala
 690 695 700
 Met Phe Ser Ser Trp Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser
 705 710 715 720
 Gly Lys Asn Ala Ile Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala
 725 730 735
 Val Ala Asp Leu Val Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys
 740 745 750
 Ser Ala Ala Ser Leu Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu
 755 760 765
 Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
 805 810 815
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
 820 825 830
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
 835 840 845

Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
 865 870 875 880
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
 885 890 895
 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
 900 905 910
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
 915 920 925
 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
 930 935 940
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
 965 970 975
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005

<210> 313

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXC02498

<400> 313

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aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa 115
 Met Ser Glu Glu Lys
 1 5

ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163
 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser
 10 15 20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211
 Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly
 25 30 35

gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259
 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys

40	45	50	
ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa			307
Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu			
55	60	65	
cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa			355
Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu			
70	75	80	85
gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt			403
Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg			
	90	95	100
ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa			451
Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu			
	105	110	115
aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca			499
Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala			
	120	125	130
gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat			547
Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp			
	135	140	145
gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac			595
Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn			
	150	155	160
act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca			643
Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro			
	170	175	180
gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc			691
Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile			
	185	190	195
gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg			739
Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu			
	200	205	210
tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg			787
Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val			
	215	220	225
acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat			835
Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp			
	230	235	240
ggg ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc			883
Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe			
	250	255	260
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Gly Pro Leu Ala Ile Val Met			
	265		

<210> 314

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

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Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
35 40 45
Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
50 55 60
Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
65 70 75 80
Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
85 90 95
Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu
100 105 110
Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe
115 120 125
Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala
130 135 140
Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu
145 150 155 160
Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu
165 170 175
Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile
180 185 190
Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu
195 200 205
Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val
210 215 220
Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu
225 230 235 240
Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly
245 250 255
Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met
260 265

<210> 315

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01491

<400> 315

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                                         Met Leu Asp Glu Ser
                                         1           5

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct 163
Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala
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ggt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg 211
Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu
                        25                30                35

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg 259
Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg
                        40                45                50

tgg tgt gca cat cag gca ctg caa gct ttg gga cga gat agc ggt gat 307
Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
                        55                60                65

ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
                        70                75                80                85

tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
                        90                95                100

cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
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ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
                        120                125                130

cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
                        135                140                145

ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
                        150                155                160                165

acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
                        170                175                180

gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
                        185                190                195

ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739

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Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210

act gca gtg act tgaactggat ggagaggata cct
 Thr Ala Val Thr
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774

<210> 316

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile
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Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
 20 25 30

Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly
 50 55 60

Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu
 65 70 75 80

Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg
 85 90 95

Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp
 100 105 110

Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala
 115 120 125

Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val
 130 135 140

His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys
 145 150 155 160

Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu
 165 170 175

Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg
 180 185 190

Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly
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Tyr Val Ile Ala Ala Thr Ala Val Thr
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<210> 317

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<400> 317

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												1				5		
att	acc	gcg	ccg	aaa	ggc	ttc	gtt	gct	tct	gca	acg	acc	gcg	gg	att	163		
Ile	Thr	Ala	Pro	Lys	Gly	Phe	Val	Ala	Ser	Ala	Thr	Thr	Ala	Gly	Ile			
				10					15					20				
aaa	gct	tct	ggc	aat	cct	gac	atg	gcg	ttg	gtg	g	aac	cag	gg	cca	211		
Lys	Ala	Ser	Gly	Asn	Pro	Asp	Met	Ala	Leu	Val	Val	Asn	Gln	Gly	Pro			
			25					30					35					
gag	ttt	tcc	gca	gcg	gcc	gtg	ttt	aca	cgt	aac	cga	gtt	ttc	gca	gcg	259		
Glu	Phe	Ser	Ala	Ala	Ala	Val	Phe	Thr	Arg	Asn	Arg	Val	Phe	Ala	Ala			
		40					45					50						
cct	gtg	aag	gtg	agc	cga	gag	aac	gtt	gct	gat	ggc	cag	atc	agg	gct	307		
Pro	Val	Lys	Val	Ser	Arg	Glu	Asn	Val	Ala	Asp	Gly	Gln	Ile	Arg	Ala			
	55					60					65							
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Val	Leu	Tyr	Asn	Ala	Gly	Asn	Ala	Asn	Ala	Cys	Asn	Gly	Leu	Gln	Gly			
70					75				80					85				
gag	aag	gat	gct	cgt	gag	tct	gtt	tct	cat	cta	gct	caa	aat	ttg	ggc	403		
Glu	Lys	Asp	Ala	Arg	Glu	Ser	Val	Ser	His	Leu	Ala	Gln	Asn	Leu	Gly			
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ttg	gag	gat	tcc	gat	att	gg	gtg	tgt	tcc	act	gg	ctt	att	gg	gag	451		
Leu	Glu	Asp	Ser	Asp	Ile	Gly	Val	Cys	Ser	Thr	Gly	Leu	Ile	Gly	Glu			
			105					110					115					
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		120					125					130						
gag	ggc	gct	ttg	gg	gac	aat	gg	gca	gct	gct	gcc	aag	gcg	atc	atg	547		
Glu	Gly	Ala	Leu	Gly	Asp	Asn	Gly	Ala	Ala	Ala	Ala	Lys	Ala	Ile	Met			
	135					140					145							
acc	act	gac	acg	gtg	gat	aag	gaa	acc	gtc	gtg	ttt	gct	gat	gg	tgg	595		
Thr	Thr	Asp	Thr	Val	Asp	Lys	Glu	Thr	Val	Val	Phe	Ala	Asp	Gly	Trp			
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act	gtc	ggc	gga	atg	ggc	aag	ggc	gtg	ggc	atg	atg	gcg	ccg	tct	ctt	643		
Thr	Val	Gly	Gly	Met	Gly	Lys	Gly	Val	Gly	Met	Met	Ala	Pro	Ser	Leu			
				170					175					180				
gcc	acc	atg	ctg	gtc	tgc	ttg	acc	act	gat	gca	tcc	gtt	act	cag	gaa	691		

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atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc 739
Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr
      200                      205                      210

ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg 787
Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu
      215                      220                      225

gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat 835
Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp
      230                      235                      240                      245

gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat 883
Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp
      250                      255                      260

gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc 931
Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr
      265                      270                      275

aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat 979
Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn
      280                      285                      290

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg 1027
Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val
      295                      300                      305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att 1075
Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile
      310                      315                      320                      325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct 1123
Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala
      330                      335                      340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga 1171
Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg
      345                      350                      355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act 1219
Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr
      360                      365                      370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct 1264
Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser
      375                      380                      385

taaaaagaaa cagcactcca act 1287

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<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val

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Val	Asn	Gln	Gly	Pro	Glu	Phe	Ser	Ala	Ala	Ala	Val	Phe	Thr	Arg	Asn
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Arg	Val	Phe	Ala	Ala	Pro	Val	Lys	Val	Ser	Arg	Glu	Asn	Val	Ala	Asp
	50					55					60				
Gly	Gln	Ile	Arg	Ala	Val	Leu	Tyr	Asn	Ala	Gly	Asn	Ala	Asn	Ala	Cys
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Asn	Gly	Leu	Gln	Gly	Glu	Lys	Asp	Ala	Arg	Glu	Ser	Val	Ser	His	Leu
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Ala	Gln	Asn	Leu	Gly	Leu	Glu	Asp	Ser	Asp	Ile	Gly	Val	Cys	Ser	Thr
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Gly	Leu	Ile	Gly	Glu	Leu	Leu	Pro	Met	Asp	Lys	Leu	Asn	Ala	Gly	Ile
	115						120					125			
Asp	Gln	Leu	Thr	Ala	Glu	Gly	Ala	Leu	Gly	Asp	Asn	Gly	Ala	Ala	Ala
	130					135					140				
Ala	Lys	Ala	Ile	Met	Thr	Thr	Asp	Thr	Val	Asp	Lys	Glu	Thr	Val	Val
145					150					155					160
Phe	Ala	Asp	Gly	Trp	Thr	Val	Gly	Gly	Met	Gly	Lys	Gly	Val	Gly	Met
			165						170					175	
Met	Ala	Pro	Ser	Leu	Ala	Thr	Met	Leu	Val	Cys	Leu	Thr	Thr	Asp	Ala
			180					185						190	
Ser	Val	Thr	Gln	Glu	Met	Ala	Gln	Ile	Ala	Leu	Ala	Asn	Ala	Thr	Ala
		195					200					205			
Val	Thr	Phe	Asp	Thr	Leu	Asp	Ile	Asp	Gly	Ser	Thr	Ser	Thr	Asn	Asp
	210					215					220				
Thr	Val	Phe	Leu	Leu	Ala	Ser	Gly	Ala	Ser	Gly	Ile	Thr	Pro	Thr	Gln
225					230					235					240
Asp	Glu	Leu	Asn	Asp	Ala	Val	Tyr	Ala	Ala	Cys	Ser	Asp	Ile	Ala	Ala
			245						250					255	
Lys	Leu	Gln	Ala	Asp	Ala	Glu	Gly	Val	Thr	Lys	Arg	Val	Ala	Val	Thr
		260						265					270		
Val	Val	Gly	Thr	Thr	Asn	Asn	Glu	Gln	Ala	Ile	Asn	Ala	Ala	Arg	Thr
		275					280					285			
Val	Ala	Arg	Asp	Asn	Leu	Phe	Lys	Cys	Ala	Met	Phe	Gly	Ser	Asp	Pro
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Asn	Trp	Gly	Arg	Val	Leu	Ala	Ala	Val	Gly	Met	Ala	Asp	Ala	Asp	Met
305					310					315					320
Glu	Pro	Glu	Lys	Ile	Ser	Val	Phe	Phe	Asn	Gly	Gln	Ala	Val	Cys	Leu
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Asp	Ser	Thr	Gly	Ala	Pro	Gly	Ala	Arg	Glu	Val	Asp	Leu	Ser	Gly	Ala
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Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
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<220>

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<222> (101)..(1051)

<223> RXA02156

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aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
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cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
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gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
                        40 45 50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
                        55 60 65

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Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
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gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
                        90 95 100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
                        105 110 115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
                        120 125 130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547

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 Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
 150 155 160 165
 ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
 Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
 170 175 180
 gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
 Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
 185 190 195
 gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739
 Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu
 200 205 210
 acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu
 215 220 225
 gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu
 230 235 240 245
 gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg
 250 255 260
 ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser
 265 270 275
 gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu
 280 285 290
 ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga 1027
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg
 295 300 305
 aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg 1074
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 310 315

<210> 320

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
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Val	Asp	Ala	Ser	Ser	Leu	Met	Asp	Ile	Ile	Glu	Ala	Gly	Arg	Ile	Pro
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Val	Val	Ser	Thr	Ile	Ala	Pro	Gly	Glu	Asp	Gly	Gln	Ile	Tyr	Asn	Ile
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	195					200						205			
Arg	Leu	Leu	Val	Leu	Thr	Asn	Val	Glu	Gly	Leu	Tyr	Thr	Asp	Trp	Pro
	210					215					220				
Asp	Lys	Ser	Ser	Leu	Val	Ser	Lys	Ile	Lys	Ala	Thr	Glu	Leu	Glu	Ala
225				230						235					240
Ile	Leu	Pro	Gly	Leu	Asp	Ser	Gly	Met	Ile	Pro	Lys	Met	Glu	Ser	Cys
			245					250						255	
Leu	Asn	Ala	Val	Arg	Gly	Gly	Val	Ser	Ala	Ala	His	Val	Ile	Asp	Gly
			260					265					270		
Arg	Ile	Ala	His	Ser	Val	Leu	Leu	Glu	Leu	Leu	Thr	Met	Gly	Gly	Ile
	275					280						285			
Gly	Thr	Met	Val	Leu	Pro	Asp	Val	Phe	Asp	Arg	Glu	Asn	Tyr	Pro	Glu
	290					295					300				
Gly	Thr	Val	Phe	Arg	Lys	Asp	Asp	Lys	Asp	Gly	Glu	Leu			
305					310					315					

<210> 321

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

cccacttgca gtttttagctg taggtgggtt tttgcatgtc taaccctct tttatgcaca 60

ccccgcgaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
 Met Ile Met His Asn
 1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
 Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
 25 30 35

tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
 Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
 40 45 50

gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
 Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
 55 60 65

gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
 Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
 70 75 80 85

gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
 Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
 90 95 100

cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
 Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
 105 110 115

ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
 Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
 120 125 130

gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547
 Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
 135 140 145

ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
 Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
 150 155 160 165

gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
 Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
 170 175 180

gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691
 Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
 185 190 195

gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
 200 205 210

tgaaagaagg cgttaccgca gaa 903

<213> Corynebacterium glutamicum

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255

Gln Pro His Leu
 260

<210> 323
 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(880)
 <223> FRXA02153

<400> 323
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cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
 Met Ile Met His Asn
 1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
 Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
 25 30 35

tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
 Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
 40 45 50

gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
 Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
 55 60 65

gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
 Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
 70 75 80 85

gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
 Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
 90 95 100

cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
 Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
 105 110 115

ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
 Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
 120 125 130

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gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
135 140 145

ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
150 155 160 165

gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
170 175 180

gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
185 190 195

gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
200 205 210

tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn
215 220 225

ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val
230 235 240 245

ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu
250 255 260

tgaaagaagg cgttaccgca gaa 903

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<210> 324

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

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Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
1 5 10 15

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Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
20 25 30

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```

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
35 40 45

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Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
50 55 60

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Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
65 70 75 80

```

```

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
85 90 95

```

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Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys

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100 105 110
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
 165 170 175
 Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190
 Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205
 Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220
 Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240
 Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255
 Gln Pro His Leu
 260

<210> 325

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02154

<400> 325

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60

caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50

ccttaaagcg gcg 414

<213> Corynebacterium glutamicum

Pro

<213> Corynebacterium glutamicum

<223> RXA02157

caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
Met Ser Thr Leu Glu
1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
 10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
 25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
 40 45 50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
 55 60 65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355
 His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu
 70 75 80 85

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403
 Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
 90 95 100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451
 Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
 105 110 115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499
 Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
 120 125 130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547
 His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
 135 140 145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595
 Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
 150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643
 Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn
 170 175 180

cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691
 Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
 185 190 195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739
 Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu
 200 205 210

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
 215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245

ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883

Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385

atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
 390

<210> 328

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
 355 360 365
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
 370 375 380
 Ala Ile Ala Glu Thr Ile Ala
 385 390

<210> 329
 <211> 1491
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1468)
 <223> RXS02970

<400> 329
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 ttattttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115
 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
 135 140 145
 cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
 150 155 160 165
 tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	
gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa	1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu	
390 395 400 405	
ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac	1363
Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His	
410 415 420	
atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg	1411

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Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
      425                        430                        435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
      440                        445                        450

gcg ttg ttc taagttttct agataacaag gcc 1491
Ala Leu Phe
      455

<210> 330
<211> 456
<212> PRT
<213> Corynebacterium glutamicum

<400> 330
Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
  1                      5                      10                      15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
      20                      25                      30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
      35                      40                      45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
      50                      55                      60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
      65                      70                      75                      80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
      85                      90                      95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
      100                     105                     110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
      115                     120                     125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
      130                     135                     140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
      145                     150                     155                     160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
      165                     170                     175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
      180                     185                     190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
      195                     200                     205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
      210                     215                     220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly

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225          230          235          240
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
          245          250          255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
          260          265          270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
          275          280          285
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
          290          295          300
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
305          310          315          320
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
          325          330          335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
          340          345          350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
          355          360          365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
          370          375          380
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385          390          395          400
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
          405          410          415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
          420          425          430
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
          435          440          445
Leu Thr Phe Ala Gly Ala Leu Phe
          450          455

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<210> 331
<211> 1330
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1330)
<223> FRXA01009

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<400> 331
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ttattttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
          1          5

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tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc 1330
 Phe Lys Glu Arg Gly
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<210> 332

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly

50	55	60
Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly 65 70 75 80		
His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg 85 90 95		
Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val 100 105 110		
Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe 115 120 125		
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala 130 135 140		
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr 145 150 155 160		
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg 165 170 175		
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro 180 185 190		
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys 195 200 205		
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala 210 215 220		
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly 225 230 235 240		
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys 245 250 255		
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe 260 265 270		
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe 275 280 285		
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala 290 295 300		
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly 305 310 315 320		
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala 325 330 335		
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile 340 345 350		
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu 355 360 365		
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile 370 375 380		

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
405 410

<210> 333

<211> 1080

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02158

<400> 333

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aaggctattg ccgagacaat cgcataaagg actcaaactt atg act tca caa cca 115
Met Thr Ser Gln Pro
1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163
Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln
10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211
Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser
25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259
Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys
40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307
Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu
55 60 65

ggt gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355
Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys
70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403
Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu
90 95 100

gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451
Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala
105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499
Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His
120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547
Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser
135 140 145

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cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595
Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu
150 155 160 165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643
Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala
170 175 180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691
Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro
185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739
Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly
200 205 210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787
Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp
215 220 225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835
Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly
230 235 240 245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883
Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val
250 255 260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931
Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala
265 270 275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979
Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser
280 285 290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg 1027
Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu
295 300 305

ctg gtg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc 1077
Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
310 315

aac 1080

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<210> 334

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

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Met Thr Ser Gln Pro Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu
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20 25 30

Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
35 40 45

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Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
  50                      55                      60
Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
  65                      70                      75                      80
Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu
                      85                      90                      95
Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn
          100                      105                      110
Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu
          115                      120                      125
Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile
  130                      135                      140
Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys
  145                      150                      155                      160
Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr
          165                      170                      175
Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro
          180                      185                      190
Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg
          195                      200                      205
Gly Gln Glu Thr Gly Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu
  210                      215                      220
Val Ala Gly Ala Asp Val Val Ile Thr Asp Thr Trp Val Ser Met Gly
  225                      230                      235                      240
Met Glu Asn Asp Gly Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln
          245                      250                      255
Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu
          260                      265                      270
His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile
          275                      280                      285
Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
  290                      295                      300
Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
  305                      310                      315

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<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<400> 335

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gtt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163
Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr
10 15 20

ctg aag aag atg att gat ggt gaa gtc atc gca gtt tcc ctc gac ctg 211
Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
25 30 35

ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259
Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
40 45 50

gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307
Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala
55 60 65

gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355
Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys
70 75 80 85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403
Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His
90 95 100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451
Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly
105 110 115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499
Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
120 125 130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547
Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala
135 140 145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595
 Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu Glu Asn Asn Val Pro
 150 155 160 165

atc gag cag tcc gtg aag tcc cca ttc tcc atc gac cag aac gtc tgg 643
Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile Asp Gln Asn Val Trp
170 175 180

ggc cgc gct att gag acc ggt tac ctg gaa gat ctg tgg aat gct cca 691
Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp Leu Trp Asn Ala Pro
185 190 195

acc aag gac atc tac gca tac acc gag gat cca gct ctg ggt aac gct 739
Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro Ala Leu Gly Asn Ala
200 205 210

Chemical	Concentration	Time	Temperature	Pressure	Flow Rate	Yield	Purity	Characterization
1,2-Dichloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	85%	98%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	78%	95%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	72%	92%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	75%	94%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	70%	90%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	73%	93%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	68%	88%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	71%	91%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	65%	85%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	69%	89%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	62%	82%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	66%	86%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	60%	80%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	63%	83%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	58%	78%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	61%	81%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	55%	75%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	59%	79%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	52%	72%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	56%	76%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	50%	70%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	53%	73%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	48%	68%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	51%	71%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	45%	65%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	49%	69%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	42%	62%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	46%	66%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	40%	60%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	43%	63%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	38%	58%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	41%	61%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	35%	55%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	39%	59%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	32%	52%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	36%	56%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	24 h	60 °C	1 atm	1.0 mL/min	30%	50%	

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cca gat gag gtc atc atc tcc ttc gag ggt ggc aag cca gtc tcc atc 787
Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly Lys Pro Val Ser Ile
    215                220                225

gat ggc cgt cca gtc tcc gta ctg cag gct att gaa gag ctg aac cgt 835
Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile Glu Glu Leu Asn Arg
230                235                240                245

cgt gca ggc gca cag ggc gtt ggc cgc ctt gac atg gtt gag gac cgt 883
Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp Met Val Glu Asp Arg
                250                255                260

ctc gtg ggc atc aag tcc cgc gaa atc tac gaa gca cca ggc gca atc 931
Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Ala Pro Gly Ala Ile
                265                270                275

gca ctg att aag gct cac gag gct ttg gaa gat gtc acc atc gag cgc 979
Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp Val Thr Ile Glu Arg
    280                285                290

gaa ctg gct cgc tac aag cgc ggc gtt gac gca cgt tgg gct gag gaa 1027
Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala Arg Trp Ala Glu Glu
    295                300                305

gta tac gac ggc ctg tgg ttc gga cct ctg aag cgc tcc ctg gac gcg 1075
Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys Arg Ser Leu Asp Ala
    310                315                320                325

ttc att gat tcc acc cag gag cac gtc acc ggc gat atc cgc atg gtt 1123
Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly Asp Ile Arg Met Val
                330                335                340

ctg cac gca ggt tcc atc acc atc aat ggt cgt cgt tcc agc cac tcc 1171
Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg Arg Ser Ser His Ser
                345                350                355

ctg tac gac ttc aac ctg gct acc tac gac acc ggc gac acc ttc gac 1219
Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr Gly Asp Thr Phe Asp
    360                365                370

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag 1267
Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
    375                380                385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct 1313
Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn
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<210> 336

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Met Thr Asn Arg Ile Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr
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Val Ala Ile Pro Tyr Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala

No.	Name	Age		Sex	Height	Weight	B.P.	Pulse	Temp.	Respiration	Systolic	Diastolic	Mean	Pulse pressure	Heart rate	Stroke volume	Cardiac output	Stroke work	Cardiac efficiency	Stroke work index	Cardiac efficiency index	Stroke work index	Cardiac efficiency index
		Year	Month																				
1	John Doe	25	10	M	175	70	120/80	72	37.5	18	120	80	93	40	5.0	100	5.0	100	100	100	100	100	100
2	Jane Smith	28	12	F	160	60	110/70	68	37.0	16	110	70	89	40	4.5	90	4.5	90	90	90	90	90	
3	Robert Johnson	30	11	M	180	75	130/90	75	37.8	20	130	90	109	40	5.5	110	5.5	110	110	110	110	110	
4	Mary White	22	9	F	155	55	105/65	65	36.8	15	105	65	85	40	4.0	85	4.0	85	85	85	85	85	
5	David Brown	35	8	M	190	85	140/100	78	38.0	22	140	100	120	40	6.0	120	6.0	120	120	120	120	120	

Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365

Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His
 370 375 380

Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
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Asn

<210> 337

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02162

<400> 337

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gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115
 Met Glu Gln His Gly
 1 5

acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20

gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu
 25 30 35

gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac 259
 Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His
 40 45 50

caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg 307
 Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly
 55 60 65

ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg 355
 Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu
 70 75 80 85

cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac 403
 Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp
 90 95 100

cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc 451
 Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg
 105 110 115

aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg 499
 Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val

120	125	130	
cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc			547
Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala			
135	140	145	
caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc			595
Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe			
150	155	160	165
cag gca gct cag ccg gtc ctt ctg gca cac cag ctg ctg gca cac gca			643
Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln Leu Leu Ala His Ala			
	170	175	180
cag cct ttg ctg cgc gat att gat cgt atc cgt gac ctg gac aag cgt			691
Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg Asp Leu Asp Lys Arg			
	185	190	195
ctt gcg gtg tct cct tac ggt tcc ggc gca ctt gct ggt tcc tct ttg			739
Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu Ala Gly Ser Ser Leu			
	200	205	210
aag ctc aac cct gaa gca atc gct gaa gaa ctc ggc ttt gat tcc gca			787
Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu Gly Phe Asp Ser Ala			
	215	220	225
gca gat aac tcc att gat gcc acc agc tcc cgc gat ttc gca tct gaa			835
Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg Asp Phe Ala Ser Glu			
	230	235	240
acc gcc ttc gtg ctg gcg cag ctt gca gtg gat atg tcc cgc ttg gct			883
Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp Met Ser Arg Leu Ala			
	250	255	260
gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg			931
Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu			
	265	270	275
tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac			979
Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn			
	280	285	290
cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt			1027
Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly			
	295	300	305
aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac			1075
Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr			
	310	315	320
aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg			1123
Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala			
	330	335	340
cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg			1171
Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu			
	345	350	355
acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc			1219
Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr			
	360	365	370

120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 1267
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 1315
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt 1363
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 1411
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 1459
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 1507
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
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tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 1554
 Trp Ala Arg Ala Gly Val Arg Arg
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<210> 338
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 338
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 Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45
 Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60
 Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80
 Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95
 Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110
 Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125
 Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val

130				135				140							
Asp	Ala	Leu	Ser	Ala	Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro
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Gly	Lys	Thr	His	Phe	Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln
				165					170					175	
Leu	Leu	Ala	His	Ala	Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg
			180						185				190		
Asp	Leu	Asp	Lys	Arg	Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu
		195					200						205		
Ala	Gly	Ser	Ser	Leu	Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu
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Gly	Phe	Asp	Ser	Ala	Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg
225					230					235					240
Asp	Phe	Ala	Ser	Glu	Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp
				245					250					255	
Met	Ser	Arg	Leu	Ala	Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe
			260						265				270		
Gly	Tyr	Ile	Thr	Leu	Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met
		275					280						285		
Pro	Gln	Lys	Lys	Asn	Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser
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Gly	Arg	Leu	Ile	Gly	Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala
305					310					315					320
Gln	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile
				325					330					335	
Val	Asp	Ser	Val	Ala	Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly
			340						345				350		
Leu	Val	Ser	Thr	Leu	Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala
		355					360						365		
Pro	Ala	Gly	Phe	Thr	Leu	Ala	Thr	Asp	Leu	Ala	Glu	Trp	Met	Val	Arg
		370				375					380				
Gln	Gly	Val	Pro	Phe	Arg	Glu	Ala	His	Glu	Ala	Ser	Gly	Ala	Cys	Val
385					390					395					400
Arg	Ile	Ala	Glu	Ser	Arg	Gly	Val	Asp	Leu	Ile	Asp	Leu	Thr	Asp	Glu
				405					410					415	
Glu	Leu	Ser	Gly	Val	Asp	Ala	Arg	Leu	Thr	Pro	Glu	Val	Arg	Glu	Val
			420						425				430		
Leu	Thr	Ile	Asp	Gly	Ala	Val	Ala	Ser	Arg	Ala	Thr	Arg	Gly	Gly	Thr
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Ala	Gly	Val	Arg	Val	Ala	Glu	Gln	Arg	Ala	Arg	Val	Asp	Ala	Ala	Ser
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<210> 339
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<213> Corynebacterium glutamicum

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<222> (101)..(883)
<223> FRXA02161
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Met Glu Gln His Gly 5																
acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163																
Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser 20																
gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211																
Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu 35																
gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac 259																
Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His 40																
caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg 307																
Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly 55																
ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg 355																
Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu 70																
cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac 403																
Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp 90																
cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc 451																
Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg 105																
aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg 499																
Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val 120																
cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc 547																
Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala 135																
caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc 595																
Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe 150																

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<212> PRT
<213> Corynebacterium glutamicum

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Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
          35          40          45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
  50          55          60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
  65          70          75          80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
          85          90          95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
          100          105          110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
          115          120          125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
          130          135          140

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Symbol	Definition	Symbol	Definition
\mathbf{A}	Matrix	\mathbf{B}	Matrix
\mathbf{C}	Matrix	\mathbf{D}	Matrix
\mathbf{E}	Matrix	\mathbf{F}	Matrix
\mathbf{G}	Matrix	\mathbf{H}	Matrix
\mathbf{I}	Matrix	\mathbf{J}	Matrix
\mathbf{K}	Matrix	\mathbf{L}	Matrix
\mathbf{M}	Matrix	\mathbf{N}	Matrix
\mathbf{O}	Matrix	\mathbf{P}	Matrix
\mathbf{Q}	Matrix	\mathbf{R}	Matrix
\mathbf{S}	Matrix	\mathbf{T}	Matrix
\mathbf{U}	Matrix	\mathbf{V}	Matrix
\mathbf{W}	Matrix	\mathbf{X}	Matrix
\mathbf{Y}	Matrix	\mathbf{Z}	Matrix
\mathbf{a}	Vector	\mathbf{b}	Vector
\mathbf{c}	Vector	\mathbf{d}	Vector
\mathbf{e}	Vector	\mathbf{f}	Vector
\mathbf{g}	Vector	\mathbf{h}	Vector
\mathbf{i}	Vector	\mathbf{j}	Vector
\mathbf{k}	Vector	\mathbf{l}	Vector
\mathbf{m}	Vector	\mathbf{n}	Vector
\mathbf{o}	Vector	\mathbf{p}	Vector
\mathbf{q}	Vector	\mathbf{r}	Vector
\mathbf{s}	Vector	\mathbf{t}	Vector
\mathbf{u}	Vector	\mathbf{v}	Vector
\mathbf{w}	Vector	\mathbf{x}	Vector
\mathbf{y}	Vector	\mathbf{z}	Vector
\mathbf{A}^T	Transpose of \mathbf{A}	\mathbf{B}^T	Transpose of \mathbf{B}
\mathbf{C}^T	Transpose of \mathbf{C}	\mathbf{D}^T	Transpose of \mathbf{D}
\mathbf{E}^T	Transpose of \mathbf{E}	\mathbf{F}^T	Transpose of \mathbf{F}
\mathbf{G}^T	Transpose of \mathbf{G}	\mathbf{H}^T	Transpose of \mathbf{H}
\mathbf{I}^T	Transpose of \mathbf{I}	\mathbf{J}^T	Transpose of \mathbf{J}
\mathbf{K}^T	Transpose of \mathbf{K}	\mathbf{L}^T	Transpose of \mathbf{L}
\mathbf{M}^T	Transpose of \mathbf{M}	\mathbf{N}^T	Transpose of \mathbf{N}
\mathbf{O}^T	Transpose of \mathbf{O}	\mathbf{P}^T	Transpose of \mathbf{P}
\mathbf{Q}^T	Transpose of \mathbf{Q}	\mathbf{R}^T	Transpose of \mathbf{R}
\mathbf{S}^T	Transpose of \mathbf{S}	\mathbf{T}^T	Transpose of \mathbf{T}
\mathbf{U}^T	Transpose of \mathbf{U}	\mathbf{V}^T	Transpose of \mathbf{V}
\mathbf{W}^T	Transpose of \mathbf{W}	\mathbf{X}^T	Transpose of \mathbf{X}
\mathbf{Y}^T	Transpose of \mathbf{Y}	\mathbf{Z}^T	Transpose of \mathbf{Z}
\mathbf{a}^T	Transpose of \mathbf{a}	\mathbf{b}^T	Transpose of \mathbf{b}
\mathbf{c}^T	Transpose of \mathbf{c}	\mathbf{d}^T	Transpose of \mathbf{d}
\mathbf{e}^T	Transpose of \mathbf{e}	\mathbf{f}^T	Transpose of \mathbf{f}
\mathbf{g}^T	Transpose of \mathbf{g}	\mathbf{h}^T	Transpose of \mathbf{h}
\mathbf{i}^T	Transpose of \mathbf{i}	\mathbf{j}^T	Transpose of \mathbf{j}
\mathbf{k}^T	Transpose of \mathbf{k}	\mathbf{l}^T	Transpose of \mathbf{l}
\mathbf{m}^T	Transpose of \mathbf{m}	\mathbf{n}^T	Transpose of \mathbf{n}
\mathbf{o}^T	Transpose of \mathbf{o}	\mathbf{p}^T	Transpose of \mathbf{p}
\mathbf{q}^T	Transpose of \mathbf{q}	\mathbf{r}^T	Transpose of \mathbf{r}
\mathbf{s}^T	Transpose of \mathbf{s}	\mathbf{t}^T	Transpose of \mathbf{t}
\mathbf{u}^T	Transpose of \mathbf{u}	\mathbf{v}^T	Transpose of \mathbf{v}
\mathbf{w}^T	Transpose of \mathbf{w}	\mathbf{x}^T	Transpose of \mathbf{x}
\mathbf{y}^T	Transpose of \mathbf{y}	\mathbf{z}^T	Transpose of \mathbf{z}

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
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Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly
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Tyr Val Pro Leu Gly
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<210> 341

<211> 786

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(763)

<223> FRXA02162

<400> 341

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Met Ser Arg Leu Ala
1 5

gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg 163
Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu
10 15 20

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 211
Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
25 30 35

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt 259
Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
40 45 50

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac 307
Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
55 60 65

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg 355
Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
70 75 80 85

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg 403
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
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 acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc 451
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
 105 110 115
 ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 499
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 120 125 130
 cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 547
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 135 140 145
 agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt 595
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 150 155 160 165
 gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 643
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 170 175 180
 gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 185 190 195
 gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
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<210> 342

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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 35 40 45
 Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60
 Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80
 Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110
 Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125
 Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140
 Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160
 Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175
 Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
 180 185 190
 Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
 195 200 205
 Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
 210 215 220

<210> 343

<211> 1269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> RXA02262

<400> 343

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tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac 115
 Met Thr Ala Thr Tyr
 1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
 40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met

70	75							80							85			
ccc Pro	gca Ala	tac Tyr	ctc Leu	ggc Gly 90	ggg Gly	cga Arg	ttc Phe	aaa Lys	aac Asn 95	acc Thr	ggc Gly	gtg Val	aag Lys	tgg Trp 100	tac Tyr	403		
gga Gly	tcc Ser	aac Asn 105	gcg Ala	gaa Glu	aac Asn	aag Lys	gcc Ala	tca Ser 110	ggc Gly	ttg Leu	cct Pro	cgc Arg	tcg Ser 115	atc Ile	cac His	451		
acc Thr	ttc Phe	gtc Val 120	ctc Leu	aac Asn	gac Asp	acg Thr	gtc Val 125	acc Thr	ggc Gly	gca Ala	cgc Pro	aag Lys 130	gcc Ala	atc Ile	atg Met	499		
tcc Ser	gcg Ala	aac Asn 135	ctg Leu	ctg Leu	tcc Ser	gcc Ala 140	tac Tyr	cgc Arg	acc Thr	ggc Gly	gcg Ala 145	gtt Val	ccc Pro	ggc Gly	gtg Val	547		
ggc Gly 150	gtg Val	aag Lys	cac His	tta Leu	gcg Ala 155	gtc Val	gcc Ala	gac Asp	gcg Ala 160	aca Thr	acc Thr	ttg Leu	gct Ala	gtc Val 165	gtc Val	595		
gga Gly	cct Pro	ggc Gly	gtc Val 170	atg Met	gcg Ala	aaa Lys	acc Thr	atc Ile	acc Thr 175	gaa Glu	gcg Ala	tgc Cys	atc Ile	gca Ala 180	gag Glu	643		
cgc Arg	cca Pro	gga Gly	atc Ile 185	acc Thr	acc Thr	atc Ile	aag Lys	atc Ile 190	aag Lys	gga Gly	cgc Arg	agc Ser	gaa Glu 195	cgc Arg	ggc Gly	691		
atc Ile	aac Asn 200	gcc Ala	ttt Phe	gca Ala	aca Thr	tgg Trp	gcg Ala 205	ttg Leu	gaa Glu	aaa Lys	ttc Phe 210	ccc Pro	gag Glu	atc Ile	gaa Glu	739		
gtg Val	gtc Val 215	gcc Ala	gtc Val	gga Gly	tct Ser	gaa Glu 220	gaa Glu	gac Asp	gtg Val	gtc Val	aaa Lys 225	gac Asp	gcc Ala	gac Asp	atc Ile	787		
gtc Val 230	atc Ile	gcc Ala	gcc Ala	acc Thr	acc Thr 235	acg Thr	gac Asp	gcc Ala	gcc Ala	ggc Gly 240	tcc Ser	tcc Ser	gcc Ala	ttc Phe	cca Pro 245	835		
tac Tyr	ttc Phe	aaa Lys	aaa Lys	gaa Glu 250	tgg Trp	ctc Leu	aag Lys	ccg Pro	ggc Gly 255	gca Ala	ttg Leu	ctg Leu	ctg Leu	ctt Leu 260	cca Pro	883		
gcc Ala	gcc Ala	ggc Gly	cgc Arg 265	ttc Phe	gac Asp	gac Asp	gct Ala	tat Tyr 270	ttg Leu	ctt Leu	gac Asp	gac Asp	gcc Ala 275	cgc Arg	ctc Leu	931		
gtt Val	gtt Val	gac Asp 280	tac Tyr	atg Met	ggg Gly	ctc Leu	tac Tyr 285	gaa Glu	gcc Ala	tgg Trp	gca Ala	gaa Glu 290	gaa Glu	tac Tyr	ggc Gly	979		
cca Pro	cag Gln 295	gcc Ala	tac Tyr	caa Gln	cta Leu	ctc Leu 300	ggc Gly	att Ile	cca Pro	gga Gly	acc Thr 305	cac His	tgg Trp	tac Tyr	gac Asp	1027		
ctg Leu 310	gcg Ala	ctg Leu	caa Gln	gga Gly	aaa Lys 315	ctc Leu	gac Asp	ctt Leu	gca Ala 320	aag Lys	att Ile	tcc Ser	cag Gln	att Ile	ggc Gly 325	1075		

gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc 1123
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile
330 335 340

atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca 1171
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
345 350 355

acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg 1219
Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
360 365 370

aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg 1266
Asn Leu Trp Glu Ser Pro Ala Leu Ala
375 380

aaa 1269

<210> 344
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 344
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Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys
20 25 30

Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
35 40 45

Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
50 55 60

Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
65 70 75 80

Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
85 90 95

Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
100 105 110

Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
115 120 125

Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
130 135 140

Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
145 150 155 160

Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
165 170 175

Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
180 185 190

Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220
 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
 370 375 380

<210> 345

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA00219

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 cacaagcact aaaacagcat taaagaaaga aagctttttc gtg gcc cgt aag aaa 115
 Val Ala Arg Lys Lys
 1 5

 aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala
 10 15 20

 ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser

	25	30	35	
tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct				259
Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser				
	40	45	50	
cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg				307
His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg				
	55	60	65	
tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca				355
Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala				
	70	75	80	85
tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc				403
Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala				
	90	95	100	
agg tat ttc gcg gat gtt tac ccg cag tca cgc aac act gtc gtg gaa				451
Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg Asn Thr Val Val Glu				
	105	110	115	
ttg gat gca gag ctt gcc cgc ctg tcg cgt gaa tgg ttc gac att ccg				499
Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu Trp Phe Asp Ile Pro				
	120	125	130	
cgc gcg cca cgg gta aag att cgt gtg gat gat gcc cga atg gtg gca				547
Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp Ala Arg Met Val Ala				
	135	140	145	
gaa tct ttc act ccc gca agc cgc gat gtg atc atc cgt gac gtt ttt				595
Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile Ile Arg Asp Val Phe				
	150	155	160	165
gcc gga gct atc acg ccg cag aac ttc acc acc gtg gag ttc ttt gag				643
Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr Val Glu Phe Phe Glu				
	170	175	180	
cac tgt cac cgt ggc ctt gct ccc ggc gga ttg tac gtt gcc aac tgt				691
His Cys His Arg Gly Leu Ala Pro Gly Gly Leu Tyr Val Ala Asn Cys				
	185	190	195	
ggc gat cat tcg gat ctg cgc gga gct aaa tct gag ctc gcg gga atg				739
Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser Glu Leu Ala Gly Met				
	200	205	210	
atg gag gtg ttc gag cac gtc gcg gtc atc gcc gat ccc ccg atg ctt				787
Met Glu Val Phe Glu His Val Ala Val Ile Ala Asp Pro Pro Met Leu				
	215	220	225	
aaa ggg cgc cgt tac ggc aac atc att ttg atg ggt tca gac acc gag				835
Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met Gly Ser Asp Thr Glu				
	230	235	240	245
ttc ttt agc tcc aac agc acg gaa gcg tcc gcg att acc cgt gag ctt				883
Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala Ile Thr Arg Glu Leu				
	250	255	260	
ctt ggc ggc ggc gtt cca gcg cag tac aag gat gaa tcc tgg gtg cgg				931
Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp Glu Ser Trp Val Arg				
	265	270	275	

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<210> 346
<211> 314
<212> PRT
<213> Corynebacterium glutamicum
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<400> 346																
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Asn	Thr	Pro	Ile	Ala	Gly	Thr	Tyr	Glu	Gly	Glu	Tyr	Ser	Val	Ile	Glu	
			20					25					30			
Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn	
		35					40					45				
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu	
	50					55					60					
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp	
65					70					75					80	
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly	
				85					90					95		
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	
			100					105					110			
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	
		115					120					125				
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	
	130					135					140					
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	
145					150					155					160	
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	
				165					170					175		
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	
			180					185					190			
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	
		195					200					205				
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	
	210					215					220					

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Asp Pro Pro Met Leu Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met
225                230                235                240

Gly Ser Asp Thr Glu Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala
                245                250                255

Ile Thr Arg Glu Leu Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp
                260                265                270

Glu Ser Trp Val Arg Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp
                275                280                285

Gly Val Ser Thr Leu Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala
                290                295                300

Glu Thr Pro Glu His Ser Asn Thr Gln Pro
305                310

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<210> 347
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1639)
<223> RXA01508

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ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115
                                   Met Ser Asp Leu Gly
                                   1 5

ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
                10                15                20

tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
                25                30                35

aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
                40                45                50

gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
                55                60                65

cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
                70                75                80                85

ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
                90                95                100

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tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc	451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val	
105 110 115	
ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc	499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu	
120 125 130	
gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct	547
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala	
135 140 145	
gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg	595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu	
150 155 160 165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc	643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile	
170 175 180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg	691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu	
185 190 195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg	739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala	
200 205 210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc	787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala	
215 220 225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa	835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln	
230 235 240 245	
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc	883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg	
250 255 260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga	931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg	
265 270 275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg	979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser	
280 285 290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc	1027
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu	
295 300 305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc	1075
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val	
310 315 320 325	
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg	1123
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met	
330 335 340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg	1171

Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu
 345 350 355
 cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat 1219
 Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp
 360 365 370
 ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag 1267
 Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu
 375 380 385
 ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg 1315
 Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val
 390 395 400 405
 gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt 1363
 Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val
 410 415 420
 gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac 1411
 Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His
 425 430 435
 gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct 1459
 Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro
 440 445 450
 gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc 1507
 Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe
 455 460 465
 ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat 1555
 Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn
 470 475 480 485
 cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg 1603
 Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val
 490 495 500
 gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac 1649
 Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp
 505 510
 gatgcgctgt gtg 1662

<210> 348

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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 20 25 30

Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile
 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys
 50 55 60
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu
 65 70 75 80
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe
 85 90 95
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala
 100 105 110
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile
 115 120 125
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala
 130 135 140
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala
 145 150 155 160
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala
 165 170 175
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val
 180 185 190
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val
 195 200 205
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser
 210 215 220
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val
 225 230 235 240
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg
 245 250 255
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr
 260 265 270
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn
 275 280 285
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala
 290 295 300
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu
 305 310 315 320
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp
 325 330 335
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp
 340 345 350
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp
 355 360 365
 Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg

Asp

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<220>  
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<222> (101)..(901)  
<223> RXA01757
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70	75	80 85	
atc gag ggt gat gcg	ctt ttt gag acg ctt	gtc gac gcc ccg agc cgc	403
Ile Glu Gly Asp	Ala Leu Phe Glu Thr	Val Asp Ala Pro Ser Arg	
	90	95 100	
ctg cgg ggt aac ccc	ata gac gct gct tca	ggc agg ttc caa gca ggg	451
Leu Arg Gly Asn Pro	Ile Asp Ala Ala Ser	Gly Arg Phe Gln Ala Gly	
	105	110 115	
gcc tcc tcg ctt gcg	ctc ggg ctt gca gcc	cag ctc aag cca gga gtt	499
Ala Ser Ser Leu Ala	Leu Gly Leu Ala Ala	Gln Leu Lys Pro Gly Val	
	120	125 130	
tta gaa ctc ggg gac	ccc gtc cat tct ctc	agt gag gaa gat ggg gaa	547
Leu Glu Leu Gly Asp	Pro Val His Ser Leu	Ser Glu Glu Asp Gly Glu	
	135	140 145	
atc gtt gtg aag tct	tcc aaa cag att gtg	agg gca aag cac gtc atc	595
Ile Val Val Lys Ser	Ser Lys Gln Ile Val	Arg Ala Lys His Val Ile	
	150	155 160 165	
att gcg gtt cca ccg	gca ctc gct gcc gag	ttg att ggt ttc acc cta	643
Ile Ala Val Pro Pro	Ala Leu Ala Ala Glu	Leu Ile Gly Phe Thr Leu	
	170	175 180	
gat tta cca gct gac	gtg cga aaa gca gcg	cat cca caa cat ata gct	691
Asp Leu Pro Ala Asp	Val Arg Lys Ala Ala	His Pro Gln His Ile Ala	
	185	190 195	
gtg atg aat tgg gca	aag gag aaa tac acc	tta ccc aca caa gcc gca	739
Val Met Asn Trp Ala	Lys Glu Lys Tyr Thr	Leu Pro Thr Gln Ala Ala	
	200	205 210	
tcg gct ggg ggt ttt	ggg cat gag ctg ttc	caa caa cca ctc gga cat	787
Ser Ala Gly Gly Phe	Gly His Glu Leu Phe	Gln Gln Pro Leu Gly His	
	215	220 225	
ggg cga att cat tgg	gca tca acg gaa gtt	gcc act gag ttt ggt gga	835
Gly Arg Ile His Trp	Ala Ser Thr Glu Val	Ala Thr Glu Phe Gly Gly	
	230	235 240 245	
cac ctt gaa ggc gca	gtt cgt gca gga att	cag gct gcg ctt caa aca	883
His Leu Glu Gly Ala	Val Arg Ala Gly Ile	Gln Ala Ala Leu Gln Thr	
	250	255 260	
gga ttt aat cta aaa	tct taaacctcgt attttccctg	ata	924
Gly Phe Asn Leu Lys	Ser		
	265		

<210> 350

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Met  Pro  Thr  Ala  Ser  Pro  Ile  Tyr  Asp  Val  Val  Val  Val  Gly  Ala  Gly
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Ile  Ser  Gly  Leu  Ile  Ala  Thr  Gln  Leu  Leu  Asp  Arg  Ala  Gly  Leu  Asn
          20              25              30

Ile  Lys  Cys  Phe  Glu  Ala  Cys  Ser  Arg  Val  Gly  Gly  Arg  Ala  Val  Ser
          35              40              45

Val  Gln  Gln  Ser  Asp  Leu  Phe  Leu  Asp  Leu  Gly  Ala  Thr  Trp  Phe  Trp
          50              55              60

Leu  Asn  Glu  Pro  Leu  Val  Gln  Gln  Leu  Val  Asn  Asn  Leu  Gly  Leu  Gly
65              70              75              80

Thr  Phe  Pro  Gln  Ala  Ile  Glu  Gly  Asp  Ala  Leu  Phe  Glu  Thr  Leu  Val
          85              90              95

Asp  Ala  Pro  Ser  Arg  Leu  Arg  Gly  Asn  Pro  Ile  Asp  Ala  Ala  Ser  Gly
          100              105              110

Arg  Phe  Gln  Ala  Gly  Ala  Ser  Ser  Leu  Ala  Leu  Gly  Leu  Ala  Ala  Gln
          115              120              125

Leu  Lys  Pro  Gly  Val  Leu  Glu  Leu  Gly  Asp  Pro  Val  His  Ser  Leu  Ser
          130              135              140

Glu  Glu  Asp  Gly  Glu  Ile  Val  Val  Lys  Ser  Ser  Lys  Gln  Ile  Val  Arg
145              150              155              160

Ala  Lys  His  Val  Ile  Ile  Ala  Val  Pro  Pro  Ala  Leu  Ala  Ala  Glu  Leu
          165              170              175

Ile  Gly  Phe  Thr  Leu  Asp  Leu  Pro  Ala  Asp  Val  Arg  Lys  Ala  Ala  His
          180              185              190

Pro  Gln  His  Ile  Ala  Val  Met  Asn  Trp  Ala  Lys  Glu  Lys  Tyr  Thr  Leu
          195              200              205

Pro  Thr  Gln  Ala  Ala  Ser  Ala  Gly  Gly  Phe  Gly  His  Glu  Leu  Phe  Gln
          210              215              220

Gln  Pro  Leu  Gly  His  Gly  Arg  Ile  His  Trp  Ala  Ser  Thr  Glu  Val  Ala
225              230              235              240

Thr  Glu  Phe  Gly  Gly  His  Leu  Glu  Gly  Ala  Val  Arg  Ala  Gly  Ile  Gln
          245              250              255

Ala  Ala  Leu  Gln  Thr  Gly  Phe  Asn  Leu  Lys  Ser
          260              265

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<210> 351

<211> 636

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXA02159

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acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163
Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg
10 15 20

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259
Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln
40 45 50

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355
Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile
70 75 80 85

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451
Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu
105 110 115

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547
Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val
135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595
Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu
150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagtccaag gct 636
Leu Ser Gly Arg Thr Thr
170

<213> Corynebacterium glutamicum

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val
1 5 10 15

Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln
 20 25 30
 Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly
 35 40 45
 Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly
 50 55 60
 Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly
 65 70 75 80
 Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys
 85 90 95
 Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly
 100 105 110
 Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala
 115 120 125
 Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala
 130 135 140
 Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys
 145 150 155 160
 Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr
 165 170

<210> 353

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXN02154

<400> 353

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60

caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50

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<210> 354
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
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<400> 354
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
  1                      5                      10                      15
Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
          20                      25                      30
Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
          35                      40                      45
Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
          50                      55                      60
Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
  65                      70                      75                      80
Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
          85                      90                      95
Pro

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<210> 355
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1279)  
<223> RXS00147
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ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115
                                         Val Ser Lys Asp Thr
                                         1           5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163

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Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser	Val	Pro	Ala	Tyr	Leu	
				10					15					20		
gtt	ctt	gca	gac	gga	cgt	acc	ttc	acc	gga	ttt	ggc	ttt	gga	gct	atc	211
Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe	Gly	Phe	Gly	Ala	Ile	
			25					30					35			
ggc	acc	acc	ctt	ggg	gag	gca	gtg	ttc	act	acc	gcc	atg	acc	ggg	tac	259
Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr	
			40				45					50				
caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg	gct	307
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
			55			60					65					
acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
					75					80					85	
70																
tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	gtt	atc	cgc	gac	ctc	403
Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu	
				90					95					100		
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu	
				105				110					115			
atg	gca	ggc	cag	ggc	atc	gtc	ggc	atc	ggc	gga	atc	gac	acc	cgc	gca	499
Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
				120			125					130				
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggg	tcc	att	gca	gcg	ggc	atc	ttc	547
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
				135		140					145					
tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gta	gag	atc	gtc	595
Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val	
					155				160						165	
150																
aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
				170					175					180		
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
				185			190						195			
gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
				200			205					210				
tct	gca	cgc	ggg	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
				215		220					225					
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
					235				240					245		
230																
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	

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                250                255                260
gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931
Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln
                265                270                275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979
Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly
                280                285                290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc 1027
His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
                295                300                305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc 1075
Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
310                315                320                325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc 1123
Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
                330                335                340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca 1171
Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
                345                350                355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca 1219
Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
                360                365                370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag 1267
Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
                375                380                385

aag aaa ggc gca taaataacat gccaaagcgt tca 1302
Lys Lys Gly Ala
390

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<210> 356

<211> 393

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 356

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Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser
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Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe
                20                25                30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
                35                40                45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50                55                60

Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65                70                75                80

Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu

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85										90					95				
Val	Ile	Arg	Asp	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr				
			100						105					110					
Ser	Leu	Gln	Gln	Glu	Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly				
		115					120					125							
Ile	Asp	Thr	Arg	Ala	Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile				
	130					135					140								
Ala	Ala	Gly	Ile	Phe	Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu				
145					150					155					160				
Leu	Val	Glu	Ile	Val	Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu				
				165					170					175					
Ser	Val	Glu	Val	Ser	Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly				
			180					185					190						
Glu	Glu	Arg	His	Thr	Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn				
		195					200					205							
Thr	Pro	Arg	Arg	Phe	Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro				
	210					215						220							
Ala	Glu	Thr	Pro	Phe	Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val				
225					230					235					240				
Phe	Ile	Ser	Asn	Gly	Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val				
				245					250					255					
Asp	Ile	Val	Arg	Glu	Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile				
			260					265						270					
Cys	Phe	Gly	Asn	Gln	Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr				
		275					280					285							
Lys	Leu	Lys	Phe	Gly	His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His				
	290					295					300								
Ile	Thr	Gly	Lys	Ile	Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu				
305					310					315					320				
Lys	Gly	Glu	Ala	Gly	Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile				
				325					330					335					
Val	Thr	His	Thr	Cys	Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Ile	Ala	Leu				
			340					345						350					
Lys	Ser	Gly	Arg	Ala	Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala				
		355					360					365							
Gly	Pro	Asn	Asp	Ala	Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met				
	370					375					380								
Asp	Ala	Asp	Ala	Gln	Lys	Lys	Gly	Ala											
385					390														

<210> 357

<211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXS00905

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 tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5
 aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20
 ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35
 cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
 40 45 50
 aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
 55 60 65
 gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
 70 75 80 85
 aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
 90 95 100
 gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
 105 110 115
 cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
 120 125 130
 ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
 135 140 145
 acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595
 Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
 150 155 160 165
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
 170 175 180
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691

Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr
185 190 195

cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739
Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr
200 205 210

gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787
Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala
215 220 225

gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835
Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg
230 235 240 245

gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883
Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys
250 255 260

ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924
Leu Glu Gly Arg Ala Leu
265

<210> 358
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 358
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Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
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Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
35 40 45

Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
50 55 60

Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
65 70 75 80

Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
85 90 95

Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
100 105 110

Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys

165	170	175
Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn		
180	185	190
Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly		
195	200	205
Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly		
210	215	220
Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val		
225	230	235
Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys		
245	250	255
Gln His His Arg Lys Leu Glu Gly Arg Ala Leu		
260	265	

<210> 359

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS00906

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gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca	115
Met Asn Thr Asp Ala	
1 5	

cgc tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct	163
Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro	
10 15 20	

tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta	211
Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val	
25 30 35	

gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg	259
Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg	
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cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca	307
Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala	
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ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg	355
Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val	
70 75 80 85	

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac	403
Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His	
90 95 100	

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp
 105 110 115

 gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser
 120 125 130

 acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val
 135 140 145

 acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
 Thr Glu Gly Ser Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu
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 Val Asn Pro

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<212> PRT

<213> Corynebacterium glutamicum

<400> 360

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 Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
 35 40 45

 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
 50 55 60

 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
 65 70 75 80

 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
 85 90 95

 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
 100 105 110

 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
 115 120 125

 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu
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 Thr Glu Leu Ile Glu Val Asn Pro
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 <213> Corynebacterium glutamicum

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 <222> (101)..(223)
 <223> RXS00907

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 Leu Ala Leu Tyr Gly
 1 5
 gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
 10 15 20
 ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35
 aac tac acc aag tagacccaaa agcaggcggtt aac 246
 Asn Tyr Thr Lys
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 <223> RXS02001

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Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu						
	10					20
cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211						
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe						
	25					35
gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259						
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly						
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atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307						
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly						
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ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355						
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu						
	70					85
att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403						
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala						
	90					100
tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451						
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr						
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ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499						
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln						
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cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547						
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly						
	135					145
gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595						
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln						
	150					165
ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643						
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met						
	170					180
gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691						
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His						
	185					195
ggt gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739						
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly						
	200					210
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc 787						
Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val						
	215					225
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat 835						
Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp						

230	235	240	245	
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc				883
Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe				
	250	255	260	
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc				931
Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val				
	265	270	275	
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac				979
Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn				
	280	285	290	
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct				1027
Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala				
	295	300	305	
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg				1075
Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser				
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cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg				1123
Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro				
	330	335	340	
ggc gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac				1171
Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn				
	345	350	355	
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc				1219
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe				
	360	365	370	
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg				1268
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cgctcgaaga tgc				1281
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Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp				
35 40 45				
Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His				
50 55 60				
Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala				
65 70 75 80				

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
 85 90 95
 Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
 100 105 110
 Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
 115 120 125
 Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
 130 135 140
 Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
 145 150 155 160
 Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
 165 170 175
 Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
 180 185 190
 Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
 195 200 205
 Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
 210 215 220
 Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
 225 230 235 240
 Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
 245 250 255
 Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
 260 265 270
 Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
 275 280 285
 Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
 290 295 300
 Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
 305 310 315 320
 Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe
 325 330 335
 Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser
 340 345 350
 Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro
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 370 375 380
 Lys Gly
 385

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<223> RXS02101
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Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
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tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211
Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu
25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259
Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val
40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
55 60 65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355
Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp
70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg
90 95 100

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atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly
      105                      110                      115

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cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
 His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
 120 125 130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
135 140 145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc gcc ggt tta 595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu
150 155 160 165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
170 175 180

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185 190 195	
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Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggg gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	1027
Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	1075
Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
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Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala	
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Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe	
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Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln	
360 365 370	
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Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala	
375 380 385	
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Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala	
390 395 400 405	
gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac	1363
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1386

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<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Phe	Asp	Cys	Glu	Val	Ile	Pro	Asn	Val	Gly	Gly	Tyr	Gly	Ile	Leu	Ala
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Val	Phe	Arg	Asn	Gly	Ser	Thr	Asp	Pro	Gly	Ala	Pro	Val	Ala	Leu	Met
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Arg	Ala	Asp	Phe	Asp	Gly	Leu	Pro	Val	Lys	Glu	Ile	Thr	Gly	Val	Pro
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Phe	Ala	Ser	Thr	Arg	Met	Arg	Pro	His	Asp	Gly	Ala	Asn	Val	His	Val
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Met	His	Ala	Cys	Gly	His	Asp	Val	His	Val	Thr	Ala	Leu	Leu	Gly	Ala
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Cys	Ala	Ile	Leu	Asp	Glu	Arg	Arg	Asp	Ala	Trp	Glu	Gly	Thr	Phe	Ile
	130					135					140				

Ala	Leu	Phe	Gln	Pro	Ser	Glu	Glu	Asn	Ser	Gln	Gly	Ala	Asn	Lys	Met
145					150					155					160

Val	Ala	Gly	Gly	Leu	Val	Asp	Leu	Ile	Pro	Arg	Pro	Asp	Val	Cys	Phe
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Gly	Gln	His	Val	Val	Pro	Gly	Ala	Ala	Gly	Thr	Val	Met	Ser	Met	Pro
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Gly	Gly	Ala	Leu	Ala	Ala	Cys	Asp	Ser	Ile	Glu	Ile	Arg	Ile	Gln	Gly
		195					200					205			

Arg	Ser	Ala	His	Gly	Ser	Met	Pro	His	Asn	Ser	Ile	Asp	Pro	Thr	Tyr
	210					215					220				

Val	Ala	Ala	Met	Ile	Val	Val	Arg	Leu	Gln	Gly	Ile	Val	Gly	Arg	Glu
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Val	Ser	Pro	Glu	Asp	Phe	Ala	Val	Ile	Ser	Val	Gly	Thr	Leu	Gln	Ser
				245					250					255	

Gly	Asn	Thr	Asn	Asn	Thr	Ile	Pro	Ala	Ser	Ala	Arg	Leu	Val	Leu	Asn
			260					265					270		

Cys	Arg	Phe	Tyr	Asn	Asp	Lys	Val	Lys	His	Lys	Val	Tyr	Arg	Ala	Ile
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275					280					285					
Glu	Arg	Val	Val	Arg	Gly	Glu	Cys	Leu	Ala	Ser	Gly	Ile	Glu	Glu	Glu
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Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro
305					310					315					320
Val	Val	Phe	Asp	Thr	Val	Arg	Pro	Val	Phe	Asp	Asp	Val	Phe	Gly	Glu
				325					330					335	
Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser
			340					345					350		
Ile	Pro	Lys	Ala	Phe	Asn	Ser	Pro	Tyr	Leu	Tyr	Trp	Thr	Ile	Gly	Val
		355					360					365			
Thr	Pro	Arg	Asp	Gln	Trp	Thr	Glu	Ala	Val	Glu	Arg	Asp	Arg	Val	Ala
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Ser	Asp	Val	Pro	Ala	Asn	His	Met	Gly	Asp	Phe	Leu	Pro	Asp	Tyr	Ala
385						390					395				400
Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr
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Tyr	Leu	Gly	Thr	Asn											
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<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3439)

<223> RXS02234

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gat	att	aac	cac	gtc	ctc	gtc	atc	ggg	tcc	ggc	ccc	atc	gtc	att	ggc	163
Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly	Pro	Ile	Val	Ile	Gly	
				10				15						20		

cag	gca	tgt	gaa	ttc	gac	tac	tcc	ggc	acc	cag	gct	tgc	cgc	gtg	ctg	211
Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln	Ala	Cys	Arg	Val	Leu	
			25					30					35			

aag	gaa	gag	gga	ctg	cgc	gtc	acc	ctc	atc	aac	tcc	aac	cca	gca	acg	259
Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	Ser	Asn	Pro	Ala	Thr	
			40				45					50				

atc	atg	acc	gac	cca	gaa	atg	gct	gac	cac	acc	tac	gtg	gag	cca	atc	307
Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr	Tyr	Val	Glu	Pro	Ile	

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Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly			
70	75	80	85
cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt			403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu			
	90	95	100
aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc			451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly			
	105	110	115
gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat			499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp			
	120	125	130
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg			547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala			
	135	140	145
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Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala			
	150	155	160
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Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly			
	170	175	180
ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct			691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala			
	185	190	195
ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa			739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu			
	200	205	210
tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc			787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr			
	215	220	225
gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg			835
Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu			
	230	235	240
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg			883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu			
	250	255	260
act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc			931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile			
	265	270	275
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc			979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile			
	280	285	290
aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg			1027
Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val			
	295	300	305

200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc	1075
Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
310 315 320 325	
aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc	1123
Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
330 335 340	
aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac	1171
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
345 350 355	
tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc	1219
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg	1267
Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
375 380 385	
tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc	1315
Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser	
390 395 400 405	
ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc	1363
Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe	
410 415 420	
gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag	1411
Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys	
425 430 435	
cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt	1459
Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu	
440 445 450	
ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg	1507
Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp	
455 460 465	
ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt	1555
Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val	
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gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg	1603
Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met	
490 495 500	
ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc	1651
Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly	
505 510 515	
gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta	1699
Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val	
520 525 530	
ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg	1747
Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro	
535 540 545	

tac	cac	tac	tcc	gca	tac	gag	ctg	gat	cca	gca	gct	gag	tct	gag	gtc	1795
Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro	Ala	Ala	Glu	Ser	Glu	Val	
550					555					560					565	
gca	cca	cag	act	gag	cgt	gaa	aag	gtc	ctg	atc	ttg	ggc	tcc	ggt	cca	1843
Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu	Ile	Leu	Gly	Ser	Gly	Pro	
				570				575						580		
aac	cgc	atc	ggc	cag	ggc	atc	gag	ttc	gac	tac	tcc	tgt	gtt	cac	gca	1891
Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp	Tyr	Ser	Cys	Val	His	Ala	
			585					590					595			
gct	ctt	gag	ctc	tcc	cgc	gtc	ggc	tac	gaa	act	gtc	atg	gtc	aac	tgc	1939
Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu	Thr	Val	Met	Val	Asn	Cys	
		600					605					610				
aac	cca	gag	acc	gtg	tcc	acc	gac	tac	gac	acc	gct	gac	cgc	ctg	tac	1987
Asn	Pro	Glu	Thr	Val	Ser	Thr	Asp	Tyr	Asp	Thr	Ala	Asp	Arg	Leu	Tyr	
	615					620					625					
ttc	gag	cca	ctg	acc	ttc	gaa	gac	gtc	atg	gag	gtc	tac	cac	gct	gag	2035
Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met	Glu	Val	Tyr	His	Ala	Glu	
630					635					640					645	
gcg	cag	tcc	ggc	acc	gtc	gca	ggg	gtt	atc	gtc	cag	ctt	ggg	ggc	cag	2083
Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile	Val	Gln	Leu	Gly	Gly	Gln	
				650					655					660		
act	cct	ctg	ggc	ttg	gca	gat	cgt	ttg	aag	aag	gct	ggc	gtc	cct	gtc	2131
Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys	Lys	Ala	Gly	Val	Pro	Val	
			665					670					675			
att	ggt	acc	tcc	cca	gag	gca	atc	gac	atg	gct	gag	gac	cgt	ggc	gag	2179
Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met	Ala	Glu	Asp	Arg	Gly	Glu	
		680					685					690				
ttc	ggt	gca	ctg	ctg	aac	cgc	gag	cag	ctt	cct	gct	cca	gca	ttc	ggc	2227
Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu	Pro	Ala	Pro	Ala	Phe	Gly	
	695				700						705					
acc	gca	acc	tct	ttc	gaa	gag	gct	cgc	aca	gta	gcc	gat	gag	atc	agc	2275
Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr	Val	Ala	Asp	Glu	Ile	Ser	
710					715					720					725	
tac	cca	gtg	ctg	gtt	cgc	cct	tcc	tac	gtc	ttg	ggt	ggc	cgt	ggc	atg	2323
Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val	Leu	Gly	Gly	Arg	Gly	Met	
				730					735					740		
gag	att	gtc	tac	gat	gag	gct	tcc	ctc	gag	gat	tac	atc	aac	cgc	gca	2371
Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu	Asp	Tyr	Ile	Asn	Arg	Ala	
			745					750					755			
act	gag	ttg	tct	tct	gac	cac	cca	gtg	ctg	gtt	gac	cgc	ttc	cta	gac	2419
Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	Val	Asp	Arg	Phe	Leu	Asp	
		760					765					770				
aac	gct	att	gag	atc	gac	gtc	gac	gca	ctg	tgc	gac	ggc	gac	gag	gtc	2467
Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu	Cys	Asp	Gly	Asp	Glu	Val	
	775					780					785					
tac	ctg	gca	ggc	gtc	atg	gag	cac	atc	gag	gaa	gcc	ggc	att	cac	tcc	2515

Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
790 795 800 805

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac 2563
Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp
810 815 820

atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt 2611
Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
825 830 835

gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc 2659
Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu
840 845 850

tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc 2707
Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val
855 860 865

tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca 2755
Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala
870 875 880 885

gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc 2803
Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr
890 895 900

gag tac gac ggc ggc tcc ttg cca ctg gac gct cca atc gct gtg aag 2851
Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys
905 910 915

gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc 2899
Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr
920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg 2947
Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met
935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc 2995
Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly
950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct 3043
Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala
970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg 3091
Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc 3139
Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc 3187
Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg
1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa 3235
Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu

1030	1035	1040	1045
ggt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac			3283
Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His			
	1050	1055	1060
gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg			3331
Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu			
	1065	1070	1075
atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc			3379
Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala			
	1080	1085	1090
ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac			3427
Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His			
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gca gtc aag gct taagccctat gacattcggc gag			3462
Ala Val Lys Ala			
1110			

<210> 368

<211> 1113

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

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Pro	Ile	Val	Ile	Gly	Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln
			20					25					30		

Ala	Cys	Arg	Val	Leu	Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn
		35					40					45			

Ser	Asn	Pro	Ala	Thr	Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr
	50					55					60				

Tyr	Val	Glu	Pro	Ile	Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys
	65				70					75					80

Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly
			85						90					95	

Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile
			100					105					110		

Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile
		115					120					125			

Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile
	130					135					140				

Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val
145					150					155					160

His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser
				165					170					175	

Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
 180 185 190
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn
 195 200 205
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu
 210 215 220
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu
 225 230 235 240
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala
 245 250 255
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln
 260 265 270
 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn
 275 280 285
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu
 290 295 300
 Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr
 305 310 315 320
 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr
 325 330 335
 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe
 340 345 350
 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe
 355 360 365
 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser
 370 375 380
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn
 385 390 395 400
 Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys
 405 410 415
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val
 420 425 430
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu
 435 440 445
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser
 450 455 460
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe
 465 470 475 480
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg
 485 490 495

Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg
 500 505 510
 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu
 515 520 525
 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe
 530 535 540
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala
 545 550 555 560
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile
 565 570 575
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr
 580 585 590
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
 595 600 605
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
 610 615 620
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val
 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu
 725 730 735
 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp
 740 745 750
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val
 755 760 765
 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys
 770 775 780
 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu
 785 790 795 800
 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr
 805 810 815
 Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu

820	825	830
Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu 835	840	845
Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg 850	855	860
Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala 865	870	875
Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu 885	890	895
Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala 900	905	910
Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg 915	920	925
Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser 930	935	940
Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala 945	950	955
Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val 965	970	975
Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile 980	985	990
Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr 995	1000	1005
Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys 1010	1015	1020
Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg 1025	1030	1035
Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser 1045	1050	1055
Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr 1060	1065	1070
Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val 1075	1080	1085
Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu 1090	1095	1100
Gln Glu Leu Asp His Ala Val Lys Ala 1105	1110	

<210> 369

<211> 3221

<212> DNA

<213> Corynebacterium glutamicum

<221> CDS

<222> (1) .. (3198)

<223> FRXA02234

<400> 369

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acc Thr	tac Tyr	gtg Val	gag Glu 20	cca Pro	atc Ile	gag Glu	ccg Pro	gaa Glu 25	tac Tyr	atc Ile	gac Asp	aag Lys	att Ile 30	ttc Phe	gct Ala	96
aag Lys	gaa Glu	atc Ile 35	gag Glu	cag Gln	ggc Gly	cac His	cca Pro 40	atc Ile	gac Asp	gcc Ala	gtc Val	ctg Leu 45	gca Ala	acc Thr	ctt Leu	144
ggc Gly 50	ggc Gly	cag Gln	act Thr	gca Ala	ctt Leu	aac Asn 55	gca Ala	gct Ala	atc Ile	cag Gln	ctg Leu 60	gat Asp	cgc Arg	ctc Leu	ggc Gly	192
atc Ile 65	ctg Leu	gaa Glu	aag Lys	tac Tyr	ggc Gly 70	gtt Val	gaa Glu	ctc Leu	atc Ile	ggc Gly 75	gca Ala	gac Asp	atc Ile	gat Asp	gcc Ala 80	240
att Ile	gag Glu	cgc Arg	ggc Gly	gaa Glu 85	gat Asp	cgc Arg	cag Gln	aag Lys	ttc Phe 90	aag Lys	gat Asp	att Ile	gtc Val	acc Thr 95	acc Thr	288
atc Ile	ggc Gly	ggc Gly	gaa Glu 100	tcc Ser	gcg Ala	cgt Arg	tcc Ser	cgc Arg 105	gtc Val	tgc Cys	cac His	aac Asn 110	atg Met	gaa Glu	gaa Glu	336
gtc Val	cac His	gag Glu 115	act Thr	gtc Val	gca Ala	gaa Glu	ctc Leu 120	ggc Gly	ctt Leu	cca Pro	gta Val	gtc Val 125	gtg Val	cgt Arg	cca Pro	384
tcc Ser	ttc Phe 130	act Thr	atg Met	ggc Gly	ggc Gly	ctg Leu 135	ggc Gly	tcc Ser	ggc Gly	ctt Leu	gca Ala 140	tac Tyr	aac Asn	acc Thr	gaa Glu	432
gac Asp 145	ctt Leu	gag Glu	cgc Arg	atc Ile	gct Ala 150	ggc Gly	gga Gly	ctt Leu	gct Ala 155	gca Ala	tct Ser	cct Pro	gaa Glu	gca Ala 160		480
aac Asn	gtc Val	ttg Leu	atc Ile	gaa Glu 165	gaa Glu	tcc Ser	atc Ile	ctt Leu 170	ggc Gly	tgg Trp	aag Lys	gaa Glu	ttc Phe	gag Glu 175	ctc Leu	528
gag Glu	ctc Leu	atg Met	cgc Arg 180	gat Asp	acc Thr	gca Ala	gac Asp	aac Asn 185	gtt Val	gtg Val	gtt Val	atc Ile	tgc Cys 190	tcc Ser	att Ile	576
gaa Glu	aac Asn	gtc Val 195	gac Asp	gca Ala	ctg Leu	ggc Gly	gtg Val 200	cac His	acc Thr	ggc Gly	gac Asp	tct Ser 205	gtc Val	acc Thr	gtg Val	624
gca Ala	cct Pro	gcc Ala	ctg Leu	acc Thr	ctg Leu	act Thr	gac Asp	cgt Arg	gaa Glu	ttc Phe	cag Gln	aag Lys	atg Met	cgc Arg	gat Asp	672

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[illegible]

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Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu	
705 710 715 720	
ggt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg	2208
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu	
725 730 735	
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag	2256
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu	
740 745 750	
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg	2304
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met	
755 760 765	
act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag	2352
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys	
770 775 780	
ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca	2400
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala	
785 790 795 800	
ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc	2448
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser	
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cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag	2496
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys	
820 825 830	
gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat	2544
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp	
835 840 845	
gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac	2592
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp	
850 855 860	
gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt	2640
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg	
865 870 875 880	
cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag	2688
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys	
885 890 895	
tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat	2736
Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr	
900 905 910	
gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc	2784
Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr	
915 920 925	
gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca	2832
Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro	
930 935 940	
atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc	2880

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Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
945                      950                      955                      960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc 2928
Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
                      965                      970                      975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat 2976
Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
                      980                      985                      990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt 3024
Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
                      995                      1000                      1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg 3072
Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
1010                      1015                      1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct 3120
Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025                      1030                      1035                      1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg 3168
Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
                      1045                      1050                      1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc 3218
Leu Gln Glu Leu Asp His Ala Val Lys Ala
                      1060                      1065

gag 3221

<210> 370
<211> 1066
<212> PRT
<213> Corynebacterium glutamicum

<400> 370
Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His
 1                      5                      10                      15

Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
20                      25                      30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
35                      40                      45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
50                      55                      60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65                      70                      75                      80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
85                      90                      95

Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
100                      105                      110

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Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
 115 120 125
 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
 130 135 140
 Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
 145 150 155 160
 Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
 165 170 175
 Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
 180 185 190
 Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
 195 200 205
 Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp
 210 215 220
 Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys
 225 230 235 240
 Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile
 245 250 255
 Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala
 260 265 270
 Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
 275 280 285
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu

435					440					445					
Arg	Glu	Ala	Lys	Phe	Met	Gly	Leu	Ser	Asp	Leu	Gln	Ile	Ala	Ala	Leu
450						455					460				
Arg	Pro	Glu	Phe	Ala	Gly	Glu	Asp	Gly	Val	Arg	Thr	Leu	Arg	Leu	Ser
465					470					475					480
Leu	Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu
				485					490					495	
Phe	Glu	Ala	Lys	Thr	Pro	Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro
			500					505					510		
Ala	Ala	Glu	Ser	Glu	Val	Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu
		515					520					525			
Ile	Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp
	530					535					540				
Tyr	Ser	Cys	Val	His	Ala	Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu
545					550					555					560
Thr	Val	Met	Val	Asn	Cys	Asn	Pro	Glu	Thr	Val	Ser	Thr	Asp	Tyr	Asp
				565					570					575	
Thr	Ala	Asp	Arg	Leu	Tyr	Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met
			580					585					590		
Glu	Val	Tyr	His	Ala	Glu	Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile
		595					600					605			
Val	Gln	Leu	Gly	Gly	Gln	Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys
	610					615					620				
Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met
625					630					635					640
Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu
				645					650					655	
Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
			660					665					670		
Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val
		675					680					685			
Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu
	690					695					700				
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu
705					710					715					720
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu
				725					730					735	
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu
			740					745					750		
Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met
		755				760						765			

Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala
 1060 1065

<210> 371

<211> 1389

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1366)

<223> RXS02565

<400> 371

ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc tttacgacga 60

aaccctcacc	ctccttcagg	aacttatccg	caacgcctgc	gtg	aat	gat	cta	acc	115
				Val	Asn	Asp	Leu	Thr	
				1				5	

cca	gat	tca	ggt	cag	gaa	att	aga	aac	gcg	gaa	agc	cta	gaa	cgt	ttc	163
Pro	Asp	Ser	Gly	Gln	Glu	Ile	Arg	Asn	Ala	Glu	Ser	Leu	Glu	Arg	Phe	
			10						15				20			

ttt	gaa	gga	acc	ccc	aac	gtt	aaa	atc	acc	aag	ctg	gaa	ccg	cat	ccg	211
Phe	Glu	Gly	Thr	Pro	Asn	Val	Lys	Ile	Thr	Lys	Leu	Glu	Pro	His	Pro	
			25					30					35			

ggc	cgg	acc	tca	att	atc	gtg	act	gtt	cca	ggc	agc	gat	cca	gat	gct	259
Gly	Arg	Thr	Ser	Ile	Ile	Val	Thr	Val	Pro	Gly	Ser	Asp	Pro	Asp	Ala	
		40				45						50				

gag	cct	tta	aca	ctg	ctt	gga	cat	act	gat	gtt	gtg	cct	gtt	gat	ctg	307
Glu	Pro	Leu	Thr	Leu	Leu	Gly	His	Thr	Asp	Val	Val	Pro	Val	Asp	Leu	
	55					60					65					

cct	aaa	tgg	act	aaa	gat	cca	ttc	ggc	gcg	gag	att	tcg	gat	gga	cag	355
Pro	Lys	Trp	Thr	Lys	Asp	Pro	Phe	Gly	Ala	Glu	Ile	Ser	Asp	Gly	Gln	
	70				75					80					85	

att	tgg	ggc	aga	ggg	tcc	gtc	gat	atg	ctc	ttt	att	acc	gca	acc	caa	403
Ile	Trp	Gly	Arg	Gly	Ser	Val	Asp	Met	Leu	Phe	Ile	Thr	Ala	Thr	Gln	
				90					95					100		

gcg	gcc	gtc	acc	cgt	caa	gta	gcc	cgt	gaa	ggc	ggc	ctg	cgt	ggc	acg	451
Ala	Ala	Val	Thr	Arg	Gln	Val	Ala	Arg	Glu	Gly	Gly	Leu	Arg	Gly	Thr	
			105					110					115			

ctg	aca	ttc	gtt	ggc	gtt	gct	gat	gag	gaa	gcc	cgc	ggc	gga	ctc	gga	499
Leu	Thr	Phe	Val	Gly	Val	Ala	Asp	Glu	Glu	Ala	Arg	Gly	Gly	Leu	Gly	
		120				125						130				

gcg	aag	tgg	ctt	tcc	gaa	gaa	cac	caa	aac	ctc	ttc	agc	tgg	aaa	aac	547
Ala	Lys	Trp	Leu	Ser	Glu	Glu	His	Gln	Asn	Leu	Phe	Ser	Trp	Lys	Asn	
	135					140					145					

tgc	ctc	tcc	gaa	tcc	ggc	gga	tcg	cac	ctt	cca	gtc	cac	gac	ggc	agc	595
Cys	Leu	Ser	Glu	Ser	Gly	Gly	Ser	His	Leu	Pro	Val	His	Asp	Gly	Ser	
	150				155					160				165		

gac	gca	gta	gta	att	aac	gtt	gga	gaa	aaa	ggc	gca	gct	caa	cgt	cgt	643
Asp	Ala	Val	Val	Ile	Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg	
				170				175						180		

att	cac	gtc	aat	ggc	gat	gct	ggc	cat	ggc	tcc	att	cct	ttc	gac	cgt	691
Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg	

185	190	195	
gac agc gct att gtc aag atc ggt gaa gtc gcc cgc cga atc gct gcc			739
Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala			
200	205	210	
gcc gat ctg aag gta gcc aag gac gat atc tgg caa ggc ttc gtc caa			787
Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln			
215	220	225	
gcg cac cgt ttc gac cca gaa acg gag cag gcg ctt ctt agc ggg acc			835
Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala Leu Leu Ser Gly Thr			
230	235	240	245
tcc cct gag gcc tac gca gag ttc ggc gga ctc tcc cgc ttc gcc cac			883
Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu Ser Arg Phe Ala His			
250	255		260
gcg gtg tct cat ctc acg atc gcc caa act gtg gtt cgt gca ggt caa			931
Ala Val Ser His Leu Thr Ile Ala Gln Thr Val Val Arg Ala Gly Gln			
265	270	275	
gcc atc aat gta ttg cca tcg cat gcg tac ttg gaa ctg gat atc cgt			979
Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu Glu Leu Asp Ile Arg			
280	285	290	
acc ctt cca ggc caa acc aat gac tat gtt gat gac acc ctg cgt gct			1027
Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp Asp Thr Leu Arg Ala			
295	300	305	
gct ctg ggc gat ctt gcc gat gaa gta gaa atc gaa cac ctc atc tct			1075
Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile Glu His Leu Ile Ser			
310	315	320	325
gaa gaa gca acg gtg agc cca act gat tcc agg ttg tat aac acc ttg			1123
Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr Leu			
330	335	340	
gaa aaa gtt ctt ggt gat ttc ttc ccc gat gcg cct gtg gtc cca att			1171
Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro Ile			
345	350	355	
att tcc tct ggt ggc tct gac ctg cgc ttt ggt cgt cga cta ggc ggt			1219
Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly Gly			
360	365	370	
gtt ggt tat ggt ttt gca gtt cat gca cgt gaa cga act ttg gcg gaa			1267
Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala Glu			
375	380	385	
gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat			1315
Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp			
390	395	400	405
ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta			1363
Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu			
410	415	420	
ggc taaaaacatg aagcaggagt ctt			1389
Gly			

<210> 372

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
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Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
 20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
 35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
 50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
 65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
 85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
 100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
 115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
 130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
 145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
 165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
 180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220

Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240

Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255

Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270

Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285

Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg
 325 330 335
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala
 340 345 350
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly
 355 360 365
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu
 370 375 380
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala
 385 390 395 400
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val
 405 410 415
 Val Arg Glu Phe Leu Gly
 420

<210> 373

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXS02937

<400> 373

gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60
 tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115
 Val Ile Ser Asn Gly
 1 5
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163
 Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met
 10 15 20
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val
 25 30 35
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His
 40 45 50
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser
 55 60 65

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cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355
His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala
70 75 80 85

gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403
Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala
90 95 100

ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451
Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu
105 110 115

gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499
Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val
120 125 130

aaa taattggcta atgaatcctt ttc 525
Lys

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<210> 374
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

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<400> 374
Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile
1 5 10 15
Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
20 25 30
Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
35 40 45
His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
50 55 60
Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
65 70 75 80
Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
85 90 95
Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp
100 105 110
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala
115 120 125
Ser Ala Trp Leu Val Lys
130

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<210> 375
<211> 966
<212> DNA
<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (101)..(943)

<223> RXA02194

<400> 375

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gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115
                                         Met Leu Lys Ile Ala
                                         1 5

gtc cca aac aaa ggc tgc ctg tcc gag cgc gcc atg gaa atc ctc gcc 163
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala
                        10 15 20

gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe
                        25 30 35

gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile
                        40 45 50

gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg
                        55 60 65

gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu
                        70 75 80 85

ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu
                        90 95 100

tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro
                        105 110 115

aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val
                        120 125 130

ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala
                        135 140 145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
                        150 155 160 165

ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
                        170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
                        185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739

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Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp
      200                      205                      210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787
Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro
      215                      220                      225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835
Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val
      230                      235                      240                      245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883
Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp
                      250                      255                      260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931
Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg
      265                      270                      275

atc gcc cgc atc tagttttaac taccctcgaa aat 966
Ile Ala Arg Ile
      280

<210> 376
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 376
Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala
  1                      5                      10                      15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys
      20                      25                      30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu
      35                      40                      45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu
      50                      55                      60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His
      65                      70                      75                      80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala
      85                      90                      95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile
      100                      105                      110

Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly
      115                      120                      125

Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile
      130                      135                      140

Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg
      145                      150                      155                      160

Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr

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165										170					175				
Ser	Glu	Ala	Val	Ile	Val	Gly	Arg	Lys	Asp	Glu	Lys	Val	Thr	Pro	Glu				
			180						185					190					
Gln	Gln	Ile	Leu	Leu	Arg	Arg	Ile	Gln	Gly	Ile	Leu	His	Ala	Gln	Asn				
		195					200					205							
Phe	Leu	Met	Leu	Asp	Tyr	Asn	Val	Asp	Arg	Asp	Asn	Leu	Asp	Ala	Ala				
	210					215					220								
Thr	Ala	Val	Thr	Pro	Gly	Leu	Ser	Gly	Pro	Thr	Val	Ser	Pro	Leu	Ala				
225					230					235					240				
Arg	Asp	Asn	Trp	Val	Ala	Val	Arg	Ala	Met	Val	Pro	Arg	Arg	Ser	Ala				
			245						250					255					
Asn	Ala	Ile	Met	Asp	Lys	Leu	Ala	Gly	Leu	Gly	Ala	Glu	Ala	Ile	Leu				
		260						265					270						
Ala	Ser	Glu	Ile	Arg	Ile	Ala	Arg	Ile											
		275					280												

<210> 377

<211> 393

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02195

<400> 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccca	aacacacatt	gataactgtt	gtgtggaaga	atg	tac	cga	gtg	aag		115
				Met	Tyr	Arg	Val	Lys		
				1				5		

aca	ttt	gac	tcg	ctg	tac	gaa	gaa	ctt	ctt	aac	cgt	gct	cag	acc	cgc		163
Thr	Phe	Asp	Ser	Leu	Tyr	Glu	Glu	Leu	Leu	Asn	Arg	Ala	Gln	Thr	Arg		
			10					15					20				

cct	gaa	ggg	tct	gga	acc	gtg	gcc	gcc	ttg	gat	aaa	ggc	atc	cat	cat		211
Pro	Glu	Gly	Ser	Gly	Thr	Val	Ala	Ala	Leu	Asp	Lys	Gly	Ile	His	His		
		25					30						35				

cta	ggt	aag	aag	gtc	atc	gaa	gaa	gcc	gga	gag	gtc	tgg	att	gca	gcc		259
Leu	Gly	Lys	Lys	Val	Ile	Glu	Glu	Ala	Gly	Glu	Val	Trp	Ile	Ala	Ala		
		40					45				50						

gag	tat	gag	acc	gat	gaa	gag	cta	gcc	gga	gaa	atc	tcc	cag	ctc	att		307
Glu	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Ala	Gly	Glu	Ile	Ser	Gln	Leu	Ile		
	55					60					65						

tat	tgg	acc	cag	gtc	atc	atg	gtt	gct	cgc	ggc	ctg	aag	cca	gaa	gat		355
Tyr	Trp	Thr	Gln	Val	Ile	Met	Val	Ala	Arg	Gly	Leu	Lys	Pro	Glu	Asp		
	70				75					80					85		

atc tac aag aac ctg taggagtttt aaagcaatca tgt 393
 Ile Tyr Lys Asn Leu
 90

<210> 378
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 378
 Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn
 1 5 10 15
 Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp
 20 25 30
 Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu
 35 40 45
 Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu
 50 55 60
 Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly
 65 70 75 80
 Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu
 85 90

<210> 379
 <211> 477
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(454)
 <223> RXA01097

<400> 379
 gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60
 taaagggagc cattaagat gcaggatttg aggtgcggaa atg agt gac aat cca 115
 Met Ser Asp Asn Pro
 1 5
 caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn
 10 15 20
 gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu
 25 30 35
 gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu
 40 45 50
 gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp

55	60	65	
atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc			355
Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala			
70	75	80	85
ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc			403
Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly			
90	95		100
ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg			451
Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu			
105	110		115
ctg taaaagcaac aacgattaag gaa			477
Leu			

<210> 380

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys
1 5 10 15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala
20 25 30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala
35 40 45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser
50 55 60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu
65 70 75 80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr
85 90 95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe
100 105 110

Asp Asn Asp Val Leu Leu
115

<210> 381

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXA01100

<400> 381

[illegible]

gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu
 230 235 240 245

ggt taatacatgg atgctcgtgg gat 861
 Gly

<210> 382

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala
 1 5 10 15

Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr
 20 25 30

Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu
 35 40 45

His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu
 50 55 60

Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr
 65 70 75 80

Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly
 85 90 95

Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp
 100 105 110

Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile
 115 120 125

Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp
 130 135 140

Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser
 145 150 155 160

Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr
 165 170 175

Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr
 180 185 190

Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val
 195 200 205

Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile
 210 215 220

Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala
 225 230 235 240

Ala Val Glu Lys Leu Gly
245

<210> 383

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA01101

<400> 383

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atcgagcta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60
cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115
                                         Met Thr Lys Thr Val
                                         1                               5

gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala
                               10                               15                               20

cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val
                               25                               30                               35

tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp
                               40                               45                               50

gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly
                               55                               60                               65

cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355
Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met
                               70                               75                               80                               85

cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly
                               90                               95                               100

tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu
                               105                               110                               115

cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg 499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met
                               120                               125                               130

ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat 547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr
                               135                               140                               145

ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca 595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro
150                               155                               160                               165

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gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg 643
 Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val
 170 175 180

gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt 691
 Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly
 185 190 195

gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc 733
 Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile
 200 205 210

taacagatag gatcaatatt cat 756

<210> 384

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg
 1 5 10 15

Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser
 20 25 30

Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly
 35 40 45

Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly
 50 55 60

His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly
 65 70 75 80

Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly
 85 90 95

Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu
 100 105 110

Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro
 115 120 125

Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr
 130 135 140

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp
 145 150 155 160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg
 165 170 175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His
 180 185 190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile
 195 200 205

Asn Tyr Ile

210

<210> 385

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01657

<400> 385

cctccgtcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc	agcaccacac	cgactcgccg	agcgcggctg	gtg	atc	gtt	gga	gtt	115
				Val	Ile	Val	Gly	Val	
				1				5	

tta	gct	ctc	cag	ggc	ggg	gtg	gaa	gaa	cac	ctc	acc	gcc	ttg	gaa	gct	163
Leu	Ala	Leu	Gln	Gly	Val	Glu	Glu	His	Leu	Thr	Ala	Leu	Glu	Ala		
			10					15					20			

ctc	gga	gcg	acg	acc	cga	aaa	gta	cgt	gtg	cca	aag	gac	ctt	gat	ggt	211
Leu	Gly	Ala	Thr	Thr	Arg	Lys	Val	Arg	Val	Pro	Lys	Asp	Leu	Asp	Gly	
			25					30					35			

ctc	gaa	ggc	atc	gtc	atc	ccc	ggc	ggg	gaa	tcc	acc	gtg	ttg	gac	aaa	259
Leu	Glu	Gly	Ile	Val	Ile	Pro	Gly	Gly	Glu	Ser	Thr	Val	Leu	Asp	Lys	
		40					45					50				

ctg	gct	cgg	aca	ttc	gac	gtg	gta	gaa	cct	cta	gcg	aat	ctc	att	cgc	307
Leu	Ala	Arg	Thr	Phe	Asp	Val	Val	Glu	Pro	Leu	Ala	Asn	Leu	Ile	Arg	
		55				60					65					

gac	ggc	cta	ccc	gtt	ttc	gct	acc	tgc	gct	ggc	ctg	atc	tat	ctg	gcg	355
Asp	Gly	Leu	Pro	Val	Phe	Ala	Thr	Cys	Ala	Gly	Leu	Ile	Tyr	Leu	Ala	
	70				75					80					85	

aaa	cac	ctc	gac	aac	cca	gca	agg	gga	caa	caa	acc	ttg	gcg	gta	gtg	403
Lys	His	Leu	Asp	Asn	Pro	Ala	Arg	Gly	Gln	Gln	Thr	Leu	Ala	Val	Val	
				90					95					100		

gac	gtg	gtg	gtg	cgt	cga	aac	gca	ttt	ggc	gcc	caa	cgc	gaa	tcc	ttc	451
Asp	Val	Val	Val	Arg	Arg	Asn	Ala	Phe	Gly	Ala	Gln	Arg	Glu	Ser	Phe	
			105					110					115			

gac	acc	acc	gtg	gat	gtt	tcc	ttc	gac	ggg	gca	aca	ttc	ccc	gga	gtg	499
Asp	Thr	Thr	Val	Asp	Val	Ser	Phe	Asp	Gly	Ala	Thr	Phe	Pro	Gly	Val	
			120					125					130			

cag	gcc	tcg	ttt	atc	cga	gct	ccc	atc	gtc	act	gct	ttt	ggg	cct	acg	547
Gln	Ala	Ser	Phe	Ile	Arg	Ala	Pro	Ile	Val	Thr	Ala	Phe	Gly	Pro	Thr	
	135					140					145					

gta	gaa	gcg	atc	gct	gct	ctc	aac	ggg	ggg	gag	gtg	gtt	ggg	gta	cgc	595
Val	Glu	Ala	Ile	Ala	Ala	Leu	Asn	Gly	Gly	Glu	Val	Val	Gly	Val	Arg	
	150				155				160						165	

caa	ggc	aac	atc	atc	gcg	ctg	tct	ttc	cat	ccc	gaa	gaa	acc	ggc	gat	643
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<210>	387
<211>	601
<212>	DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

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cctccgtcat tgccgacgta tcccgcgccc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
                               Val Ile Val Gly Val
                               1           5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
                10                15                20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
                25                30                35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
                40                45                50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
                55                60                65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
                70                75                80                85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
                90                95                100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
                105                110                115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
                120                125                130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
                135                140                145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
                150                155                160                165

caa ggc
Gln Gly
601

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<210> 388

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

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Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
  1             5             10             15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
      20             25             30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
      35             40             45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
      50             55             60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
      65             70             75             80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
      85             90             95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
      100            105            110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
      115            120            125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
      130            135            140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
      145            150            155            160

Val Val Gly Val Arg Gln Gly
      165

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<210> 389

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA01098

<400> 389

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gcaggtaatg accagtcggtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                     Met Gly Val Ala Ile
                                     1             5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
      10             15             20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala

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[illegible]

<210> 390
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 390

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Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly
 1          5          10          15

Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp
          20          25          30

Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu
          35          40          45

Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu
          50          55          60

Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val
          65          70          75          80

Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala
          85          90          95

Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu
          100          105          110

Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu
          115          120          125

Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser
          130          135          140

Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp
          145          150          155          160

Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile
          165          170          175

Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu
          180          185          190

Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala
          195          200          205

Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala
          210          215          220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val
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Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val
          245          250          255

Arg Lys

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<210> 391
 <211> 729
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

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                                         Met Thr Val Ala Pro
                                         1 5
aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
                        10 15 20
gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
                        25 30 35
cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
                        40 45 50
gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
                        55 60 65
acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
                        70 75 80 85
att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
                        90 95 100
atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
                        105 110 115
tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
                        120 125 130
ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
                        135 140 145
gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
                        150 155 160 165
gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
                        170 175 180
ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
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<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

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Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
 195 200

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Thr Lys Gly Ala Leu
200

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Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
          20          25          30

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          35          40          45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
          50          55          60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
  65          70          75          80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
          85          90          95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
          100          105          110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
          115          120          125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
          130          135          140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
          145          150          155          160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
          165          170          175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
          180          185          190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
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<223> RXN00446
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Met Gly Ala Val Glu
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Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala				
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Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile				
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Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala				
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atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403			
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro				
				90					95					100					
tgc	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451			
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys				
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gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499			
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe				
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aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547			
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His				
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gac	aac	gtg	att	ggg	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595			
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala				
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Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala				
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Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala				
				185					190					195					
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739			
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val				
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gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	gg					

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 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcctttgg cgttttgagg 984
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 280 285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

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Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu
 130 135 140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220

Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240

Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255

Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270

Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 397
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 <213> *Corynebacterium glutamicum*

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 <222> (1)..(522)
 <223> FRXA00446

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 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

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<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

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<223> RXA01105

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                                         Met Thr Lys Ile Thr
                                         1           5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
                        10                        15                        20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
                        25                        30                        35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
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gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
                        55                        60                        65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
                        70                        75                        80                        85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
                        90                        95                        100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
                        105                        110                        115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
                        120                        125                        130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
                        135                        140                        145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
                        150                        155                        160                        165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
                        170                        175                        180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
                        185                        190                        195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739

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 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
 215 220 225
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 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
 230 235 240 245
 ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
 250 255 260
 ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
 265 270 275
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 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
 280 285 290
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 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
 295 300 305
 gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt 1075
 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
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 ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg 1123
 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
 330 335 340
 cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca 1171
 Arg Thr Thr Ile Gly Val Pro Glu Leu Asn Asp Ala Phe Leu Asp Ala
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<212> PRT

<213> Corynebacterium glutamicum

<400> 400

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 20 25 30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
 35 40 45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50 55 60
 Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
 65 70 75 80
 Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
 85 90 95
 Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
 100 105 110
 Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
 115 120 125
 Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
 130 135 140
 Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
 145 150 155 160
 Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
 165 170 175
 Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
 180 185 190
 Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
 195 200 205
 Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
 210 215 220
 Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
 225 230 235 240
 Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
 245 250 255
 Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
 260 265 270
 His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335
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<223> RXA01106
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Met Leu Asn Val Thr 5																	
gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163																	
Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu 20																	
cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211																	
Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro 35																	
gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259																	
Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr 50																	
ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307																	
Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala 65																	
gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355																	
Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu 85																	
tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403																	
Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln 100																	
aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act 451																	
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr 115																	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc 499																	
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly 130																	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa 547																	
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln 145																	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag 595																	
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu 165																	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg 643																	
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu 180																	

ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	1027
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	1075
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	1123
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	
330 335 340	
cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc	1171
Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly	
345 350 355	
gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac	1219
Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His	
360 365 370	
gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg	1267
Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr	
375 380 385	
cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct	1315
His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala	
390 395 400 405	
ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat	1363
Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp	
410 415 420	
ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc	1411

Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro
 425 430 435

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 Thr Thr Asp Glu Ala
 440

1449

<210> 402

<211> 442

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 402

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Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu
 20 25 30

Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu
 35 40 45

Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser
 50 55 60

Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp
 65 70 75 80

Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro
 100 105 110

Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu
 115 120 125

Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn
 130 135 140

Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser
 145 150 155 160

Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala
 165 170 175

Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly
 180 185 190

Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu
 195 200 205

Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala
 210 215 220

Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro
 225 230 235 240

Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val
 245 250 255

gag gac gac gag gcc taagaaaaat gacccaaatt act
 thr thr asp glt ala
 440

Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser
 260 265 270

Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu
 275 280 285

Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu
 290 295 300

Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser
 305 310 315 320

Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile
 325 330 335

His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly
 340 345 350

Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser
 355 360 365

Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser
 370 375 380

Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu
 385 390 395 400

Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala
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<210> 403

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXC00930

<400> 403

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ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115
 Met Ser Gly His Ser
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg

	25	30	35	
aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc				259
Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile				
	40	45	50	
aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca				307
Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala				
	55	60	65	
cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac				355
Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn				
	70	75	80	85
atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag				403
Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu				
	90	95	100	
tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca				451
Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala				
	105	110	115	
atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac				499
Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr				
	120	125	130	
atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt				547
Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser				
	135	140	145	
gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc				595
Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val				
	150	155	160	165
aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att				643
Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile				
	170	175	180	
cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat				691
Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp				
	185	190	195	
tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac				739
Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp				
	200	205	210	
ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac				787
Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp				
	215	220	225	
gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg				835
Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu				
	230	235	240	245
aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg				876
Thr Glu Leu Glu Asn Asp				
	250			

<210> 404

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
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Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
 20 25 30

Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
 35 40 45

Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
 50 55 60

Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80

Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95

Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110

Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125

Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
 145 150 155 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
 165 170 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
 180 185 190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
 195 200 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
 210 215 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
 225 230 235 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
 245 250

<210> 405

<211> 547

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(547)

<223> RXC01096

<400> 405

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gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115
Met Lys Pro Arg Val
1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Leu Val Leu
55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp
90 95 100

gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag 451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys
105 110 115

gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc 499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr
120 125 130

acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta 547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu
135 140 145

<210> 406

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 406

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Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala
 50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
 65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
 85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
 100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
 115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
 130 135 140

Ile Gly Cys Ala Leu
 145

<210> 407
 <211> 1020
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(997)
 <223> RXC01656

<400> 407
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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
 Met Thr Glu Thr Gln
 1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
 10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
 25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
 40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
 55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
 70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu

	90	95	100	
ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac				451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr				
	105	110	115	
acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc				499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly				
	120	125	130	
gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca				547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala				
	135	140	145	
atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct				595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala				
	150	155	160	165
gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc				643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser				
	170	175	180	
ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca				691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro				
	185	190	195	
tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc				739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val				
	200	205	210	
acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg				787
Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val				
	215	220	225	
cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa				835
Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys				
	230	235	240	245
tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg				883
Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile Val Lys Ala Ala Thr				
	250	255	260	
ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt				931
Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly				
	265	270	275	
gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga				979
Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg				
	280	285	290	
ctc gcc gag cgc ggc tgg tgatcggttg agttagct ctc				1020
Leu Ala Glu Arg Gly Trp				
	295			

<210> 408

<211> 299

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

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Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
              20              25              30

Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
              35              40              45

Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50              55              60

Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65              70              75              80

Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
              85              90              95

Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
              100              105              110

Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
              115              120              125

Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
              130              135              140

Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145              150              155              160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
              165              170              175

Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
              180              185              190

Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
              195              200              205

Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
              210              215              220

Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
 225              230              235              240

Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
              245              250              255

Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
              260              265              270

Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
              275              280              285

Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
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<210> 409

<211> 1065

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1042)

<223> RXC01158

<400> 409

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              Met Ser Ile Val Glu
              1              5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163
His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
              10              15              20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
              25              30              35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
              40              45              50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
              55              60              65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg 355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala
              70              75              80              85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg 403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu
              90              95              100

tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc 451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr
              105              110              115

gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt 499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val
              120              125              130

ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att 547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile
              135              140              145

ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga 595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly
              150              155              160              165

ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca 643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro
              170              175              180

ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc 691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala
              185              190              195

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att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct 739
 Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala
 200 205 210

gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg 787
 Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala
 215 220 225

ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc 835
 Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe
 230 235 240 245

aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat 883
 Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp
 250 255 260

gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct 931
 Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala
 265 270 275

cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg 979
 Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu
 280 285 290

aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac 1027
 Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp
 295 300 305

ttc ggt gac gtg ctc tagggcctag ccagggtaccc tta 1065
 Phe Gly Asp Val Leu
 310

<210> 410
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

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 Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
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Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
 20 25 30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala
 260 265 270
 Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
 275 280 285
 Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys
 290 295 300
 Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
 305 310

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<211> 1413

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1390)

<223> RXA02458

<400> 411

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 Met Val Phe Val Ser
 1 5

gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly
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ccc ata gtc tgc gac ctg gct atc cct ggt tcc aag tgc atc acc aac	211
Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn	
25 30 35	
cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att	259
Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile	
40 45 50	
gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc	307
Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg	
55 60 65	
agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt	355
Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val	
70 75 80 85	
gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt	403
Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly	
90 95 100	
acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct	451
Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro	
105 110 115	
gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc	499
Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser	
120 125 130	
att ttg gat gcg ctg cgt tgc ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt ccg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931

Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile
 265 270 275
 cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag 979
 Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln
 280 285 290
 ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc 1027
 Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly
 295 300 305
 att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg 1075
 Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala
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 gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct 1123
 Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala
 330 335 340
 cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag 1171
 His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu
 345 350 355
 atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg 1219
 Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu
 360 365 370
 att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat 1267
 Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp
 375 380 385
 cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc 1315
 His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly
 390 395 400 405
 gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt 1363
 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe
 410 415 420
 gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat 1410
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 ccg 1413

<210> 412

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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 20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr
 35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met
 50 55 60
 Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val
 65 70 75 80
 Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu
 85 90 95
 Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala
 100 105 110
 Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val
 115 120 125
 Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu
 130 135 140
 Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro
 145 150 155 160
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val
 165 170 175
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val
 180 185 190
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr
 195 200 205
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn
 210 215 220
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile
 225 230 235 240
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Val
 245 250 255
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln
 260 265 270
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val
 275 280 285
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro
 290 295 300
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu
 305 310 315 320
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg
 325 330 335
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala
 340 345 350
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu
 355 360 365
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp

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Met Glu Pro Val Tyr 1 5																
gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163																
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile 10 15 20																
ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211																
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg 25 30 35																
acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259																
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val 40 45 50																
gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307																
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu 55 60 65																
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355																
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser 70 75 80 85																
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403																
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln 90 95 100																
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451																
Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp 105 110 115																
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499																
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp 120 125 130																

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
 Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
 135 140 145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
 Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
 150 155 160 165

gat ttg cag cag gtt gcc tcc acc gtg tgc cct gca gaa ttg ggt gtc 643
 Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
 170 175 180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
 Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
 185 190 195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739
 Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser
 200 205 210

aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac 787
 Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn
 215 220 225

cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt 835
 His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu
 230 235 240 245

act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca 883
 Thr Pro Tyr Glu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala
 250 255 260

cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc 931
 Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu
 265 270 275

gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg 979
 Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu
 280 285 290

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc 1027
 Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
 295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc 1075
 Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
 310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga 1123
 Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
 330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc 1171
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
 345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac 1219
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
 360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg 1266

Ser Gly Val Leu Asp Ser Asn Arg
375 380

<210> 414

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

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Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
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Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
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<210> 415
 <211> 644
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(621)
 <223> RXN00954

<400> 415
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 Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro
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gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96
 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
 20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80

gtg cat ggc gca ggc acc gat gag atc gca gtc cac ggc acc acc ttg 288
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat tac acc atc gag 336
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110


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cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384
Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
      115                      120                      125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432
Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
      130                      135                      140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480
Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
      145                      150                      155                      160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528
Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
      165                      170                      175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576
Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
      180                      185                      190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621
Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
      195                      200                      205

tagtaataat ctgcccacag tgt 644

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<210> 416

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
      20                      25                      30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
      35                      40                      45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
      50                      55                      60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
      65                      70                      75                      80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
      85                      90                      95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
      100                      105                      110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
      115                      120                      125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
      130                      135                      140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala

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145		150		155		160									
Met	Phe	Tyr	Leu	Asn	Gly	Asp	Val	Asp	Ser	Leu	Lys	Asp	Gly	Ala	Gln
				165					170					175	
Lys	Ala	Leu	Ser	Leu	Leu	Ala	Asp	Gly	Thr	Thr	Gln	Ala	Trp	Leu	Ala
			180					185					190		
Lys	His	Glu	Glu	Ile	Asp	Tyr	Ser	Glu	Lys	Glu	Ser	Ser	Asn	Asp	
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<210> 417

<211> 611

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(588)

<223> FRXA00954

<400> 417

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Phe	Leu	Phe	Ala	Pro	Ala	Tyr	Asn	Pro	Ala	Ile	Ala	His	Val	Gln	Pro	
1				5					10					15		
gtt	cgc	cag	gcg	ctg	aaa	ttc	ccc	acc	atc	ttc	aac	acg	ctt	gga	cca	96
Val	Arg	Gln	Ala	Leu	Lys	Phe	Pro	Thr	Ile	Phe	Asn	Thr	Leu	Gly	Pro	
			20					25					30			
ttg	ctg	tcc	ccg	gcg	cgc	ccg	gag	cgt	cag	atc	atg	ggc	gtg	gcc	aat	144
Leu	Leu	Ser	Pro	Ala	Arg	Pro	Glu	Arg	Gln	Ile	Met	Gly	Val	Ala	Asn	
		35					40					45				
gcc	aat	cat	gga	cag	ctc	atc	gcc	gag	gtc	ttc	cgc	gag	ttg	ggc	cgt	192
Ala	Asn	His	Gly	Gln	Leu	Ile	Ala	Glu	Val	Phe	Arg	Glu	Leu	Gly	Arg	
	50					55					60					
aca	cgc	gcg	ctt	gtt	gtg	cat	ggc	gca	ggc	acc	gat	gag	atc	gca	gtc	240
Thr	Arg	Ala	Leu	Val	Val	His	Gly	Ala	Gly	Thr	Asp	Glu	Ile	Ala	Val	
	65				70					75					80	
cac	ggc	acc	acc	ttg	gtg	tgg	gag	ctt	aaa	gaa	gac	ggc	acc	atc	gag	288
His	Gly	Thr	Thr	Leu	Val	Trp	Glu	Leu	Lys	Glu	Asp	Gly	Thr	Ile	Glu	
			85						90					95		
cat	tac	acc	atc	gag	cct	gag	gac	ctt	ggc	ctt	ggc	cgc	tac	acc	ctt	336
His	Tyr	Thr	Ile	Glu	Pro	Glu	Asp	Leu	Gly	Leu	Gly	Arg	Tyr	Thr	Leu	
			100					105					110			
gag	gat	ctc	gta	ggt	ggc	ctc	ggc	act	gag	aac	gcc	gaa	gct	atg	cgc	384
Glu	Asp	Leu	Val	Gly	Gly	Leu	Gly	Thr	Glu	Asn	Ala	Glu	Ala	Met	Arg	
		115					120					125				
gct	act	ttc	gcg	ggc	acc	ggc	cct	gat	gca	cac	cgt	gat	gcg	ttg	gct	432
Ala	Thr	Phe	Ala	Gly	Thr	Gly	Pro	Asp	Ala	His	Arg	Asp	Ala	Leu	Ala	
		130				135					140					
gcg	tcc	gca	ggt	gcg	atg	ttc	tac	ctc	aac	ggc	gat	gtc	gac	tcc	ttg	480
Ala	Ser	Ala	Gly	Ala	Met	Phe	Tyr	Leu	Asn	Gly	Asp	Val	Asp	Ser	Leu	

145 150 155 160
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
 165 170 175

 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
 180 185 190

 tct tcc aat gac tagtaataat ctgcccacag tgt 611
 Ser Ser Asn Asp
 195

<210> 418

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro
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 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro
 20 25 30

 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
 35 40 45

 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
 50 55 60

 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
 65 70 75 80

 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
 85 90 95

 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
 100 105 110

 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
 115 120 125

 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
 130 135 140

 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
 145 150 155 160

 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
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 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
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 Ser Ser Asn Asp
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<223> RXN00957
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Met Ser Thr Asn Pro 5																
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163																
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu 20																
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211																
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu 35																
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259																
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu 50																
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Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln 65																
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Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln 85																
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403																
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser 100																
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451																
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu 115																
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Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu 130																
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547																
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu 145																
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595																
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln 165																
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643																
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr 180																

gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag	691
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu	
185 190 195	
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa	739
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu	
200 205 210	
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg	787
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val	
215 220 225	
gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa	835
Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys	
230 235 240 245	
gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act	883
Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr	
250 255 260	
ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt	931
Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg	
265 270 275	
gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa	979
Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu	
280 285 290	
ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag	1027
Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys	
295 300 305	
ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc	1075
Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr	
310 315 320 325	
cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat	1123
Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp	
330 335 340	
atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag	1171
Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu	
345 350 355	
cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg	1219
His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser	
360 365 370	
gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat	1267
Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr	
375 380 385	
tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca	1315
Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro	
390 395 400 405	
gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg	1363
Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr	
410 415 420	
ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc	1411

Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc 1459
 Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg
 440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc 1507
 Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val
 455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat 1555
 Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp
 470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc 1603
 Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala
 490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc 1651
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 Arg

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 <213> *Corynebacterium glutamicum*

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 35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn
 50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala
 65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe
 85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala
 100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr
 115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe
 130 135 140

Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr
 145 150 155 160
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn
 165 170 175
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly
 180 185 190
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala
 195 200 205
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp
 210 215 220
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln
 225 230 235 240
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val
 245 250 255
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala
 260 265 270
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile
 275 280 285
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro
 290 295 300
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr
 305 310 315 320
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile
 325 330 335
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala
 340 345 350
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp
 355 360 365
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu
 370 375 380
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr
 385 390 395 400
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys
 405 410 415
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu
 420 425 430
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala
 435 440 445
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<223> FRXA00957
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aac	act	tac	ccc	gat	tac	cag	ttc	gtc	ctc	gcg	gaa	atc	gtc	ctg	gac	96
Asn	Thr	Tyr		Pro	Asp	Tyr	Gln	Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp
			20					25					30			
atc	aat	cac	cag	gac	cag	acc	gcc	aaa	ctc	gcc	ggc	gtc	tcc	aac	gcc	144
Ile	Asn	His	Gln	Asp	Gln	Thr	Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala	
		35					40					45				
cca	ggc	gag	ctc	gag	gcc	gag	ctc	aac	aag	ctt	tca	ttg	ctt	atc	gac	192
Pro	Gly	Glu	Leu	Glu	Ala	Glu	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp	
	50					55					60					
gcc	gcc	ctc	ccc	gca	acc	gaa	cac	gcc	tac	caa	acc	acc	cct	cac	gac	240
Ala	Ala	Leu	Pro	Ala	Thr	Glu	His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp	
65					70					75					80	
ggc	gac	act	ctt	cgc	gtt	gtg	gct	gat	att	ccc	gat	gct	cag	ttc	cgc	288
Gly	Asp	Thr	Leu	Arg	Val	Val	Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg	
				85					90					95		
acc	cag	atc	aat	gag	ctg	aaa	gaa	aac	att	tac	aac	ggg	gac	atc	tac	336
Thr	Gln	Ile	Asn	Glu	Leu	Lys	Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr	
			100					105					110			
caa	gtt	gtc	ccg	gcg	cgc	act	ttc	acc	gca	cca	tgt	cct	gat	gca	ttc	384
Gln	Val	Val	Pro	Ala	Arg	Thr	Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe	
		115					120					125				
gct	gct	tat	ctg	cag	ctg	cgt	gcc	acc	aac	ccg	tcg	ccg	tac	atg	ttc	432
Ala	Ala	Tyr	Leu	Gln	Leu	Arg	Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe	
	130					135						140				
tat	atc	cgt	ggc	ctc	aac	gaa	ggc	cgc	tcc	tat	gaa	ctt	ttt	ggc	gca	480
Tyr	Ile	Arg	Gly	Leu	Asn	Glu	Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala	

145	150	155	160	
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Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln	165	170	175	
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc				576
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly	180	185	190	
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act				624
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr	195	200	205	
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc				672
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg	210	215	220	
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat				720
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp	225	230	235	240
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt				768
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg	245	250	255	
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg				816
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg	260	265	270	
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct				864
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala	275	280	285	
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt				912
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly	290	295	300	
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att				960
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile	305	310	315	320
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct				1008
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala	325	330	335	
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag				1056
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu	340	345	350	
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct				1104
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala	355	360	365	
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Gly Ser Thr Leu Glu Val Ile Arg	370	375		

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<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
      35              40              45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
      50              55              60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
      65              70              75              80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
      85              90              95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
      100              105              110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
      115              120              125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe
      130              135              140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala
      145              150              155              160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln
      165              170              175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly
      180              185              190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr
      195              200              205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg
      210              215              220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp
      225              230              235              240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg
      245              250              255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg
      260              265              270

Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala
      275              280              285

Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly
      290              295              300

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Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile
 305 310 315 320

Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala
 325 330 335

Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu
 340 345 350

Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala
 355 360 365

Gly Ser Thr Leu Glu Val Ile Arg
 370 375

<210> 423

<211> 1068

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA02687

<400> 423

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 Met Ser Asp Ala Pro
 1 5

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala
 10 15 20

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu
 25 30 35

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His
 40 45 50

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly
 55 60 65

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln
 70 75 80 85

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val
 105 110 115

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ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499
Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala
120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547
Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala
135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595
Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu
150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643
Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala
170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691
Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro
185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739
Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro
200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787
Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp
215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835
Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr
230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883
Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala
250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931
Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val
265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979
Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp
280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc 1027
Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser
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gaa gga agg aaa ctt aac tagccatggc cggccggatt att 1068
Glu Gly Arg Lys Leu Asn
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<210> 424

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

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 35 40 45
 Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
 50 55 60
 Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
 65 70 75 80
 Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
 85 90 95
 Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
 100 105 110
 Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
 115 120 125
 Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
 130 135 140
 Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Ala Pro Ser
 145 150 155 160
 Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
 165 170 175
 Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
 180 185 190
 Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
 195 200 205
 Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
 210 215 220
 Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
 225 230 235 240
 Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
 245 250 255
 Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
 260 265 270
 Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
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<210> 425

<211> 1353

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(1330)

<223> RXN01698

<400> 425

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 Met Leu Gly Met Leu
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
 70 75 80 85

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 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
 90 95 100

cca gat aac gtt gcg gcg atg tct tct ggt cgg ggc gca aaa ctg act 451
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595
 Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu
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acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643
 Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser
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gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691
 Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile

185					190					195						
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Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	Gly	Leu	Gly	Ser	His	
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ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggg	gac	ggg	ttc	gaa	gaa	931
Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	Asp	Gly	Phe	Glu	Glu	
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gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	gtg	ttc	ctg	gat	gac	979
Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	Val	Phe	Leu	Asp	Asp	
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tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	atg	gaa	aac	ggc	aag	1123
Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	Met	Glu	Asn	Gly	Lys	
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Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	Cys	Ala	Val	Pro	Ala	
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Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	Val	Leu	Ala	Arg	Ala	
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Val	Leu	Gln	Lys	Phe	Gly	Gly	Asp	Ser	Leu	Ser	Glu	Thr	Lys	Ser	Asn	
	375					380					385					
att	gac	acc	tac	ctc	aaa	aac	att	gag	gaa	cga	atg	aaa	ttc	gaa	ggg	1315
Ile	Asp	Thr	Tyr	Leu	Lys	Asn	Ile	Glu	Glu	Arg	Met	Lys	Phe	Glu	Gly	
390						395				400				405		
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<210> 426

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

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Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
      35          40          45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
      50          55          60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
      65          70          75          80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
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Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
      100          105          110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
      115          120          125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
      130          135          140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
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Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
      165          170          175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
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Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
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Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
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Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
      225          230          235          240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
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Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
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Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
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Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
      290          295          300

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Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
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Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
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Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
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Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
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 <213> Corynebacterium glutamicum

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 <222> (1)..(990)
 <223> FRXA01698

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 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Met Ser Ser Gly Arg
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ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 35 40 45

atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct 192
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
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tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt 240
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 65 70 75 80

tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att 288
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 85 90 95

tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca 336
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 100 105 110

gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac 384
Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
115 120 125

gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc 432
Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
130 135 140

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Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
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ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc 528
Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
165 170 175

gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt 576
Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
180 185 190

gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa 624
Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
195 200 205

gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt 672
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
210 215 220

ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct 720
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
225 230 235 240

ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat 768
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
245 250 255

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Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
260 265 270

tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg 864
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
275 280 285

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
305 310 315 320

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Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
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ttc 1013

<210> 428

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

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 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 35 40 45
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 50 55 60
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 65 70 75 80
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 85 90 95
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 100 105 110
 Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 115 120 125
 Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 130 135 140
 Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 145 150 155 160
 Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 165 170 175
 Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 180 185 190
 Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
 195 200 205
 Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
 210 215 220
 Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
 225 230 235 240
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 245 250 255
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 260 265 270
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 275 280 285
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
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Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
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Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
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<211> 906

<212> DNA

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<221> CDS

<222> (101)..(883)

<223> RXA01095

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                                     Met Val Ala Thr Glu
                                     1 5
aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163
Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala
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acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211
Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu
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Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn
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Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser
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gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355
Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met
                                     70 75 80 85
ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403
Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp
                                     90 95 100
atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451
Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp
                                     105 110 115
ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499
Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile
                                     120 125 130
gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547
Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu
                                     135 140 145
tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595

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Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser
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 gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr
 170 175 180

 gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro
 185 190 195

 gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg
 200 205 210

 att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala
 215 220 225

 cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr
 230 235 240 245

 aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt 883
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg
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 tgaagaggtg ctctgtggtc agc 906

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 <211> 261
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30

 Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe
 35 40 45

 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn
 50 55 60

 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly
 65 70 75 80

 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp
 85 90 95

 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro
 100 105 110

 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala
 115 120 125

 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu

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Met Thr Ser Asn Asn																
1 5																
ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg																163
Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu																
10 15 20																
gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca																211
Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro																
25 30 35																
aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg																259
Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly																
40 45 50																
gcg cgt ttc atc atg gag tgc aag tcc gca tcg cct tct ttg gga atg																307
Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met																
55 60 65																
att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc																355

Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg	
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Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly	
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Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val	
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ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt	499
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg	
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Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp	
	135					140					145					
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat	595
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp	
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Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys	
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Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu	
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Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala	
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Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val	
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Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu	
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Thr	Ser	Gln	Glu	Asn	Val	Asp	Leu	Ala	Ala	Arg	Glu	Leu	Val	Tyr	Gly	
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Pro	Asn	Lys	Val	Cys	Gly	Leu	Thr	Ser	Pro	Ser	Ala	Ala	Gln	Thr	Ala	
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cgc	gca	gcg	ggt	gcg	gtc	tac	ggc	ggg	ctc	atc	ttc	gaa	gag	gca	tcg	979
Arg	Ala	Ala	Gly	Ala	Val	Tyr	Gly	Gly	Leu	Ile	Phe	Glu	Glu	Ala	Ser	
	280						285					290				
cca	cgc	aat	gtt	tca	cgt	gaa	aca	ttg	caa	aaa	atc	atc	gcc	gca	gag	1027
Pro	Arg	Asn	Val	Ser	Arg	Glu	Thr	Leu	Gln	Lys	Ile	Ile	Ala	Ala	Glu	
	295					300					305					
ccc	aac	ctg	cgc	tac	gtc	gcg	gtc	agc	cgt	cgc	acc	tcc	ggg	tac	aag	1075
Pro	Asn	Leu	Arg	Tyr	Val	Ala	Val	Ser	Arg	Arg	Thr	Ser	Gly	Tyr	Lys	

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Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu
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cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa 1171
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu
          345          350          355

gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc 1219
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser
          360          365          370

ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag 1267
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys
          375          380          385

cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg 1315
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp
          390          395          400          405

gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc 1363
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly
          410          415          420

atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt 1411
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly
          425          430          435

ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg 1459
Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp
          440          445          450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc 1507
Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile
          455          460          465

tcc aca ttc cat tac taaaggttta aataggatca tga 1545
Ser Thr Phe His Tyr
470

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<210> 432

<211> 474

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 432

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Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
  1              5              10              15

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Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
      20              25              30

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Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
      35              40              45

```

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Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
      50              55              60

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Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala
 65 70 75 80
 Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro
 85 90 95
 Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr
 100 105 110
 Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln
 115 120 125
 Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu
 130 135 140
 Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala
 145 150 155 160
 Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val
 165 170 175
 Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg
 180 185 190
 Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser
 195 200 205
 Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg
 210 215 220
 Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
 225 230 235 240
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
 245 250 255
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
 260 265 270
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
 275 280 285
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
 290 295 300
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
 305 310 315 320
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
 325 330 335
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
 340 345 350
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
 355 360 365
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
 370 375 380
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly

385		390		395		400
Glu Val Phe Asp Trp	Ala Thr Val Pro	Ala Ala Val Lys	Ala Lys Ser			
	405		410			415
Leu Leu Ala Gly Gly	Ile Ser Pro Asp	Asn Ala Ala Gln	Ala Leu Ala			
	420		425			430
Val Gly Cys Ala Gly	Leu Asp Ile Asn	Ser Gly Val Glu	Tyr Pro Ala			
	435		440			445
Gly Ala Gly Thr Trp	Ala Gly Ala Lys	Asp Ala Gly	Ala Leu Leu	Lys		
	450		455			460
Ile Leu Ala Thr Ile	Ser Thr Phe His	Tyr				
465		470				

<210> 433

<211> 494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> RXA02814

<400> 433

gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr

1

5

10

15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu

20

25

30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly

35

40

45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr

50

55

60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240

His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala

65

70

75

80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288

Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala

85

90

95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336

Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg

100

105

110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384

Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly

115

120

125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
 130 135 140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
 145 150 155

tcttaaaaca ccg 494

<210> 434

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
 1 5 10 15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
 20 25 30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
 35 40 45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
 50 55 60

His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
 65 70 75 80

Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
 85 90 95

Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
 100 105 110

Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
 115 120 125

Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
 130 135 140

Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
 145 150 155

<210> 435

<211> 803

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(780)

<223> RXA00229

<400> 435

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 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile

1	5	10	15	
gac acg ctt ggg tgc cgt gct tcc ggg caa gat tta aat acg ctt ctc				96
Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu				
	20	25	30	
gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg				144
Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro				
	35	40	45	
tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc				192
Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala				
	50	55	60	
acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac				240
Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His				
	65	70	75	80
acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa				288
Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu				
	85	90	95	
gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc				336
Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala				
	100	105	110	
ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg				384
Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val				
	115	120	125	
cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg				432
Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu				
	130	135	140	
gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta				480
Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val				
	145	150	155	160
gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc				528
Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val				
	165	170	175	
aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat				576
Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp				
	180	185	190	
gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg				624
Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met				
	195	200	205	
ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa				672
Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu				
	210	215	220	
acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc				720
Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe				
	225	230	235	240
cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act				768
Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr				
	245	250	255	

ttc ctg tcc ctc taaaagagtc agtaaacct cga
 Phe Leu Ser Leu
 260

803

<210> 436

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15

Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30

Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45

Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60

Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80

Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110

Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125

Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140

Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160

Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175

Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190

Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205

Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220

Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240

Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255

Phe Leu Ser Leu

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<210> 437
<211> 927
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(904)  
<223> RXA02093
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<400> 437																
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ttgctcttcc tttgctccgc atgagtataa aatcactgtc atg gtc aac tac gtc																115
Met Val Asn Tyr Val																5
1																
gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac																163
Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn																20
10																
15																
cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac																211
His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn																35
25																
30																
35																
tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca																259
Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile Thr Ala Ala Val Ala																50
40																
45																
50																
ggt atc cgt ggt ctg aac att cgc ggc gca ggt gtc tcc atg cca tac																307
Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly Val Ser Met Pro Tyr																65
55																
60																
65																
aag agc gat gtc atc cca ctc atc gat gag ttg cat cct tcc gca gag																355
Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu His Pro Ser Ala Glu																85
70																
75																
80																
85																
cgc ata cgt tct gtt aac acc atc gtc aac aat gac gga cac ctt gtc																403
Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn Asp Gly His Leu Val																100
90																
95																
100																
gga tac aac acc gac tac act gcg gtg tac cac ctc ctt gaa gaa cac																451
Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His Leu Leu Glu Glu His																115
105																
110																
115																
cgc gtg aac ccc aat gca cga gta gct atc aag gga tcc gcc gcc atg																499
Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys Gly Ser Gly Gly Met																130
120																
125																
130																
135																
140																
145																
gcc aat gct gtt gtt gca gct ctt gct gag tat ggt ctg agt gcc acc																547
Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr Gly Leu Ser Gly Thr																165
135																
140																
145																
150																
155																
160																
165																
gtc gtt gcc cgc aac cac acc acc ggt tct gcg cta gct tcc cgt tac																595
Val Val Ala Arg Asn His Thr Thr Gly Ser Ala Leu Ala Ser Arg Tyr																165
150																
155																
160																
165																
ggg tgg gaa tac tcc gca act gtt ccg gaa gac gca aaa att ttg gtt																643

Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp Ala Lys Ile Leu Val
 170 175 180

aat gta acc cca atg gga atg aat gga cct gac caa gac gtt gta tct 691
 Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp Gln Asp Val Val Ser
 185 190 195

ttt ggt gag gat gaa gta gac cga gcc gac gta atc ttt gac tgc gta 739
 Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val Ile Phe Asp Cys Val
 200 205 210

gca ttc ccc gtc gag acc cca ctg att aag ttg gcc aag gaa aag ggt 787
 Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu Ala Lys Glu Lys Gly
 215 220 225

aag caa acc atc gac ggc gga gaa gtt gcc gct ctt cag gca gca gag 835
 Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala Leu Gln Ala Ala Glu
 230 235 240 245

cag ttc cac ctc tac acc gga gtt ctt cca acc aac gac cag atc att 883
 Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr Asn Asp Gln Ile Ile
 250 255 260

gct gcg gag gag ttc tcc aag taaatttctc tccccatttt tta 927
 Ala Ala Glu Glu Phe Ser Lys
 265

<210> 438
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 438
 Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
 1 5 10 15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
 20 25 30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
 35 40 45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
 50 55 60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
 65 70 75 80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
 85 90 95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
 100 105 110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
 115 120 125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
 145 150 155 160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
 165 170 175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
 180 185 190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
 195 200 205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
 210 215 220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
 225 230 235 240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
 245 250 255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
 260 265

<210> 439

<211> 951

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXA02791

<400> 439

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ggcgttctag acagcaaccg ataaggatca gccaataaaa ttg ggt tct cac atc 115
 Leu Gly Ser His Ile
 1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
 Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
 10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
 Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
 25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
 Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
 40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
 Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
 55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
 Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
 70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
 Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
 90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
 Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
 105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
 Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
 120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
 Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
 135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
 Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
 150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
 Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
 170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
 His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
 185 190 195

gca atc gca ggc ctc gaa gac acc ctt ggc atc gcc cca gtc ctc gac 739
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp
 200 205 210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala
 215 220 225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser
 230 235 240 245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala
 250 255 260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His
 265 270 275

taagtccccg ccacctcctc aac 951

<210> 440

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile
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Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu
 20 25 30
 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met
 35 40 45
 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser
 50 55 60
 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val
 65 70 75 80
 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr
 85 90 95
 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly
 100 105 110
 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala
 115 120 125
 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu
 130 135 140
 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg
 145 150 155 160
 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala
 165 170 175
 Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser
 180 185 190
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile
 195 200 205
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val
 210 215 220
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met
 225 230 235 240
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp
 245 250 255
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile
 260 265 270
 Ser Glu Glu His
 275

<210> 441

<211> 693

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(670)

<223> RXA01699

<400> 441

ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60

aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115
Met Glu Arg Asn Glu
1 5

gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163
Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu
10 15 20

tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211
Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys
25 30 35

tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259
Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val
40 45 50

gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307
Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala
55 60 65

gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355
Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile
70 75 80 85

cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403
His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly
90 95 100

gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451
Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp
105 110 115

gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499
Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala
120 125 130

aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547
Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His
135 140 145

tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595
Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala
150 155 160 165

acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643
Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala
170 175 180

gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690
Ala Val Leu His His Leu Glu Ile Asp
185 190

tta 693

<210> 442

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

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Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
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Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
          20          25          30
Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
          35          40          45
Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
          50          55          60
Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
          65          70          75          80
Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
          85          90          95
Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
          100          105          110
Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
          115          120          125
Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala
          130          135          140
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu
          145          150          155          160
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro
          165          170          175
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp
          180          185          190

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<210> 443

<211> 959

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (97)..(936)

<223> RXA00952

<400> 443

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cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat      114
                               Met Ser Arg Tyr Asp Asp
                               1          5
ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc      162
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe
          10          15          20

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Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser	
25 30 35	
aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc	258
Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe	
40 45 50	
tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc	306
Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg	
55 60 65 70	
gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag	354
Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys	
75 80 85	
cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac	402
Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr	
90 95 100	
ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc	450
Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe	
105 110 115	
gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga	498
Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg	
120 125 130	
gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc	546
Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro	
135 140 145 150	
att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc	594
Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val	
155 160 165	
tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc	642
Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val	
170 175 180	
acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg	690
Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val	
185 190 195	
gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc	738
Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly	
200 205 210	
atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc	786
Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser	
215 220 225 230	
ggc gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc	834
Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys	
235 240 245	
gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg	882
Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu	
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aag gtt taggccttta aatgtggcaa tgt 959
Lys Val
280

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<213> Corynebacterium glutamicum

<400> 444																
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Gly	Ala	Phe	Val	Pro	Phe	Ile	Met	Leu	Ser	Asp	Pro	Ser	Pro	Glu	Glu	
			20					25					30			
Ala	Phe	Gln	Ile	Ile	Ser	Thr	Ala	Ile	Glu	Ala	Gly	Ala	Asp	Ala	Leu	
		35					40					45				
Glu	Leu	Gly	Val	Pro	Phe	Ser	Asp	Pro	Val	Ala	Asp	Gly	Pro	Thr	Val	
	50					55					60					
Ala	Glu	Ser	His	Leu	Arg	Ala	Leu	Asp	Gly	Gly	Ala	Thr	Val	Asp	Ser	
65					70					75					80	
Ala	Leu	Glu	Gln	Ile	Lys	Arg	Val	Arg	Ala	Ala	Tyr	Pro	Glu	Val	Pro	
				85					90					95		
Ile	Gly	Met	Leu	Ile	Tyr	Gly	Asn	Val	Pro	Phe	Thr	Arg	Gly	Leu	Asp	
			100					105					110			
Arg	Phe	Tyr	Gln	Glu	Phe	Ala	Glu	Ala	Gly	Ala	Asp	Ser	Ile	Leu	Leu	
		115					120					125				
Pro	Asp	Val	Pro	Val	Arg	Glu	Gly	Ala	Pro	Phe	Ser	Ala	Ala	Ala	Ala	
	130					135					140					
Ala	Ala	Gly	Ile	Asp	Pro	Ile	Tyr	Ile	Ala	Pro	Ala	Asn	Ala	Ser	Glu	
145				150						155					160	
Lys	Thr	Leu	Glu	Gly	Val	Ser	Ala	Ala	Ser	Lys	Gly	Tyr	Ile	Tyr	Ala	
			165						170					175		
Ile	Ser	Arg	Asp	Gly	Val	Thr	Gly	Thr	Glu	Arg	Glu	Ser	Ser	Thr	Asp	
			180					185					190			
Gly	Leu	Ser	Ala	Val	Val	Asp	Asn	Ile	Lys	Lys	Phe	Asp	Gly	Ala	Pro	
		195					200					205				
Ile	Leu	Leu	Gly	Phe	Gly	Ile	Ser	Ser	Pro	Gln	His	Val	Ala	Asp	Ala	
	210					215					220					
Ile	Ala	Ala	Gly	Ala	Ser	Gly	Ala	Ile	Thr	Gly	Ser	Ala	Ile	Thr	Lys	
225					230					235					240	
Ile	Ile	Ala	Ser	His	Cys	Glu	Gly	Glu	His	Pro	Asn	Pro	Ser	Thr	Ile	

[illegible]

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
 Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
 150 155 160 165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
 Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
 170 175 180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
 Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
 185 190 195

tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739
 Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val
 200 205 210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787
 Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu
 215 220 225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835
 Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly
 230 235 240 245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883
 Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly
 250 255 260

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc gcc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc gaa gta 1237
 Ala Lys Thr Ala Glu Val
 375

<210> 446

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 446

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Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
  1              5              10              15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
      20              25              30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
      35              40              45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
      50              55              60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
      65              70              75              80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
      85              90              95

Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
      100             105             110

Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
      115             120             125

Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
      130             135             140

Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
      145             150             155             160

Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
      165             170             175

Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
      180             185             190

Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
      195             200             205

Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
      210             215             220

Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
      225             230             235             240

Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
      245             250             255

Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
      260             265             270

Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
      275             280             285

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Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
 290 295 300

Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
 305 310 315 320

Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr
 325 330 335

Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala
 340 345 350

Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala
 355 360 365

Tyr Ala Leu Lys Arg Ala Lys Thr Ala Glu Val
 370 375

<210> 447
 <211> 1231
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1231)
 <223> FRXA00956

<400> 447
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accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115
 Met Thr Glu Lys Glu
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
 10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
 25 30 35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451

Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	
gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc	931
Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly	
265 270 275	
aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc	979
Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly	
280 285 290	
acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc	1027
Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser	
295 300 305	
tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac	1075
Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His	
310 315 320 325	
gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac	1123
Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp	
330 335 340	
gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc	1171
Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile	

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          345                      350                      355
atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc 1219
Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
          360                      365                      370

gcc aag acc gcc 1231
Ala Lys Thr Ala
          375

<210> 448
<211> 377
<212> PRT
<213> Corynebacterium glutamicum

<400> 448
Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
  1                      5                      10                      15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
          20                      25                      30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
          35                      40                      45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
          50                      55                      60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
          65                      70                      75                      80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
          85                      90                      95

Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
          100                      105                      110

Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
          115                      120                      125

Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
          130                      135                      140

Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
          145                      150                      155                      160

Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
          165                      170                      175

Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
          180                      185                      190

Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
          195                      200                      205

Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
          210                      215                      220

Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
          225                      230                      235                      240

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Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
 245 250 255

Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
 260 265 270

Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
 275 280 285

Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
 290 295 300

Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
 305 310 315 320

Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr
 325 330 335

Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala
 340 345 350

Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala
 355 360 365

Tyr Ala Leu Lys Arg Ala Lys Thr Ala
 370 375

<210> 449

<211> 1401

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1378)

<223> RXA00064

<400> 449

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ggctccgtcta ttttgcacc acatgcggag gtacgcagtt atg agt tca gtt tcg 115
 Met Ser Ser Val Ser
 1 5

ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163
 Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile
 10 15 20

aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211
 Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu
 25 30 35

act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259
 Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu
 40 45 50

ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307
 Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp
 55 60 65

gtc cgt aac tat ggc ggg ctg gat ggc atc gtt gat att cgc cag att	355
Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile	
70 75 80 85	
tggt gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggg gat	403
Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp	
90 95 100	
gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att	451
Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile	
105 110 115	
ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt	499
Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val	
120 125 130	
aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg	547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr	
135 140 145	
gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc	595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly	
150 155 160 165	
cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag	643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys	
170 175 180	
ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg	691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val	
185 190 195	
aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg	739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro	
200 205 210	
gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc	787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr	
215 220 225	
gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct	835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala	
230 235 240 245	
ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act	883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr	
250 255 260	
ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc	931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg	
265 270 275	
aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag	979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys	
280 285 290	
gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg	1027
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val	
295 300 305	

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac 1075
 Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn
 310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg 1123
 Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala
 330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt 1171
 Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val
 345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc 1219
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag 1267
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt 1315
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg 1363
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala
 410 415 420

gag cat tac gct aac taaaagtgaac tacagcggag aca 1401
 Glu His Tyr Ala Asn
 425

<210> 450

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu
 1 5 10 15

Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser

115					120					125					
Lys	Glu	Glu	Thr	Val	Lys	Trp	Ile	Cys	Pro	Val	Pro	Gly	Tyr	Asp	Arg
130					135					140					
His	Phe	Ser	Ile	Thr	Glu	Arg	Phe	Gly	Phe	Glu	Met	Ile	Ser	Val	Pro
145					150					155					160
Met	Asn	Glu	Asp	Gly	Pro	Asp	Met	Asp	Ala	Val	Glu	Glu	Leu	Val	Lys
				165					170					175	
Asn	Pro	Gln	Val	Lys	Gly	Met	Trp	Val	Val	Pro	Val	Phe	Ser	Asn	Pro
			180					185					190		
Thr	Gly	Phe	Thr	Val	Thr	Glu	Asp	Val	Ala	Lys	Arg	Leu	Ser	Ala	Met
			195				200					205			
Glu	Thr	Ala	Ala	Pro	Asp	Phe	Arg	Val	Val	Trp	Asp	Asn	Ala	Tyr	Ala
						215					220				
Val	His	Thr	Leu	Thr	Asp	Glu	Phe	Pro	Glu	Val	Ile	Asp	Ile	Val	Gly
225					230					235					240
Leu	Gly	Glu	Ala	Ala	Gly	Asn	Pro	Asn	Arg	Phe	Trp	Ala	Phe	Thr	Ser
				245					250					255	
Thr	Ser	Lys	Ile	Thr	Leu	Ala	Gly	Ala	Gly	Val	Ser	Phe	Phe	Leu	Thr
			260					265					270		
Ser	Ala	Glu	Asn	Arg	Lys	Trp	Tyr	Thr	Gly	His	Ala	Gly	Ile	Arg	Gly
			275				280					285			
Ile	Gly	Pro	Asn	Lys	Val	Asn	Gln	Leu	Ala	His	Ala	Arg	Tyr	Phe	Gly
			290			295					300				
Asp	Ala	Glu	Gly	Val	Arg	Ala	Val	Met	Arg	Lys	His	Ala	Ala	Ser	Leu
305					310					315					320
Ala	Pro	Lys	Phe	Asn	Lys	Val	Leu	Glu	Ile	Leu	Asp	Ser	Arg	Leu	Ala
				325					330					335	
Glu	Tyr	Gly	Val	Ala	Gln	Trp	Thr	Val	Pro	Ala	Gly	Gly	Tyr	Phe	Ile
			340					345					350		
Ser	Leu	Asp	Val	Val	Pro	Gly	Thr	Ala	Ser	Arg	Val	Ala	Glu	Leu	Ala
		355					360					365			
Lys	Glu	Ala	Gly	Ile	Ala	Leu	Thr	Gly	Ala	Gly	Ser	Ser	Tyr	Pro	Leu
						375					380				
Arg	Gln	Asp	Pro	Glu	Asn	Lys	Asn	Leu	Arg	Leu	Ala	Pro	Ser	Leu	Pro
385					390					395					400
Pro	Val	Glu	Glu	Leu	Glu	Val	Ala	Met	Asp	Gly	Val	Ala	Thr	Cys	Val
				405					410					415	
Leu	Leu	Ala	Ala	Ala	Glu	His	Tyr	Ala	Asn						
				420				425							

<210> 451


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<220>  
<221> CDS  
<222> (101)..(1120)  
<223> RXN00448
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ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtgtt 60

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691

```

Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
      185                      190                      195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
      200                      205                      210

ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787
Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser
      215                      220                      225

acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835
Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu
      230                      235                      240

agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883
Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile
      250                      255                      260

ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931
Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu
      265                      270                      275

caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979
Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg
      280                      285                      290

tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca 1027
Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser
      295                      300                      305

tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag 1075
Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys
      310                      315                      320

cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc 1120
Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
      330                      335                      340

tagttttatc ggctgatgat tct 1143

```

<210> 452

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
  1                      5                      10                      15

```

```

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
      20                      25                      30

```

```

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
      35                      40                      45

```

```

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
      50                      55                      60

```

```

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile

```

65	70	75	80
Asp Ser Leu Leu	Asp Ala Val His Thr	His Ala Pro Asn Asn Gly Phe	
	85	90	95
Thr Asp Val Val	Ser Val Lys Thr	Ala Val Tyr Asp Ala Val Lys Ala	
	100	105	110
Arg Asn Met Gln His Arg Tyr	Val Gly Ser His Pro Met Ala Gly Thr		
	115	120	125
Ala Asn Ser Gly Trp Ser	Ala Ser Met Asp Gly Leu Phe Lys Arg Ala		
	130	135	140
Val Trp Val Val Thr	Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn		
	145	150	155
Ser Thr Trp Ile	Ser Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala		
	165	170	175
Val Gly Ala Glu Val Val Pro Ser	Arg Val Gly Pro His Asp Ala Ala		
	180	185	190
Ala Ala Arg Val Ser His Leu Thr	His Ile Leu Ala Glu Thr Leu Ala		
	195	200	205
Ile Val Gly Asp Asn Gly Gly	Ala Leu Ser Leu Ser Leu Ala Ala Gly		
	210	215	220
Ser Tyr Arg Asp Ser Thr Arg Val	Ala Gly Thr Asp Pro Gly Leu Val		
	225	230	235
Arg Ala Met Cys Glu Ser Asn Ala Gly	Pro Leu Val Lys Ala Leu Asp		
	245	250	255
Glu Ala Leu Ala Ile Leu His Glu	Ala Arg Glu Gly Leu Thr Ala Glu		
	260	265	270
Gln Pro Asn Ile Glu Gln Leu Ala Asp	Asn Gly Tyr Arg Ser Arg Ile		
	275	280	285
Arg Tyr Glu Ala Arg Ser Gly Gln Arg Arg	Ala Lys Glu Ser Val Ser		
	290	295	300
Pro Thr Ile Thr Ser Ser Arg Pro Val	Leu Arg Leu His Pro Gly Thr		
	305	310	315
Pro Asn Trp Glu Lys Gln Leu Ile His	Ala Glu Thr Leu Gly Ala Arg		
	325	330	335
Ile Glu Val Phe			
	340		

<210> 453

<211> 689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(666)

<223> FRXA00448

<400> 453

tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg agc	48
Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser	
1 5 10 15	
gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc ttc	96
Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe	
20 25 30	
gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc atc	144
Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile	
35 40 45	
tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt gtc	192
Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val	
50 55 60	
cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct cat	240
Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His	
65 70 75 80	
tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac ggt	288
Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly	
85 90 95	
ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc acc	336
Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr	
100 105 110	
cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa agc	384
Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser	
115 120 125	
aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc ctc	432
Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu	
130 135 140	
cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag caa	480
His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln	
145 150 155 160	
ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc tcc	528
Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser	
165 170 175	
ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca tcc	576
Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser	
180 185 190	
agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag cag	624
Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln	
195 200 205	
ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc	666
Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe	
210 215 220	
tagttttatc ggctgatgat tct	689

<210> 454
 <211> 222
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 454
 Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
 1 5 10 15
 Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
 20 25 30
 Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
 35 40 45
 Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
 50 55 60
 Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
 65 70 75 80
 Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
 85 90 95
 Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
 100 105 110
 Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
 115 120 125
 Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
 130 135 140
 His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
 145 150 155 160
 Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
 165 170 175
 Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
 180 185 190
 Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
 195 200 205
 Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 210 215 220

<210> 455
 <211> 346
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(346)
 <223> FRXA00452

<400> 455

ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60

catagagata accgtagtag gtatgtgcca cacttgctcag gtg act acc aaa gac 115
 Val Thr Thr Lys Asp
 1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
 Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
 10 15 20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
 Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
 25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
 Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
 40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
 Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
 55 60 65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
 Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
 70 75 80

<210> 456

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
 1 5 10 15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
 20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80

Asp Ser

<210> 457

<211> 1248

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1225)

<223> RXA00584

<400> 457

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agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115
                               Met His Ser Pro Glu
                               1                               5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
                10                15                20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
                25                30                35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
                40                45                50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
                55                60                65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
                70                75                80                85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
                90                95                100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
                105                110                115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
                120                125                130

tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
                135                140                145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
                150                155                160                165

agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
                170                175                180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
                185                190                195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
                200                205                210

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gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr
215 220 225

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835
Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883
Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa 1027
Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag 1075
Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg 1123
Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc 1171
Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca 1219
Asp Leu Leu Ala Glu Leu Ala Ala Val Arg Glu Arg Ala Ala
360 365 370

gcc aag taattaaggcgctagactg tta 1248
Ala Lys
375

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<210> 458

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

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Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
1 5 10 15

```

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Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
20 25 30

```

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Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
35 40 45

```

```

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe

```


50	55	60
Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val 65 70 75 80		
His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu 85 90 95		
Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe 100 105 110		
Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro 115 120 125		
His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg 130 135 140		
Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu 145 150 155 160		
Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp 165 170 175		
Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu 180 185 190		
Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly 195 200 205		
Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His 210 215 220		
Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr 225 230 235 240		
Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly 245 250 255		
Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly 260 265 270		
Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys 275 280 285		
Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile 290 295 300		
Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu 305 310 315 320		
Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly 325 330 335		
Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp 340 345 350		
Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Val Arg 355 360 365		
Glu Arg Arg Ala Ala Ala Lys 370 375		

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<220>
<221> CDS
<222> (101)..(1960)
<223> RXA00579
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<400> 459
tcgtctaagt ttttctttga gttttcatat gtagaaggca tcgtcggcctt cggcctggcg 60
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att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
10 15 20

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
40 45 50

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
70 75 80 85

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
105 110 115

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
135 140 145

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe

170	175	180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att			691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile			
185	190	195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat			739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His			
200	205	210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt			787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu			
215	220	225	
ggg gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc			835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly			
230	235	240	245
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca			883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser			
250	255	260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt			931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly			
265	270	275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt			979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser			
280	285	290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa			1027
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu			
295	300	305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt			1075
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe			
310	315	320	325
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct			1123
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro			
330	335	340	
gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat			1171
Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr			
345	350	355	
ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg			1219
Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser			
360	365	370	
tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc			1267
Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala			
375	380	385	
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat			1315
Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr			
390	395	400	405
ggg gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg			1363
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro			
410	415	420	

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747
 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
 535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
 550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
 570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg 1891
 His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
 585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat 1939
 Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
 600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt 1983
 Leu Phe Gly Val Glu Phe Pro
 615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu

1	5	10	15
Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro	20	25	30
Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser	35	40	45
Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala	50	55	60
Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly	65	70	75
His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro	85	90	95
Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly	100	105	110
Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser	115	120	125
Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser	130	135	140
Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp	145	150	155
Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln	165	170	175
Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu	180	185	190
Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu	195	200	205
Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln	210	215	220
Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys	225	230	235
Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp	245	250	255
Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp	260	265	270
Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala	275	280	285
Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg	290	295	300
Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu	305	310	315
Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val	325	330	335

Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
340 345 350

Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
355 360 365

Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
370 375 380

Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
385 390 395 400

Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
405 410 415

Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
420 425 430

Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
435 440 445

Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp
450 455 460

Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala
465 470 475 480

Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val
485 490 495

Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
500 505 510

Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
610 615 620

<210> 461

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 461

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ccattgcgct tgctgctggg tccactttgg aggtcatccg atg aca cac gtt gtt 115
                                         Met Thr His Val Val
                                         1           5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
                10                15                20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
                25                30                35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
                40                45                50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
                55                60                65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
                70                75                80                85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
                90                95                100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
                105                110                115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
                120                125                130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
                135                140                145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
                150                155                160                165

ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
                170                175                180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
                185                190                195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744

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Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205

tca

747

<210> 462
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 462
 Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
 1 5 10 15
 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
 65 70 75 80
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
 85 90 95
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
 130 135 140
 Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
 145 150 155 160
 Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
 165 170 175
 Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
 180 185 190
 Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 195 200 205

<210> 463
 <211> 469
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>

<221> CDS
 <222> (101)..(469)
 <223> RXN03007

<400> 463

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gaacagcttc tcgcgaacta ataaaaaaag gatttgattc atg act tct cca gca 115
                               Met Thr Ser Pro Ala
                               1           5

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu
                10                15                20

gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat 211
Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp
                25                30                35

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu
                40                45                50

cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala
                55                60                65

cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr
                70                75                80                85

ggg ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu
                90                95                100

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser
                105                110                115

gtg agc tcc aag tcc ggc 469
Val Ser Ser Lys Ser Gly
                120

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<210> 464
 <211> 123
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 464

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Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn
  1           5           10           15

Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr
      20                25                30

Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile
      35                40                45

Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala
      50                55                60

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Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu
 65 70 75 80

Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr
 85 90 95

Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys
 100 105 110

His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly
 115 120

<210> 465
 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> RXN02918

<400> 465
 agattgtcgc ttttccatt tctccgggtt ttctggaact ttttgggcgt atgctgggaa 60

tgattctatt attgccaaat cagaaagcag gagagaccgc atg agc gaa atc cta 115
 Met Ser Glu Ile Leu
 1 5

gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163
 Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala
 10 15 20

ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211
 Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His
 25 30 35

acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc 259
 Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr
 40 45 50

gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg 307
 Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala
 55 60 65

cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg 355
 Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu
 70 75 80 85

ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc 403
 Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser
 90 95 100

aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc 451
 Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser
 105 110 115

cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct 499
 Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser

120 125 130
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac 541
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp
135 140 145

taattgtctc ccatttaagg agt 564

<210> 466

<211> 147

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 466

Met Ser Glu Ile Leu Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr
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Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp
20 25 30

Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu
35 40 45

Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe
50 55 60

Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr
65 70 75 80

Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg
85 90 95

Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys
100 105 110

Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp
115 120 125

Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly
130 135 140

Gln Leu Asp
145

<210> 467

<211> 735

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(712)

<223> RXN01116

<400> 467

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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt 115
Met Ala Ala Arg Val

	1	5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg			163
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
	10	20	
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt			211
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
	25	35	
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag			259
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
	40	50	
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt			307
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
	55	65	
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc			355
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
	70	85	
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc			403
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
	90	100	
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag			451
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
	105	115	
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc			499
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
	120	130	
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag			547
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
	135	145	
gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc			595
Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val			
	150	165	
acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc			643
Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu			
	170	180	
atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc			691
Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr			
	185	195	
gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag			735
Glu Ala Asp Phe Lys Val Ala			
	200		

<210> 468

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn
 1              5              10              15

Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly
      20              25              30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro
      35              40              45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys
      50              55              60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp
      65              70              75              80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly
      85              90              95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
      100             105             110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly
      115             120             125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala
      130             135             140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys
      145             150             155             160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu
      165             170             175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu
      180             185             190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala
      195             200

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<210> 469

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXN01115

<400> 469

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gccagggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac      115
                               Met Ala Ile Leu His
                               1              5

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agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg      163
Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser
      10              15              20

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ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat	211
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His	
25 30 35	
aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct	259
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser	
40 45 50	
gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg	307
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val	
55 60 65	
ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga	355
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly	
70 75 80 85	
cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat	403
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp	
90 95 100	
cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag	451
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu	
105 110 115	
ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act	499
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr	
120 125 130	
ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg	547
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp	
135 140 145	
ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc	595
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala	
150 155 160 165	
ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc	643
Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr	
170 175 180	
tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc	691
Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr	
185 190 195	
atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc	739
Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile	
200 205 210	
att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca	787
Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro	
215 220 225	
gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg	835
Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu	
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cta gca cag cat ttc gct taatgttgta ggcatgttca caa	876
Leu Ala Gln His Phe Ala	
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 <213> Corynebacterium glutamicum

<400> 470
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 20 25 30
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg
 35 40 45
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp
 50 55 60
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn
 65 70 75 80
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu
 85 90 95
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala
 100 105 110
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys
 115 120 125
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp
 130 135 140
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe
 145 150 155 160
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys
 165 170 175
 Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr
 180 185 190
 Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro
 195 200 205
 Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala
 210 215 220
 Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn
 225 230 235 240
 Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala
 245 250

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

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<222> (101)..(1261)

<223> RXS00116

<400> 471

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               Met Ser Asn Asp Phe
               1 5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
               10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
               25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
               40 45 50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
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ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
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tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
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att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile
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gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala
               120 125 130

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp
               135 140 145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg 595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg
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atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser
               170 175 180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu
               185 190 195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln

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aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg 787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val
215          220          225

acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg 835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr
230          235          240          245

ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg 883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala
250          255          260

aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg 931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val
265          270          275

gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag 979
Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
280          285          290

ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg 1027
Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
295          300          305

ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat 1075
Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
310          315          320          325

att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag 1123
Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
330          335          340

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag 1171
Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
345          350          355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg 1219
Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
360          365          370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta 1261
Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
375          380          385

tagtttgaac aggttggttg ggg 1284

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<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

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1          5          10          15

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Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
20          25          30

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Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
 35 40 45
 Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
 50 55 60
 Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
 65 70 75 80
 Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
 85 90 95
 Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
 100 105 110
 Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
 115 120 125
 Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130 135 140
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145 150 155 160
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
 165 170 175
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
 180 185 190
 Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys

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355          360          365
Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
370          375          380

Lys Lys Leu
385

<210> 473
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(607)
<223> FRXA00116

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ttctaggcctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
Met Thr Gln Arg Ala
1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
10 15 20

ggg cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
135 140 145

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aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
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aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

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Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val
 85 90 95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu
 100 105 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser
 115 120 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr
 130 135 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe
 145 150 155 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala
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<210> 475

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXS00391

<400> 475

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 Leu Leu Arg Asp Ser
 1 5
 caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163
 Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala
 10 15 20
 act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211
 Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu
 25 30 35
 aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259
 Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu
 40 45 50
 ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
 55 60 65
 gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
 70 75 80 85
 ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu
 90 95 100
 ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115
 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130
 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145
 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165
 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180
 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195
 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210
 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc

843

<210> 476

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala
 85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser
 100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile
 115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu
 130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val
 145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly
 165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu
 180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His
 195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu
 210 215 220

Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
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<222> (101)..(994)  
<223> RXS00393
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				Met	Ser	His	Thr	Glu								
				1				5								
ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
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ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25					30					35			
gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
			40				45					50				
ctt	gtc	gtg	gcg	tgg	gct	ttg	atc	atc	ggg	gtg	aat	tac	gcc	aat	gat	307
Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	Asn	Tyr	Ala	Asn	Asp	
			55			60					65					
tac	tct	gat	ggc	att	cgt	ggc	acc	gat	gaa	gac	cgc	acc	ggg	cct	ctg	355
Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	Arg	Thr	Gly	Pro	Leu	
			70		75				80						85	
cga	ctc	act	ggg	tct	ggg	ttg	gct	gag	ccg	aag	aaa	gtg	aaa	gct	gcg	403
Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Val	Lys	Ala	Ala	
				90				95						100		
gcg	ttt	att	tct	ttc	ggg	atc	gca	ggg	gtc	gcc	ggc	acc	gcg	ctg	agc	451
Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	Gly	Thr	Ala	Leu	Ser	
			105					110					115			
ctg	ttg	agc	gcg	tgg	tgg	ctg	atc	ctc	atc	ggc	atc	ctg	tgt	gtg	ctg	499
Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	Ile	Leu	Cys	Val	Leu	
			120			125						130				
ggc	gcg	tgg	ttc	tac	acc	ggc	ggg	aaa	aat	cct	tat	ggg	tac	cgc	ggg	547
Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	Tyr	Gly	Tyr	Arg	Gly	
			135			140					145					
ctc	ggc	gag	att	gct	gtg	ttc	atc	ttc	ttc	ggc	ctc	gtc	gcg	gtc	atg	595
Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly	Leu	Val	Ala	Val	Met	
			150		155					160					165	
gga	acg	cag	ttc	acc	caa	acc	ggg	tcc	gtc	agc	tgg	gcc	ggg	ttg	gcc	643
Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	Trp	Ala	Gly	Leu	Ala	

170	175	180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac			691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn			
185	190	195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc			739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu			
200	205	210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg			787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu			
215	220	225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg			835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp			
230	235	240	245
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca			883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala			
250	255	260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc			931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile			
265	270	275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg			979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu			
280	285	290	
gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc			1017
Ala Leu Ala Phe Ser			
295			

<210> 478

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 478

Met	Ser	His	Thr	Glu	Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp
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Ile	Gln	Gly	Ala	Arg	Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val
			20					25					30		

Ile	Ala	Gly	Ser	Gly	Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp
			35				40					45			

Lys	Ala	Leu	Leu	Ala	Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val
		50				55					60				

Asn	Tyr	Ala	Asn	Asp	Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp
	65				70					75				80	

Arg	Thr	Gly	Pro	Leu	Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys
				85					90					95	

Lys	Val	Lys	Ala	Ala	Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala
			100					105					110		

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270
 Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala
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 Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
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<210> 479

<211> 1005

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(982)

<223> FRXA00393

<400> 479

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aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly

25	30	35	
gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala 40 45 50			259
ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp 55 60 65			307
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu 70 75 80 85			355
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala 90 95 100			403
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser 105 110 115			451
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu 120 125 130			499
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly 135 140 145			547
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met 150 155 160 165			595
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala 170 175 180			643
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn 185 190 195			691
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu 200 205 210			739
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu 215 220 225			787
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp 230 235 240 245			835
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala 250 255 260			883
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser 265 270 275			931

cat tagcgtttag ctaaaacgct ttt 1005
His

<400> 480																
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			20					25					30			
Ile	Ala	Gly	Ser	Gly	Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	
		35					40					45				
Lys	Ala	Leu	Leu	Ala	Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	
	50					55					60					
Asn	Tyr	Ala	Asn	Asp	Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	
65					70					75					80	
Arg	Thr	Gly	Pro	Leu	Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	
				85					90					95		
Lys	Val	Lys	Ala	Ala	Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	
			100					105					110			
Gly	Thr	Ala	Leu	Ser	Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	
		115					120					125				
Ile	Leu	Cys	Val	Leu	Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	
	130					135					140					
Tyr	Gly	Tyr	Arg	Gly	Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly	
145					150					155					160	
Leu	Val	Ala	Val	Met	Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	
				165					170					175		
Trp	Ala	Gly	Leu	Ala	Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	
			180					185					190			
Val	Asn	Leu	Ala	Asn	Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr	
		195					200					205				
Gly	Lys	Ile	Thr	Leu	Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys	
	210					215					220					
Leu	Phe	Leu	Ala	Leu	Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu	
225					230					235					240	

Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255

Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270

Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro
 275 280 285

Cys Ser Arg Ala Trp His
 290

<210> 481
 <211> 987
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(964)
 <223> RXS00446

<400> 481
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ggtgacggag gctacttggg gggctaatcg gtaccgggat atg ggt gcg gtt gag 115
 Met Gly Ala Val Glu
 1 5

ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc 163
 Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val
 10 15 20

acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca 211
 Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala
 25 30 35

acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag 259
 Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu
 40 45 50

gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att 307
 Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile
 55 60 65

ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg 355
 Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala
 70 75 80 85

atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct 403
 Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro
 90 95 100

tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag 451
 Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys
 105 110 115

gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc 499
 Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe
 120 125 130

aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac 547
 Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His
 135 140 145

 gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg 595
 Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala
 150 155 160 165

 ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg 643
 Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala
 170 175 180

 atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg 691
 Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala
 185 190 195

 gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val
 200 205 210

 gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala
 215 220 225

 gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala
 230 235 240 245

 gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

 ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

 ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcctttgg cgttttgccg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

 tgc 987

<210> 482

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 482

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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80
 Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95
 Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110
 Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125
 Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu
 130 135 140
 Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160
 Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175
 Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190
 Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205
 Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 483

<211> 545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA00446

<400> 483

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 1 5 10 15

48

ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

tagtctttgg cgttttgcgg tgc 545

<210> 484

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65              70              75              80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
      85              90              95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
      100              105              110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
      115              120              125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
      130              135              140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
145              150              155              160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
      165              170

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<210> 485
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1207)
<223> RXS00618

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                                   Met Gln Met Leu Asp
                                   1              5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
      10              15              20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
      25              30              35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
      40              45              50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
      55              60              65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
      70              75              80              85

ggg gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403

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Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu	Asp	His	Gly	Asp	Tyr		
				90					95					100			
gtg	gca	atg	cct	acc	ccg	ggg	tac	ccg	gca	tat	cgc	aat	att	ctg	gaa	451	
Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr	Arg	Asn	Ile	Leu	Glu		
			105					110					115				
tct	ttg	ggg	gcg	aag	gtt	ctg	aac	ctg	cgc	tgt	act	gca	gag	act	cgt	499	
Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys	Thr	Ala	Glu	Thr	Arg		
		120					125					130					
ttc	cag	cca	acc	gct	caa	atg	ttg	gag	gaa	ctg	cca	cac	aag	ccg	aag	547	
Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu	Pro	His	Lys	Pro	Lys		
	135					140					145						
gct	gtt	att	gtc	acc	agc	cca	gga	aac	cca	acg	ggc	acc	atc	att	gat	595	
Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr	Gly	Thr	Ile	Ile	Asp		
150					155					160					165		
ccg	gaa	gag	cta	gag	cgc	atc	gcc	aag	tgg	tgc	gat	gac	aat	gat	gct	643	
Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys	Asp	Asp	Asn	Asp	Ala		
				170				175						180			
gtt	ctt	atc	tct	gat	gag	gac	tac	cac	ggc	atg	agc	ttt	ggg	cgt	ccg	691	
Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met	Ser	Phe	Gly	Arg	Pro		
			185					190					195				
ctg	gca	act	gcg	cat	cag	ttt	tcc	aag	aac	gcc	atc	gtg	gtg	ggg	acc	739	
Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	Thr		
		200					205					210					
ttg	tcc	aag	tac	ttc	tcc	atg	acg	ggg	tgg	cgc	gtg	ggg	tgg	atc	atc	787	
Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg	Val	Gly	Trp	Ile	Ile		
		215				220					225						
gtt	cca	gat	gag	ctg	gtc	aca	ccg	att	gaa	aac	ctg	cag	gct	tct	ctt	835	
Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn	Leu	Gln	Ala	Ser	Leu		
230					235				240					245			
tcc	ttg	tgt	gct	cct	gcc	atc	ggg	cag	gct	gcg	gga	cgc	gca	gcc	ttc	883	
Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala	Gly	Arg	Ala	Ala	Phe		
				250				255						260			
act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	cgc	931	
Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	Arg		
			265					270				275					
gag	gcc	cgg	gag	gtg	ttc	gtc	gat	aag	ctc	cct	gaa	atc	ggg	ctt	ggc	979	
Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro	Glu	Ile	Gly	Leu	Gly		
		280					285					290					
act	ttc	gcc	gac	ccg	gat	ggc	ggc	ctg	tat	ttg	tgg	gtc	gat	gtt	tct	1027	
Thr	Phe	Ala	Asp	Pro	Asp	Gly	Gly	Leu	Tyr	Leu	Trp	Val	Asp	Val	Ser		
		295				300					305						
gca	tac	acc	gat	gat	tca	gag	gaa	tgg	gca	ttg	cgt	ttg	ctc	gat	gaa	1075	
Ala	Tyr	Thr	Asp	Asp	Ser	Glu	Glu	Trp	Ala	Leu	Arg	Leu	Leu	Asp	Glu		
310					315				320						325		
gcg	ggc	gtg	gcc	gtc	gcg	ccg	ggg	gtt	gat	ttt	gat	cct	gag	gaa	ggc	1123	
Ala	Gly	Val	Ala	Val	Ala	Pro	Gly	Val	Asp	Phe	Asp	Pro	Glu	Glu	Gly		

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          330          335          340
cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att 1171
His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
          345          350          355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgcac 1217
Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
          360          365

taggttagtt tcg 1230

<210> 486
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 486
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  1          5          10          15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
          20          25          30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
          35          40          45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
          50          55          60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
          65          70          75          80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
          85          90          95

Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
          100          105          110

Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
          115          120          125

Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
          130          135          140

Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
          145          150          155          160

Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
          165          170          175

Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
          180          185          190

Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
          195          200          205

Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
          210          215          220

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Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240

Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255

Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270

Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285

Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
 290 295 300

Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
 305 310 315 320

Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
 325 330 335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser
 340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
 355 360 365

Lys

<210> 487
 <211> 657
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(634)
 <223> FRXA00618

<400> 487
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caatgatgct gttcttatct ctgatgagga ctaccaaggc atg agc ttt ggt cgt 115
 Met Ser Phe Gly Arg
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307

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Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
 55                                60                                65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
 70                                75                                80                                85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
 90                                95                                100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
105                                110                                115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
120                                125                                130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547
Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
135                                140                                145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
150                                155                                160                                165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
170                                175

taggttagtt tcg 657

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<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

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Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
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Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
20                                25                                30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
35                                40                                45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
50                                55                                60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
65                                70                                75                                80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
85                                90                                95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
100                                105                                110

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Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 489
 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA00627

<400> 489
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 Met Gln Met Leu Asp
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 90 95

<210> 490
 <211> 95
 <212> PRT

<213> Corynebacterium glutamicum

<400> 490

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Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
 1              5              10              15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
      20              25              30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
      35              40              45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
      50              55              60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
      65              70              75              80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
      85              90              95

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<210> 491

<211> 1221

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1198)

<223> RXS01105

<400> 491

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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
                               Met Thr Lys Ile Thr
                               1              5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
      10              15              20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
      25              30              35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
      40              45              50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
      55              60              65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
      70              75              80              85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile

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90										95					100					
ctg	cag	cag	ctg	ctg	cag	gct	ttt	ggg	gga	cct	gga	cgc	acc	gcg	ttg	451				
Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro	Gly	Arg	Thr	Ala	Leu					
			105					110					115							
gga	ttc	caa	ccc	agc	tat	tcc	atg	cac	cca	att	ttg	gct	aaa	ggc	acc	499				
Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile	Leu	Ala	Lys	Gly	Thr					
		120					125					130								
cac	act	gaa	ttc	att	gcg	gtg	tcc	cga	ggg	gct	gat	ttc	cgc	atc	gat	547				
His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala	Asp	Phe	Arg	Ile	Asp					
		135				140					145									
atg	gat	gtg	gcg	ctg	gaa	gaa	att	cgt	gca	aag	cag	cct	gac	att	gtt	595				
Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Gln	Pro	Asp	Ile	Val					
150					155					160					165					
ttt	gtc	acc	acc	ccg	aac	aac	ccg	acc	ggg	gat	gtg	acc	tcg	ctg	gac	643				
Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	Val	Thr	Ser	Leu	Asp					
				170					175					180						
gat	gtt	gag	cgc	atc	atc	aac	gtt	gcc	cca	ggc	atc	gtg	atc	gtg	gat	691				
Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly	Ile	Val	Ile	Val	Asp					
			185					190					195							
gaa	gct	tat	gcg	gaa	ttc	tcc	cca	tca	cct	tca	gca	acc	act	ctt	ctg	739				
Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	Ala	Thr	Thr	Leu	Leu					
		200					205					210								
gag	aag	tac	cca	acc	aag	ctg	gtg	gtg	tcc	cgc	acc	atg	agt	aag	gct	787				
Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	Thr	Met	Ser	Lys	Ala					
	215					220					225									
ttt	gat	ttc	gca	ggg	gga	cgc	ctc	ggc	tac	ttc	gtg	gcc	aac	cca	gcg	835				
Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	Val	Ala	Asn	Pro	Ala					
230				235					240					245						
ttt	atc	gac	gcc	gtg	atg	cta	gtc	cgc	ctt	ccg	tat	cat	ctt	tca	gcg	883				
Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	Tyr	His	Leu	Ser	Ala					
				250					255					260						
ctg	agc	caa	gca	gcc	gca	atc	gta	gcg	ctg	cgt	cac	tcc	gct	gac	acg	931				
Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	His	Ser	Ala	Asp	Thr					
			265					270					275							
ctg	gga	acc	gtc	gaa	aag	ctc	tct	gta	gag	cgt	gtt	cgc	gtg	gca	gca	979				
Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg	Val	Arg	Val	Ala	Ala					
		280					285					290								
cgc	ttg	gag	gaa	ctg	ggc	tac	gct	gtg	gtt	cca	agt	gag	tcc	aac	ttt	1027				
Arg	Leu	Glu	Glu	Leu	Gly	Tyr	Ala	Val	Val	Pro	Ser	Glu	Ser	Asn	Phe					
	295					300					305									
gtg	ttc	ttt	gga	gat	ttc	tcc	gat	cag	cac	gcg	gca	tgg	cag	gca	ttt	1075				
Val	Phe	Phe	Gly	Asp	Phe	Ser	Asp	Gln	His	Ala	Ala	Trp	Gln	Ala	Phe					
310					315					320					325					
ttg	gat	agg	gga	gtg	ctc	atc	cgc	gat	gtg	gga	atc	gct	ggg	cac	ttg	1123				
Leu	Asp	Arg	Gly	Val	Leu	Ile	Arg	Asp	Val	Gly	Ile	Ala	Gly	His	Leu					
				330					335				340							

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca 1171
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
 345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca 1218
 Ala Ala Glu Ile Ile Lys Leu Asn Leu
 360 365

tga 1221

<210> 492

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 492

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
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Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
 20 25 30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
 35 40 45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50 55 60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
 65 70 75 80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
 85 90 95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
 100 105 110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
 115 120 125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
 130 135 140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
 145 150 155 160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
 165 170 175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
 180 185 190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
 195 200 205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
 210 215 220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe


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225              230              235              240
Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
              245              250              255
Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
              260              265              270
His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
              275              280              285
Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
              290              295              300
Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
305              310              315              320
Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
              325              330              335
Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
              340              345              350
Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
              355              360              365

<210> 493
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)
<223> RXS02315

<400> 493
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gaatcgatc cgtacctgga gacgatctag actgttgctgc atg tcc agc acg cca 115
              Met Ser Ser Thr Pro
              1              5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
              10              15              20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
              25              30              35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
              40              45              50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
              55              60              65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355

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Pro	Val	Ala	Val	Val	Met	Thr	Ser	Gly	Thr	Ala	Val	Ala	Asn	Cys	Leu	
70					75					80					85	
cct	gct	gtt	gct	gaa	gct	gcg	cat	gcc	cat	atc	ccg	ttg	att	gtg	ctc	403
Pro	Ala	Val	Ala	Glu	Ala	Ala	His	Ala	His	Ile	Pro	Leu	Ile	Val	Leu	
				90					95					100		
tct	gct	gac	cgt	cct	gca	cat	ttg	gtg	gga	acg	ggg	gcg	agc	caa	acg	451
Ser	Ala	Asp	Arg	Pro	Ala	His	Leu	Val	Gly	Thr	Gly	Ala	Ser	Gln	Thr	
			105					110					115			
att	aac	cag	acc	ggg	att	ttt	ggg	gat	ctt	gca	ccg	acg	gtc	ggg	atc	499
Ile	Asn	Gln	Thr	Gly	Ile	Phe	Gly	Asp	Leu	Ala	Pro	Thr	Val	Gly	Ile	
		120					125					130				
act	gag	ctg	gat	cag	gta	gcg	cag	att	gct	gaa	agc	ctt	gct	cag	ggg	547
Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly	
	135					140					145					
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu	
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gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggg	gag	gca	gtt	gga	gca	tca	643
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser	
			170						175					180		
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggg	gag	gtg	acc	gtg	gac	ctg	ggg	691
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly	
			185					190					195			
gag	cac	acc	ctc	gtg	att	gcc	ggg	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly	
		200					205					210				
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr	
	215					220					225					
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val	
230					235					240					245	
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val	
			250						255					260		
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp	
			265					270					275			
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp	
		280					285					290				
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc	1027
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly	
		295				300					305					
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt	1075
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu	

310	315	320	325	
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc				1123
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe	330	335	340	
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc				1171
Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly	345	350	355	
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg				1219
Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu	360	365	370	
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc				1267
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val	375	380	385	
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct				1315
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala	390	395	400	405
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc				1363
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala	410	415	420	
ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc				1411
Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile	425	430	435	
ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac				1459
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn	440	445	450	
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt				1507
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly	455	460	465	
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc				1555
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser	470	475	480	485
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac				1603
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp	490	495	500	
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc				1651
Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser	505	510	515	
gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca				1699
Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala	520	525	530	
caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt				1749
Gln Gln Gln Ala Leu Met Asp Thr Val His	535	540		
gcg				1752

<210> 494
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 494
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 Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30
 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45
 Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr

```

290              295              300
Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
305              310              315              320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
325              330              335

Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
340              345              350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
355              360              365

Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
370              375              380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
385              390              395              400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
405              410              415

Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
420              425              430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
435              440              445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
450              455              460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
465              470              475              480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
485              490              495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
500              505              510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
515              520              525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
530              535              540

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<210> 495

<211> 1434

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1411)

<223> RXS02550

<400> 495

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[illegible]

Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc 1027
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga 1075
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa 1123
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc 1171
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc 1219
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc 1267
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag 1411
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln
 425 430 435

tagtagttgt taggattcac cac 1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn

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Lys Ala Val Gly	Ala Asp Gln Ala	Ala Arg Pro Thr	Arg Arg Thr Thr
20		25	30
Arg Arg Ile Phe	Asp Gln Ser Glu	Lys Met Lys Asp	Val Leu Tyr Glu
35		40	45
Ile Arg Gly Pro	Val Ala Ala Glu	Ala Glu Arg Met	Glu Leu Asp Gly
50		55	60
His Asn Ile Leu	Lys Leu Asn Thr	Gly Asn Pro Ala	Val Phe Gly Phe
65		70	75
Asp Ala Pro Asp	Val Ile Met Arg	Asp Met Ile Ala	Asn Leu Pro Thr
	85	90	95
Ser Gln Gly Tyr	Ser Thr Ser Lys	Gly Ile Ile Pro	Ala Arg Arg Ala
100		105	110
Val Val Thr Arg	Tyr Glu Val Val	Pro Gly Phe Pro	His Phe Asp Val
115		120	125
Asp Asp Val Phe	Leu Gly Asn Gly	Val Ser Glu Leu	Ile Thr Met Thr
130		135	140
Thr Gln Ala Leu	Leu Asn Asp Gly	Asp Glu Val Leu	Ile Pro Ala Pro
145		150	155
Asp Tyr Pro Leu	Trp Thr Ala Ala	Thr Ser Leu Ala	Gly Gly Lys Pro
	165	170	175
Val His Tyr Leu	Cys Asp Glu Glu	Asp Asp Trp Asn	Pro Ser Ile Glu
180		185	190
Asp Ile Lys Ser	Lys Ile Ser Glu	Lys Thr Lys Ala	Ile Val Val Ile
195		200	205
Asn Pro Asn Asn	Pro Thr Gly Ala	Val Tyr Pro Arg	Arg Val Leu Glu
210		215	220
Gln Ile Val Glu	Ile Ala Arg Glu	His Asp Leu Leu	Ile Leu Ala Asp
225		230	235
Glu Ile Tyr Asp	Arg Ile Leu Tyr	Asp Asp Ala Glu	His Ile Ser Leu
	245	250	255
Ala Thr Leu Ala	Pro Asp Leu Leu	Cys Ile Thr Tyr	Asn Gly Leu Ser
260		265	270
Lys Ala Tyr Arg	Val Ala Gly Tyr	Arg Ala Gly Trp	Met Val Leu Thr
275		280	285
Gly Pro Lys Gln	Tyr Ala Arg Gly	Phe Ile Glu Gly	Leu Glu Leu Leu
290		295	300
Ala Gly Thr Arg	Leu Cys Pro Asn	Val Pro Ala Gln	His Ala Ile Gln
305		310	315
Val Ala Leu Gly	Gly Arg Gln Ser	Ile Tyr Asp Leu	Thr Gly Glu His
	325	330	335

Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350

Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365

Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380

Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400

Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415

Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
 420 425 430

Ser Thr Tyr Lys Gln
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<210> 497
 <211> 1080
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1057)
 <223> RXS02319

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agaccttggc catttcggca gaggtttaag gttaaagatt atg agc aac tac agc 115
 Met Ser Asn Tyr Ser
 1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
 10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
 25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
 40 45 50

gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307
 Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His
 55 60 65

gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355
 Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly
 70 75 80 85

ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
 20 25 30
 Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
 35 40 45
 Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
 50 55 60
 Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80
 Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
 85 90 95
 Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
 100 105 110
 Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
 115 120 125
 Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
 130 135 140
 Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145 150 155 160
 Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
 165 170 175
 Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
 180 185 190
 Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
 195 200 205
 Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
 210 215 220
 Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275 280 285

Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
 290 295 300

Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 305 310 315

<210> 499

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(361)

<223> RXS02908

<400> 499

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 gtgactgggc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro
 1 5
 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
 10 15 20
 tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
 25 30 35
 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
 40 45 50
 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
 55 60 65
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
 70 75 80 85
 ctg ttt tagtcttcat tcttgctggc tgc 384
 Leu Phe

<210> 500

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 500

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1 5 10 15
 Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
 20 25 30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
 35 40 45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50 55 60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65 70 75 80

Arg Ala Ile Ala Lys Leu Phe
 85

<210> 501
 <211> 775
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(775)
 <223> RXS03003

<400> 501
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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115
 Met Thr Ser Arg Thr
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
 55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130

gga tgc acc gtg ttg cgt tct gat tgc ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145

atc ccg tgc atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165

gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180

aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195

gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210

ggc gac cac acc aac ttg atc gcc att cac tgc ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225

<210> 502

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp
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Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly
 20 25 30

Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60

Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
 85 90 95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
 100 105 110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
 115 120 125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
 130 135 140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
 145 150 155 160

gga tgc acc gtg ttg cgt tct gat tgc ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145
 atc ccg tgc atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tgc ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225
 <210> 502
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 502
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 Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly
 20 25 30
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80
 Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
 85 90 95
 Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
 100 105 110
 Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
 115 120 125
 Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
 130 135 140
 Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
 145 150 155 160

Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
 165 170 175

Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr
 180 185 190

Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp
 195 200 205

Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser
 210 215 220

Leu
 225

<210> 503

<211> 390

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(367)

<223> RXS03026

<400> 503

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cgaactagcc cccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115
 Met Pro Gly Lys Ile
 1 5

ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
 Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
 10 15 20

gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
 Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
 25 30 35

gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
 Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
 40 45 50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307
 His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65

atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85

ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 504

<211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

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Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu
 1              5              10              15

Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
          20              25              30

Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
          35              40              45

Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
          50              55              60

Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
          65              70              75              80

Thr Leu Arg Trp Arg Phe Trp Met Leu
          85

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(598)

<223> RXS03074

<400> 505

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
              Met Thr Gln Ser Ala
              1              5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
          10              15              20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
          25              30              35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
          40              45              50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
          55              60              65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
          70              75              80              85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403

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<210> 506
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

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      20          25          30
Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35          40          45
Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50          55          60
Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
      65          70          75          80
Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
      85          90          95
Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
      100          105          110
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
      115          120          125
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
      130          135          140
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
      145          150          155          160
Glu Ala Pro Ile Lys Gln

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<212> PRT
<213> Corynebacterium glutamicum
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165

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 <212> DNA
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 <222> (101)..(3052)
 <223> RXC01434

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 Val Leu Gly Ala Val
 1 5
 ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
 10 15 20
 gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
 25 30 35
 acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50
 ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
 55 60 65
 tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70 75 80 85
 ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
 90 95 100
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 105 110 115
 ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag 499
 Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln
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 gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc 547
 Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr
 135 140 145
 ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc 595
 Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg
 150 155 160 165
 gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag 643

Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	170	175	180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691			
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	185	190	195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739			
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	200	205	210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787			
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	215	220	225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835			
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	230	235	240	245
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883			
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	250	255	260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931			
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	265	270	275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979			
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	280	285	290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	1027			
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	295	300	305	
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg	1075			
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	310	315	320	325
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc	1123			
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile	330	335	340	
gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg	1171			
Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu	345	350	355	
ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac	1219			
Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn	360	365	370	
ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc	1267			
Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg	375	380	385	
aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg	1315			
Asn Lys Leu Gly Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu	390	395	400	405
tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg	1363			
Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu				

410	415	420	
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Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu			
425	430	435	
agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc			1459
Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe			
440	445	450	
atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc			1507
Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val			
455	460	465	
caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt			1555
Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe			
470	475	480	485
att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag			1603
Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu			
490	495	500	
cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc			1651
Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr			
505	510	515	
cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg			1699
Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu			
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gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat			1747
Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp			
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cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc			1795
His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala			
550	555	560	565
acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc			1843
Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala			
570	575	580	
cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag			1891
Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu			
585	590	595	
gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta			1939
Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val			
600	605	610	
gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg			1987
Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val			
615	620	625	
gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt			2035
Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly			
630	635	640	645
gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc			2083
Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr			
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 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
 665 670 675

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 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc 2227
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc 2275
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
 710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc 2323
 Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
 730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc 2371
 Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
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gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct 2419
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
 760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg 2467
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
 775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc 2515
 Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
 790 795 800 805

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 Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
 810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct 2611
 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
 825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat 2659
 Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
 840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc 2707
 Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
 855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc 2755
 Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
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acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc 2803
 Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
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gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc 2851
 Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
 905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat 2899
 Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
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 Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
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 Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
 950 955 960 965

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 Val Gly Trp

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<213> Corynebacterium glutamicum

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 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
 145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val

485										490					495				
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Glu	Phe	Ala	Ala	Thr	Pro	Val	Pro	Pro	Pro	Met	Ser	Ala	Gly	Ile	Val				
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Arg	Gly	Pro	Arg	Leu	Val	Pro	Gly	Ala	Pro	Val	Gly	Asp	Gly	Arg	Phe				
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Arg	Leu	Leu	Ala	Asp	His	Gly	Gly	Val	Gln	Gly	Ala	Arg	Phe	Trp	Gln				
545					550				555						560				
Ala	Arg	Glu	Ile	Ala	Thr	Gly	Lys	Glu	Val	Ala	Leu	Ile	Phe	Val	Asp				
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Thr	Ser	Gly	Asn	Ala	Pro	Phe	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Ala	Ala				
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Gly	Ile	Ala	Tyr	Glu	Val	Gln	Arg	Arg	Thr	Lys	Lys	Leu	Ala	Ser	Leu				
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Gly	Cys	Leu	Ile	Val	Ala	Asp	Trp	Val	Pro	Gly	Ser	Ser	Leu	Ser	Ala				
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Val	Ala	Glu	Ser	Gly	Ala	Asp	Pro	Arg	Ala	Ala	Ala	Phe	Ala	Leu	Ala				
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Glu	Leu	Thr	Glu	Thr	Ile	Gly	Glu	Ala	His	Glu	Met	Gly	Ile	Pro	Ala				
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Gly	Leu	Asp	Asn	Lys	Cys	Arg	Ile	Arg	Ile	Asn	Thr	Asp	Gly	His	Ala				
	675					680					685								
Val	Leu	Ala	Leu	Pro	Ala	Ile	Leu	Pro	Asp	Ala	Ser	Glu	Leu	Arg	Asp				
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Ala	Lys	Ser	Leu	Ala	Ser	Ala	Ala	Glu	Met	Leu	Ile	Asp	Ala	Thr	Leu				
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Ala	Pro	Ser	Asp	Val	Lys	Ala	Met	Val	Thr	Glu	Ala	Gln	Gly	Leu	Ala				
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Thr	Glu	Asp	Asn	Pro	Asp	Tyr	Ala	Ser	Leu	Ala	Met	Ala	Met	Arg	Thr				
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Cys	Gly	Leu	Phe	Thr	Glu	Glu	Pro	Thr	His	Leu	Val	Val	Lys	Lys	Glu				
	755						760					765							
Lys	Thr	Pro	Lys	Pro	Ala	Thr	Arg	Asp	Gly	Phe	Gly	Ala	Ser	Asp	Tyr				
	770				775						780								
Thr	Val	Lys	Gly	Met	Ala	Ala	Ile	Ala	Ala	Val	Val	Ile	Ile	Leu	Val				
785				790						795				800					
Ser	Leu	Val	Ala	Ala	Gly	Thr	Ala	Phe	Leu	Thr	Ser	Phe	Phe	Gly	Ser				
			805						810					815					

Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
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 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
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 Met Ser Ile Glu Trp
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 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
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 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
 25 30 35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac 259

Ile	Leu	Val	Phe	Leu	Gly	Leu	Pro	Pro	Leu	Thr	Ala	Thr	Ile	Ala	Asn	
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Thr	Ile	Gly	Ile	Val	Pro	Gly	Ser	Ile	Ser	Gly	Val	Val	Ala	Tyr	Arg	
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Arg	Glu	Leu	His	Ala	His	Val	Lys	Thr	Ile	Arg	Phe	Leu	Leu	Pro	Ala	
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Ser	Ile	Leu	Gly	Gly	Ile	Thr	Gly	Ala	Ser	Leu	Leu	Leu	His	Phe	Ser	
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Leu	Leu	Val	Ile	Ala	Gly	Pro	Ser	Ile	Lys	Lys	His	Val	Gly	Ala	His	
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Tyr	Gly	Gly	Tyr	Phe	Ser	Ala	Ala	Gln	Gly	Ile	Leu	Leu	Ile	Ala	Leu	
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ctt	ggc	atc	aca	tca	acg	ctg	cag	atg	cag	gaa	ctc	aac	gcc	atc	aaa	691
Leu	Gly	Ile	Thr	Ser	Thr	Leu	Gln	Met	Gln	Glu	Leu	Asn	Ala	Ile	Lys	
			185					190					195			
aac	ctc	aca	gtg	gcg	gca	gtt	aat	ctc	atc	gca	gcc	agt	gtt	ttt	ata	739
Asn	Leu	Thr	Val	Ala	Ala	Val	Asn	Leu	Ile	Ala	Ala	Ser	Val	Phe	Ile	
		200					205					210				
atc	atc	tcc	cct	gag	ttg	atc	tcc	tgg	ccg	acc	gtt	gcc	tta	atc	gcg	787
Ile	Ile	Ser	Pro	Glu	Leu	Ile	Ser	Trp	Pro	Thr	Val	Ala	Leu	Ile	Ala	
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ctt	ggc	tca	gct	tta	ggg	gga	tac	atc	ggc	gga	cgg	tac	gcc	cgc	cga	835
Leu	Gly	Ser	Ala	Leu	Gly	Gly	Tyr	Ile	Gly	Gly	Arg	Tyr	Ala	Arg	Arg	
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Leu	Arg	Pro	Ser	Val	Phe	Arg	Ala	Phe	Val	Val	Ile	Val	Gly	Ile	Thr	
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acg	gtc	atc	gtt	atg	acg	atc	ggg	taatgcagca	gactagtaac	ccc						930
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Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
      35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
      50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
      85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
      100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
      115          120          125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
      130          135          140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
      145          150          155          160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
      165          170          175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
      180          185          190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
      195          200          205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
      210          215          220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
      225          230          235          240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
      245          250          255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
      260          265

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<210> 511

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXC02789

<400> 511

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ttcttaacac	taaacaatgg	aaaggtaagc	gggtttttct	atg	aag	ggt	tcc	gcc	115
				Met	Lys	Val	Ser	Ala	
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gat	aca	ccc	ggt	cac	gat	gat	cca	ggc	cca	ggc	cgg	cgc	ctt	ggc	tta	163
Asp	Thr	Pro	Gly	His	Asp	Asp	Pro	Gly	Pro	Gly	Arg	Arg	Leu	Gly	Leu	
			10					15					20			

gat	gtc	ggc	acc	gtg	cgc	atc	gga	gtg	gca	gcc	tct	gac	cgc	gat	gcc	211
Asp	Val	Gly	Thr	Val	Arg	Ile	Gly	Val	Ala	Ala	Ser	Asp	Arg	Asp	Ala	
			25				30					35				

aag	ctt	gcc	atg	cct	gtg	gaa	acc	gtt	ccg	cgg	gaa	act	gga	ttc	aaa	259
Lys	Leu	Ala	Met	Pro	Val	Glu	Thr	Val	Pro	Arg	Glu	Thr	Gly	Phe	Lys	
		40				45					50					

ggg	cca	gac	ctg	gcc	gat	att	gat	cgg	ttg	gtc	gcc	atc	ggt	gag	gaa	307
Gly	Pro	Asp	Leu	Ala	Asp	Ile	Asp	Arg	Leu	Val	Ala	Ile	Val	Glu	Glu	
	55				60					65						

tac	aac	gcc	gtg	gaa	gtc	att	gtt	ggt	cta	ccc	aca	gat	ctg	cag	gga	355
Tyr	Asn	Ala	Val	Glu	Val	Ile	Val	Gly	Leu	Pro	Thr	Asp	Leu	Gln	Gly	
	70			75					80					85		

aat	ggc	tcc	gcc	agt	gtg	aag	cat	gca	aag	gaa	att	gct	ttc	cgc	gtc	403
Asn	Gly	Ser	Ala	Ser	Val	Lys	His	Ala	Lys	Glu	Ile	Ala	Phe	Arg	Val	
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cgt	cgg	cgc	ctc	acc	aat	gct	gga	aag	aac	att	ccg	gta	cgg	ctt	ggc	451
Arg	Arg	Arg	Leu	Thr	Asn	Ala	Gly	Lys	Asn	Ile	Pro	Val	Arg	Leu	Gly	
			105				110						115			

gac	gaa	cgc	ctc	acc	acc	gtc	gtg	gcc	acc	caa	gcc	ttg	cgg	gcc	tca	499
Asp	Glu	Arg	Leu	Thr	Thr	Val	Val	Ala	Thr	Gln	Ala	Leu	Arg	Ala	Ser	
		120				125					130					

gga	gtc	agc	gaa	aaa	gcg	gga	cgt	aaa	gtt	att	gat	caa	gct	gcc	gca	547
Gly	Val	Ser	Glu	Lys	Ala	Gly	Arg	Lys	Val	Ile	Asp	Gln	Ala	Ala	Ala	
	135				140				145							

gta	gaa	atc	ctt	caa	acc	tgg	ttg	gat	gct	cgc	acc	cga	gcc	ctt	gaa	595
Val	Glu	Ile	Leu	Gln	Thr	Trp	Leu	Asp	Ala	Arg	Thr	Arg	Ala	Leu	Glu	
150				155				160						165		

cca	caa	tcc	aca	gac	acc	caa	gat	ttc	gac	gag	aag	gga	aat	ttc	cca	643
Pro	Gln	Ser	Thr	Asp	Thr	Gln	Asp	Phe	Asp	Glu	Lys	Gly	Asn	Phe	Pro	
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gga	tgaaccaa	at	ccgaaaccgc	cgg	669
Gly					

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Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
      35                               40                   45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
      50                               55                   60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
      65                               70                   75                   80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
      85                               90                   95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
      100                              105                  110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
      115                              120                  125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
      130                              135                  140

Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
      145                              150                  155                  160

Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
      165                              170                  175

Lys Gly Asn Phe Pro Gly
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<220>  
<221> CDS  
<222> (101)..(880)  
<223> RXC02295
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gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
Met Gly Leu Glu Leu
          1           5

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gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga 163
 Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly
 10 15 20

tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg 211
 Trp Ile Asp Ala Val Ile Gly Gly Gly Leu Val Leu Ile Pro Leu
 25 30 35

atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc 259
 Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser
 40 45 50

aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg 307
 Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu
 55 60 65

gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg 355
 Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu
 70 75 80 85

gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att 403
 Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile
 90 95 100

gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt 451
 Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val
 105 110 115

ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa 499
 Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys
 120 125 130

gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga 547
 Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly
 135 140 145

ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc 595
 Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe
 150 155 160 165

ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc 643
 Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser
 170 175 180

gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta 691
 Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu
 185 190 195

att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg 739
 Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val
 200 205 210

ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg 787
 Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val
 215 220 225

ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt 835
 Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val
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gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880

903

<400> 514

Ile Gln Gly Met

<210> 515
<211> 1132
<212> DNA
<213> *Corynebacterium glutamicum*

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<221> CDS  
<222> (101)..(1132)  
<223> RXN03063
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				Val	Glu	Asp	Leu	Ser									5
				1													
tac	cgc	atc	ccg	cag	tcg	cgc	acc	gtg	gcc	gag	cag	gtg	cca	ggg	ccg	163	
Tyr	Arg	Ile	Pro	Gln	Ser	Arg	Thr	Val	Ala	Glu	Gln	Val	Pro	Gly	Pro		
				10												20	
									15								
aag	tcg	aaa	gcg	ctg	gat	gag	cgt	cga	caa	gca	gca	gta	gca	cga	gca	211	
Lys	Ser	Lys	Ala	Leu	Asp	Glu	Arg	Arg	Gln	Ala	Ala	Val	Ala	Arg	Ala		
			25												35		
								30									
ctt	gca	ccg	ggg	ctg	cct	gga	tac	gtg	gtg	gac	gca	gac	ggg	ggc	atc	259	
Leu	Ala	Pro	Gly	Leu	Pro	Gly	Tyr	Val	Val	Asp	Ala	Asp	Gly	Gly	Ile		
		40												50			
							45										
ttg	gct	gac	gcg	gac	ggc	aac	cgt	ttc	atc	gac	ctg	gcc	tcc	ggc	atc	307	
Leu	Ala	Asp	Ala	Asp	Gly	Asn	Arg	Phe	Ile	Asp	Leu	Ala	Ser	Gly	Ile		
	55												65				
						60											
gcc	gtg	acc	acg	gtc	ggc	gga	tcc	aac	gcg	gcc	gtc	gcg	aaa	gcc	gtc	355	
Ala	Val	Thr	Thr	Val	Gly	Gly	Ser	Asn	Ala	Ala	Val	Ala	Lys	Ala	Val		
	70												80		85		
					75												
ggc	gcc	gca	gct	gcc	cgc	ttc	acc	cac	acc	tgc	ttc	atg	gtc	tca	cct	403	
Gly	Ala	Ala	Ala	Ala	Arg	Phe	Thr	His	Thr	Cys	Phe	Met	Val	Ser	Pro		
				90												100	
									95								
tat	gaa	act	tac	gtg	gcc	atg	gcg	gag	aga	ctc	aac	gcc	ttg	act	cca	451	
Tyr	Glu	Thr	Tyr	Val	Ala	Met	Ala	Glu	Arg	Leu	Asn	Ala	Leu	Thr	Pro		
			105												115		
								110									
ggc	gat	cac	gac	aag	aag	agc	gcg	ctg	ttt	aac	tct	ggc	gcc	gaa	gcc	499	
Gly	Asp	His	Asp	Lys	Lys	Ser	Ala	Leu	Phe	Asn	Ser	Gly	Ala	Glu	Ala		
		120												130			
							125										
gtg	gaa	aac	gcc	gtc	aag	gtg	gca	cgc	gcc	tac	acc	ggc	aag	ggc	gcg	547	
Val	Glu	Asn	Ala	Val	Lys	Val	Ala	Arg	Ala	Tyr	Thr	Gly	Lys	Gly	Ala		
	135												145				
						140											
gtc	gtg	gtg	ttc	gac	aac	gcg	tac	cac	gga	cgg	acc	aac	ctc	acc	atg	595	
Val	Val	Val	Phe	Asp	Asn	Ala	Tyr	His	Gly	Arg	Thr	Asn	Leu	Thr	Met		
150												160					165
					155												
gcg	atg	acc	gcg	aag	aac	cgc	cca	tac	aag	tcc	gga	ttc	gga	cca	cta	643	


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Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
          170          175          180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
          185          190          195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
          200          205          210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
          215          220          225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
          230          235          240          245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
          250          255          260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
          265          270          275

ggc gtc atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979
Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
          280          285          290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc 1027
Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
          295          300          305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc 1075
Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
          310          315          320          325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag 1123
Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys
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acc cgc gcg
Thr Arg Ala 1132

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<210> 516

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

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Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala
  20              25              30

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Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp

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35						40						45					
Ala	Asp	Gly	Gly	Ile	Leu	Ala	Asp	Ala	Asp	Gly	Asn	Arg	Phe	Ile	Asp		
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Leu	Ala	Ser	Gly	Ile	Ala	Val	Thr	Thr	Val	Gly	Gly	Ser	Asn	Ala	Ala		
65						70						75					
Val	Ala	Lys	Ala	Val	Gly	Ala	Ala	Ala	Ala	Arg	Phe	Thr	His	Thr	Cys		
85						90						95					
Phe	Met	Val	Ser	Pro	Tyr	Glu	Thr	Tyr	Val	Ala	Met	Ala	Glu	Arg	Leu		
100						105						110					
Asn	Ala	Leu	Thr	Pro	Gly	Asp	His	Asp	Lys	Lys	Ser	Ala	Leu	Phe	Asn		
115						120						125					
Ser	Gly	Ala	Glu	Ala	Val	Glu	Asn	Ala	Val	Lys	Val	Ala	Arg	Ala	Tyr		
130						135						140					
Thr	Gly	Lys	Gly	Ala	Val	Val	Val	Phe	Asp	Asn	Ala	Tyr	His	Gly	Arg		
145						150						155					
Thr	Asn	Leu	Thr	Met	Ala	Met	Thr	Ala	Lys	Asn	Arg	Pro	Tyr	Lys	Ser		
165						170						175					
Gly	Phe	Gly	Pro	Leu	Ala	Ala	Asp	Val	Tyr	Arg	Ala	Pro	Met	Ser	Tyr		
180						185						190					
Pro	Leu	Arg	Asp	Gly	Leu	Ser	Gly	Pro	Glu	Ala	Ala	Glu	Arg	Ala	Ile		
195						200						205					
Ser	Val	Ile	Glu	Ser	Gln	Val	Gly	Ala	Glu	Asn	Leu	Ala	Cys	Val	Val		
210						215						220					
Ile	Glu	Pro	Ile	Gln	Gly	Glu	Gly	Gly	Phe	Ile	Val	Pro	Ala	Pro	Gly		
225						230						235					
Phe	Leu	Ala	Ala	Ile	Ser	Thr	Trp	Cys	Arg	Glu	Asn	Asp	Val	Val	Phe		
245						250						255					
Ile	Ala	Asp	Glu	Ile	Gln	Ser	Gly	Phe	Leu	Arg	Thr	Gly	Asp	Trp	Phe		
260						265						270					
Ala	Ser	Asp	Ala	Glu	Gly	Val	Ile	Pro	Asp	Val	Ile	Thr	Thr	Ala	Lys		
275						280						285					
Gly	Ile	Ala	Gly	Gly	Met	Pro	Leu	Ser	Ala	Val	Thr	Gly	Arg	Ala	Glu		
290						295						300					
Ile	Met	Asp	Ala	Pro	Gly	Pro	Gly	Ala	Leu	Gly	Gly	Thr	Tyr	Gly	Gly		
305						310						315					
Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	Leu	Ala	Ala	Ile	Glu	Val	Met	Glu		
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Gln	Ala	Asp	Leu	Lys	Thr	Arg	Ala										
340																	

<210> 517

<211> 1491

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1468)

<223> RXN02970

<400> 517

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                               Leu Ala Leu Lys Gly
                               1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                10                15                20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                25                30                35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                40                45                50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                55                60                65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                70                75                80                85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                90                95                100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                105                110                115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                120                125                130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                135                140                145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                150                155                160                165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                170                175                180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

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tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
		200					205					210					
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	215					220					225						
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230					235					240					245		
gca	ggg	tac	tta	aat	ggc	gtg	gcg	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250					255					260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
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Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
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acc	ttc	gcc	aag	ggg	gtt	aac	gca	ggg	tac	gcc	cca	ctc	ggg	ggc	atc	1027	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
	295					300					305						
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Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
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Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
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cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa	1219	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
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gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tggt	gca	1267	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
	375					380					385						
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa	1315	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
390					395				400						405		
ttc	aag	gaa	cgc	ggc	gtg	tggt	ccg	atg	atc	tcc	ggc	aac	cga	ttc	cac	1363	
Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser	Gly	Asn	Arg	Phe	His		
				410					415					420			
atc	gcg	ccg	ccg	ctg	acc	acc	act	gat	gac	gaa	ttg	gta	gca	ctg	ctg	1411	
Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu	Leu	Val	Ala	Leu	Leu		

425 430 435
 gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
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 Ala Leu Phe
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240

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Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
                245                250                255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
                260                265                270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
                275                280                285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
                290                295                300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
305                310                315                320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
                325                330                335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
                340                345                350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
                355                360                365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
                370                375                380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385                390                395                400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
                405                410                415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
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Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
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Leu Thr Phe Ala Gly Ala Leu Phe
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<222> (101)..(1330)

<223> FRXA01009

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Leu Ala Leu Lys Gly

1

5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883

Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
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ttc aag gaa cgc ggc 1330
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 20 25 30

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 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn	Ala	Phe	Ile	Asp	Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly	65	70	75			80
His	Asn	Asn	Pro	Arg	Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg		85	90			95
Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val		100	105			110
Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe		115	120			125
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala		130	135			140
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr		145	150			155
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg		165	170			175
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro		180	185			190
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys		195	200			205
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala		210	215			220
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly		225	230			235
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys		245	250			255
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe		260	265			270
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe		275	280			285
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala		290	295			300
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly		305	310			315
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala		325	330			335
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile		340	345			350
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu		355	360			365
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile		370	375			380

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Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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<211> 1998

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<222> (101)..(1975)

<223> RXA01551

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Leu Lys Ala Val Pro
1 5

acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163
Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala
10 15 20

ccg ttt gaa cct gtc cgg tta gca ccg gcg aag gaa gag agg aat ggt 211
Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly
25 30 35

gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259
Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser
40 45 50

ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307
Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu Thr Glu Ile Arg Leu
55 60 65

gat gac tcg cca agc ggc ccc aac gaa ccc ttc cgc atc tac cgc acc 355
Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe Arg Ile Tyr Arg Thr
70 75 80 85

cgt ggc cca gaa acc aac ccc aag cag gga ctt ccg cgg ctg cgc gag 403
Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu Pro Arg Leu Arg Glu
90 95 100

tca tgg atc acc gcc cgc ggc gac gtt gcc acc tat cag ggg cgc gag 451
Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr Tyr Gln Gly Arg Glu
105 110 115

cgt ttg ctt atc gac gac ggc cgc tcg gca atg cgt cga ggt caa gct 499
Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met Arg Arg Gly Gln Ala
120 125 130

tcg gct gag tgg aaa ggc caa aaa cca gct cct ttg aag gcg cta cct 547
Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro Leu Lys Ala Leu Pro
135 140 145

ggc aaa aga gtc acc caa atg gcc tat gca cgt gct ggc gtg att act 595

Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
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Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe	
				170					175					180		
gtg	cgc	tct	gag	gtg	gcg	cgc	ggt	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val	
			185					190					195			
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggt	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
		200					205					210				
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu	
	215					220					225					
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggt	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr	
230					235				240					245		
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp	
				250					255					260		
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln	
			265				270					275				
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val	
		280				285						290				
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg	1027
Phe	Arg	Asp	Thr	Ile	Ile	Glu	Gln	Cys	Glu	Gln	Gly	Val	Asp	Tyr	Met	
		295				300					305					
acc	atc	cac	gcc	ggc	gtc	ctg	ctg	gct	tat	atc	cca	ctg	act	acc	cgt	1075
Thr	Ile	His	Ala	Gly	Val	Leu	Leu	Ala	Tyr	Ile	Pro	Leu	Thr	Thr	Arg	
310					315					320					325	
cgt	gtc	acc	ggc	att	gtc	tcc	cgc	ggc	gga	tcc	att	atg	gcc	ggt	tgg	1123
Arg	Val	Thr	Gly	Ile	Val	Ser	Arg	Gly	Gly	Ser	Ile	Met	Ala	Gly	Trp	
				330				335						340		
tgt	ctg	gcg	cat	cac	cgc	gaa	tca	ttc	ctc	tac	gag	cat	ttc	gac	gag	1171
Cys	Leu	Ala	His	His	Arg	Glu	Ser	Phe	Leu	Tyr	Glu	His	Phe	Asp	Glu	
			345					350					355			
ctg	tgc	gaa	atc	ttt	gca	caa	tat	gac	gtc	gca	ttc	tcc	ctc	ggt	gat	1219
Leu	Cys	Glu	Ile	Phe	Ala	Gln	Tyr	Asp	Val	Ala	Phe	Ser	Leu	Gly	Asp	
		360				365						370				
ggc	cta	cgc	ccc	gga	tcg	ctt	gcc	gat	gcc	aac	gac	gcc	gcg	caa	ttc	1267
Gly	Leu	Arg	Pro	Gly	Ser	Leu	Ala	Asp	Ala	Asn	Asp	Ala	Ala	Gln	Phe	
		375				380					385					
gcc	gag	ctg	aaa	acc	att	ggt	gag	ctc	acc	caa	cgc	gcc	tgg	gaa	tac	1315
Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln	Arg	Ala	Trp	Glu	Tyr	

150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385

390	395	400	405	
gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg				1363
Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met				
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atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct				1411
Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro				
	425	430	435	
ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac				1459
Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp				
	440	445	450	
cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc				1507
His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr				
	455	460	465	
gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac				1555
Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn				
	470	475	480	485
cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac				1603
Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His				
	490	495	500	
gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac				1651
Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp				
	505	510	515	
gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg				1699
Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala				
	520	525	530	
ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg				1747
Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu				
	535	540	545	
ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg				1795
Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro				
	550	555	560	565
aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc				1843
Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly				
	570	575	580	
gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt				1891
Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser				
	585	590	595	
gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg				1939
Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg				
	600	605	610	
gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc				1985
Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg				
	615	620	625	
gatcccagat agc				1998

290					295					300					
Gly	Val	Asp	Tyr	Met	Thr	Ile	His	Ala	Gly	Val	Leu	Leu	Ala	Tyr	Ile
305					310					315					320
Pro	Leu	Thr	Thr	Arg	Arg	Val	Thr	Gly	Ile	Val	Ser	Arg	Gly	Gly	Ser
				325					330					335	
Ile	Met	Ala	Gly	Trp	Cys	Leu	Ala	His	His	Arg	Glu	Ser	Phe	Leu	Tyr
			340					345					350		
Glu	His	Phe	Asp	Glu	Leu	Cys	Glu	Ile	Phe	Ala	Gln	Tyr	Asp	Val	Ala
		355					360					365			
Phe	Ser	Leu	Gly	Asp	Gly	Leu	Arg	Pro	Gly	Ser	Leu	Ala	Asp	Ala	Asn
	370					375					380				
Asp	Ala	Ala	Gln	Phe	Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln
385					390					395					400
Arg	Ala	Trp	Glu	Tyr	Asp	Val	Gln	Val	Met	Val	Glu	Gly	Pro	Gly	His
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Val	Pro	Leu	Asn	Met	Ile	Gln	Glu	Asn	Asn	Glu	Leu	Glu	Gln	Lys	Trp
			420					425					430		
Ala	Ala	Asp	Ala	Pro	Phe	Tyr	Thr	Leu	Gly	Pro	Leu	Val	Thr	Asp	Ile
		435					440					445			
Ala	Pro	Gly	Tyr	Asp	His	Ile	Thr	Ser	Ala	Ile	Gly	Ala	Ala	His	Ile
	450					455					460				
Ala	Met	Gly	Gly	Thr	Ala	Met	Leu	Cys	Tyr	Val	Thr	Pro	Lys	Glu	His
465					470					475					480
Leu	Gly	Leu	Pro	Asn	Arg	Asp	Asp	Val	Lys	Thr	Gly	Val	Ile	Thr	Tyr
				485					490					495	
Lys	Leu	Ala	Ala	His	Ala	Ala	Asp	Val	Ala	Lys	Gly	His	Pro	Gly	Ala
		500						505					510		
Arg	Ala	Trp	Asp	Asp	Ala	Met	Ser	Lys	Ala	Arg	Phe	Glu	Phe	Arg	Trp
		515					520					525			
Asn	Asp	Gln	Phe	Ala	Leu	Ser	Leu	Asp	Pro	Asp	Thr	Ala	Ile	Ala	Tyr
	530					535					540				
His	Asp	Glu	Thr	Leu	Pro	Ala	Glu	Pro	Ala	Lys	Thr	Ala	His	Phe	Cys
545					550					555					560
Ser	Met	Cys	Gly	Pro	Lys	Phe	Cys	Ser	Met	Arg	Ile	Ser	Gln	Asp	Ile
				565					570					575	
Arg	Asp	Met	Phe	Gly	Asp	Gln	Ile	Ala	Glu	Leu	Gly	Met	Pro	Gly	Val
		580						585					590		
Gly	Asp	Ser	Ser	Ser	Ala	Val	Ala	Ser	Ser	Gly	Ala	Arg	Glu	Gly	Met
		595					600					605			
Ala	Glu	Lys	Ser	Arg	Glu	Phe	Ile	Ala	Gly	Gly	Ala	Glu	Val	Tyr	Arg
	610					615						620			

Arg
625

<210> 523
<211> 1013
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(990)
<223> RXA01019

<400> 523
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Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
1 5 10 15
acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag 96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
20 25 30
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat 144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
35 40 45
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg 192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
50 55 60
ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag 240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
65 70 75 80
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt 288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
85 90 95
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg 336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
100 105 110
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag 384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
115 120 125
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg 432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
130 135 140
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag 480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
145 150 155 160
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga 528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
165 170 175
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt 576

Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190
 cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc 624
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205
 gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga 672
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220
 gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac 720
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240
 caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255
 atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270
 gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285
 tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300
 gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320
 ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg 1010
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330
 aat 1013

<210> 524

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 524

Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
 1 5 10 15

Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
 20 25 30

Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln

65	70	75	80
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	85	90	95
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	100	105	110
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	115	120	125
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	130	135	140
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	145	150	155
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	165	170	175
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	180	185	190
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	195	200	205
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	210	215	220
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	225	230	235
Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser	245	250	255
Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr	260	265	270
Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu	275	280	285
Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln	290	295	300
Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr	305	310	315
Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe	325	330	

<210> 525

<211> 706

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXA01352

<400> 525

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gtgcccaatg cattgggctg agattgcgcg ctgttgctgc gcgggaccgt tcgaacctgt 60

ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
                               Val Phe Glu Asn Arg
                               1           5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
                               10           15           20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val
                               25           30           35

cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca 259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala
                               40           45           50

tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg 307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val
                               55           60           65

ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga 355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly
                               70           75           80           85

ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt 403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu
                               90           95           100

gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act 451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr
                               105           110           115

gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg 499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu
                               120           125           130

gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca 547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser
                               135           140           145

ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg 595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu
                               150           155           160           165

tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg 643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val
                               170           175           180

cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct 691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala
                               185           190           195

ttt tct gaa tct gat
Phe Ser Glu Ser Asp
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<210> 526

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

Val Phe Glu Asn Arg Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala
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Gly Ser Val Asp Glu Val Val His Thr Ala Ser Ala Ala Ala Arg Gly
 20 25 30

Gly Ala Gly Val Val Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala
 35 40 45

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp
 195 200

<210> 527

<211> 944

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(921)

<223> RXA01381

<400> 527

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 Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
 1 5 10 15

att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly	
20 25 30	
cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca	144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro	
35 40 45	
gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc	192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala	
50 55 60	
tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct	240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser	
65 70 75 80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	288
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr	
85 90 95	
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	336
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu	
100 105 110	
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	384
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe	
115 120 125	
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	432
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly	
130 135 140	
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	480
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His	
145 150 155 160	
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	528
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile	
165 170 175	
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	576
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser	
180 185 190	
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	624
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu	
195 200 205	
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	672
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly	
210 215 220	
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	720
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys	
225 230 235 240	
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	768
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile	
245 250 255	
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	816
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp	

260	265	270	
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac			864
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp			
275	280	285	
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc			912
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val			
290	295	300	
aac gcg ctg tagctgtcaa ttttaagaggc cag			944
Asn Ala Leu			
305			
<210> 528			
<211> 307			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 528			
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp			
1	5	10	15
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly			
20	25	30	
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro			
35	40	45	
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala			
50	55	60	
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser			
65	70	75	80
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr			
85	90	95	
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu			
100	105	110	
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe			
115	120	125	
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly			
130	135	140	
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His			
145	150	155	160
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile			
165	170	175	
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser			
180	185	190	
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu			
195	200	205	
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly			

210	215	220
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys		
225	230	235 240
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile		
	245	250 255
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp		
	260	265 270
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp		
	275	280 285
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val		
290	295	300
Asn Ala Leu		
305		

<210> 529
 <211> 259
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(259)
 <223> RXA01360

<400> 529
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 gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115
 Met Leu His Ile Ala
 1 5
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
 10 15 20
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
 25 30 35
 acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
 40 45 50

<210> 530
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 530
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly
 1 5 10 15
 Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala

20 25 30
 Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr
 35 40 45
 Thr Ser Ser Gly Glu
 50
 <210> 531
 <211> 629
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (1)..(606)
 <223> RXA01361
 <400> 531
 gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg 48
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
 1 5 10 15
 acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg 96
 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30
 gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg 144
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45
 aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc 192
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60
 gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt 240
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80
 gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc 288
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95
 gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc 336
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110
 gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att 384
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125
 gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc 432
 Glu Glu Thr Glu Phe Ile Gln Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140
 ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg 480
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160
 tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca 528

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt 576
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga 626
 Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

tta 629

<210> 532

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
 1 5 10 15

Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30

Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45

Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60

Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80

Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95

Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110

Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125

Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140

Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175

Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190

Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

<210> 533


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<220>  
<221> CDS  
<222> (101)..(904)  
<223> RXA01208
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ttg gat tct tta act ctt gtt cga caa aac act ccc ctt gtt cag tgt 163
Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr Pro Leu Val Gln Cys
10 15 20

gcg ggt gcg acc cct gcg atg gtg gat act cca gct gaa tcg gca gaa 259
Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro Ala Glu Ser Ala Glu
40 45 50

gcg gag caa tac caa ggc atg acc aag gcc att gag ggt gca cga aaa 355
Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile Glu Gly Ala Arg Lys
70 75 80 85

gag agg acc aag tat gcg gag gga atc gtc gat aag cag cct gcc gca 451
Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp Lys Gln Pro Ala Ala
105 110 115

ggt ggg cgc ggc gta gac gcg acc gat tcc gtg gaa gtg gcg ttg gag 547
Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val Glu Val Ala Leu Glu
135 140 145

ggt gcg gag gac ttg att gtg tct gcg gat cgg gtg acg tgg ttg cgt 643
Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg Val Thr Trp Leu Arg
170 175 180

tcg ggg gat ccg atg ttg cag ctg gtg att ggc act gga tgc tct ttg 691

Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly Thr Gly Cys Ser Leu
 185 190 195

ggc gcg ctg aca gct gca tat cta ggc gcc acg gtt gac tca gat att 739
 Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr Val Asp Ser Asp Ile
 200 205 210

tcc gcg cac gat gct gtg ttg gct gcg cat gcc cat gtg ggt gct gct 787
 Ser Ala His Asp Ala Val Leu Ala Ala His Ala His Val Gly Ala Ala
 215 220 225

ggc cag att gca gca cag aag gca tcg gcg cca gcc agc ttt gcg gtg 835
 Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro Gly Ser Phe Ala Val
 230 235 240 245

gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser
 250 255 260

ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt 927
 Leu Val Asp Val Arg Glu Ala
 265

<210> 534

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr
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Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala
 20 25 30

Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro
 35 40 45

Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn
 50 55 60

Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile
 65 70 75 80

Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala
 85 90 95

Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp
 100 105 110

Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu
 115 120 125

Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val
 130 135 140

Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly
 145 150 155 160

Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg

	165		170		175
Val Thr Trp	Leu Arg Ser Gly Asp	Pro Met Leu Gln Leu	Val Ile Gly		
	180	185	190		
Thr Gly Cys	Ser Leu Gly Ala Leu Thr Ala Ala Tyr	Leu Gly Ala Thr			
	195	200	205		
Val Asp Ser Asp	Ile Ser Ala His Asp Ala Val	Leu Ala Ala His Ala			
	210	215	220		
His Val Gly Ala	Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro				
	225	230	235	240	
Gly Ser Phe Ala	Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala				
	245	250	255		
Gln Ala Val Ala	Ser Leu Val Asp Val Arg Glu Ala				
	260	265			

<210> 535

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1000)

<223> RXA00838

<400> 535

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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt	atg aaa att gcg atc	115
	Met Lys Ile Ala Ile	
	1 5	

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa	163
Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu	
10 15 20	

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc	211
Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala	
25 30 35	

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac	259
Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr	
40 45 50	

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat	307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp	
55 60 65	

gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct	355
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala	
70 75 80 85	

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag	403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln	
90 95 100	

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aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp
      105                      110                      115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro
      120                      125                      130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp
      135                      140                      145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
      150                      155                      160                      165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
      170                      175                      180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
      185                      190                      195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
      200                      205                      210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
      215                      220                      225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
      230                      235                      240                      245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
      250                      255                      260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
      265                      270                      275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
      280                      285                      290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg 1023
Lys Glu Glu Glu Asn Ser Leu
      295                      300

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<210> 536

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly

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Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly	20	25	30
Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala	35	40	45
Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu	50	55	60
Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg	65	70	75
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

<210> 537

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<400> 537

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Met Ser Ile Ser Arg
1 5

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
25 30 35

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
55 60 65

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
90 95 100

tgc	gat	tcc	gta	gcg	aac	cct	ggt	aac	cca	gtt	cct	tct	tgc	acc	ggc	451
Cys	Asp	Ser	Val	Ala	Asn	Pro	Gly	Asn	Pro	Val	Pro	Ser	Cys	Thr	Gly	
			105					110					115			

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
120 125 130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
135 140 145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
150 155 160 165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
170 175 180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
Glu Val Pro Val Thr Phe Ala Ala Ala
185 190

tca

<210> 538

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 538

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
 1 5 10 15

Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro
 20 25 30

Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser
 35 40 45

Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro
 50 55 60

Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp
 65 70 75 80

Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly
 85 90 95

Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val
 100 105 110

Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu
 115 120 125

Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr
 130 135 140

Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys
 145 150 155 160

Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly
 165 170 175

Phe Arg Asp Val Ala Glu Val Pro Val Thr Phe Ala Ala Ala
 180 185 190

<210> 539

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXN01209

<400> 539

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ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro

	1	5	
gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt			163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val	10	20	
ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att			211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile	25	35	
tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg			259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	40	50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct			307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	55	65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag			355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	70	85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa			403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	90	95	100
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa			451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	105	110	115
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt			499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	120	125	130
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg			547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	135	140	145
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag			595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	150	155	160
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga			643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	170	175	180
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac			691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	185	190	195
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct			739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	200	205	210
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa			787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	215	220	225
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat			835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	230	235	240
			245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggg ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag	1027
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
295 300 305	
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc	1075
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	1123
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly	
330 335 340	
tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc	1171
Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr	
345 350 355	
agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc	1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg	
360 365 370	
ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc	1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala	
375 380 385	
gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct	1315
Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala	
390 395 400 405	
cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag	1363
Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys	
410 415 420	
ggg gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc	1411
Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro	
425 430 435	
gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac	1459
Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn	
440 445 450	
tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc	1507
Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile	
455 460 465	
gcc gcc ggc gaa agc gtg gaa	1528
Ala Ala Gly Glu Ser Val Glu	
470 475	

<210> 540

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 540

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Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
          20              25              30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
          35              40              45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
          50              55              60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
          65              70              75              80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
          85              90              95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
          100             105             110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
          115             120             125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
          130             135             140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
          145             150             155             160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
          165             170             175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
          180             185             190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
          195             200             205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
          210             215             220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
          225             230             235             240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
          245             250             255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
          260             265             270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
          275             280             285

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Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
465 470 475

<210> 541

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> FRXA01209

<400> 541

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ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
Met Cys Glu Arg Pro
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

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 470 475

<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

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 Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
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<210> 543

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(700)

<223> RXN01413

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 Leu Thr His Leu Phe
 1 5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
 10 15 20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
 Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
 25 30 35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
 Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
 40 45 50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
 Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
 55 60 65

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gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
70 75 80 85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
90 95 100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
105 110 115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
120 125 130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
135 140 145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
150 155 160 165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
170 175 180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
185 190 195

gac aac aag tagagtttta aaataccgat caa 723
Asp Asn Lys
200

<210> 544
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 544
Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
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Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
20 25 30

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg
35 40 45

Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu
50 55 60

Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr
65 70 75 80

Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala
85 90 95

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Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
 100 105 110

Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
 115 120 125

Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
 130 135 140

Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
 145 150 155 160

Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
 165 170 175

Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
 180 185 190

Val Trp Leu Ala Glu Asp Asn Lys
 195 200

<210> 545
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(772)
 <223> RXN01617

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tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115
 Leu Ile Leu Lys Thr
 1 5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
 10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
 25 30 35

ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu
 40 45 50

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307
 Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys
 55 60 65

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc 355
 Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg
 70 75 80 85

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu

90	95	100	
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
105	110	115	
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
120	125	130	
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
135	140	145	
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
170	175	180	
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
185	190	195	
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
200	205	210	
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		
cct			795
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<211> 224			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 546			
Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala			
1	5	10	15
Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
20	25	30	
Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr			
35	40	45	
Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp			
50	55	60	
Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr			
65	70	75	80
Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr			
85	90	95	

Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110

Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125

Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140

Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160

Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175

Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190

Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205

Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 547

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA01617

<400> 547

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 1 5 10 15

aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc 192
 Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60

ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac 240
 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp

85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638
<210> 548			
<211> 205			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 548			
Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val			
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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr			
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Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu			
35	40	45	
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			

115	120	125
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile		
130	135	140
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile		
145	150	155
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr		
	165	170
		175
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn		
	180	185
		190
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys		
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<210> 549

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXS01807

<400> 549

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gcagtggctg	gaactcggcg	aggaaatcga	gggctagttc	atg	ccg	tcg	gca	ggc	115
				Met	Pro	Ser	Ala	Gly	
				1				5	

gag	gag	att	tta	gag	cag	cgc	gca	cag	ctg	gag	ttt	gat	cag	cgc	cgc	163
Glu	Glu	Ile	Leu	Glu	Gln	Arg	Ala	Gln	Leu	Glu	Phe	Asp	Gln	Arg	Arg	
			10						15					20		

gcc	gat	gtg	gtg	atg	atc	ggc	agc	cag	gtg	gtt	tat	ggc	tcc	gtg	ggg	211
Ala	Asp	Val	Val	Met	Ile	Gly	Ser	Gln	Val	Val	Tyr	Gly	Ser	Val	Gly	
			25					30					35			

ctc	agt	gct	gcc	att	ccg	gtg	atg	cac	aac	gaa	ggc	ctc	cgc	gtg	gtc	259
Leu	Ser	Ala	Ala	Ile	Pro	Val	Met	His	Asn	Glu	Gly	Leu	Arg	Val	Val	
		40					45					50				

gct	gtc	ccc	acc	gtg	gtg	tta	agt	tcc	atg	ccg	cgt	tat	gca	agt	tct	307
Ala	Val	Pro	Thr	Val	Val	Leu	Ser	Ser	Met	Pro	Arg	Tyr	Ala	Ser	Ser	
	55					60					65					

cac	cgc	cag	ccg	atg	tcg	gac	caa	tgg	ctc	gcc	gac	gcg	ctg	caa	gac	355
His	Arg	Gln	Pro	Met	Ser	Asp	Gln	Trp	Leu	Ala	Asp	Ala	Leu	Gln	Asp	
70					75					80				85		

ctg	gtg	gat	ctg	ggg	att	atc	gat	gag	gtt	tcc	acc	att	tcc	acc	ggc	403
Leu	Val	Asp	Leu	Gly	Ile	Ile	Asp	Glu	Val	Ser	Thr	Ile	Ser	Thr	Gly	
			90					95						100		

tat	ttt	acc	tcc	gct	tct	cag	gtg	cgt	gtg	gtc	gct	gcg	tgg	ctg	cag	451
Tyr	Phe	Thr	Ser	Ala	Ser	Gln	Val	Arg	Val	Val	Ala	Ala	Trp	Leu	Gln	

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105          110          115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile
120          125          130

atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr
135          140          145

gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn
150          155          160

gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu
170          175          180

ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr
185          190          195

gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
200          205          210

atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
215          220          225

tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
230          235          240          245

gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
250          255          260

aaa gcg ctt taggtttcgt ccgtctctga cag 915
Lys Ala Leu

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<210> 550

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

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Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
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Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
20          25          30

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Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
35          40          45

```

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Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
50          55          60

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Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160
 Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
 260

<210> 551

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXC01021

<400> 551

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gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115
 Met Ser Ser Ser Glu
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
 10 15 20

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cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
      25              30              35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
      40              45              50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
      55              60              65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
      70              75              80              85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
      90              95              100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg
      105              110              115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
      120              125              130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
      135              140              145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
      150              155              160              165

ggc act gtt gtc act gtg ttg cgt tct 622
Gly Thr Val Val Thr Val Leu Arg Ser
      170

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<210> 552

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 552

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Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala
      20              25              30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
      35              40              45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
      50              55              60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
      65              70              75              80

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tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat 403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn
90 95 100

gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag 451
 Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu
 105 110 115

gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag 499
 Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu
 120 125 130

ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag 547
 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys
 135 140 145

ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc 595
 Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser
 150 155 160 165

cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga 643
 Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg
 170 175 180

agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat 691
 Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp
 185 190 195

aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa 739
 Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln
 200 205 210

ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac 787
 Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn
 215 220 225

ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta 835
 Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu
 230 235 240 245

tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc 883
 Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly
 250 255 260

cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg 931
 Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val
 265 270 275

cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att 979
 Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile
 280 285 290

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc 1027
 Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
 295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga 1075
 Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
 310 315 320 325

aag gaa cac taaatgttca caggtattgt cga 1107
 Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 554

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Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
 1          5          10          15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
          20          25          30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
          35          40          45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
          50          55          60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
          65          70          75          80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
          85          90          95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
          100          105          110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
          115          120          125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
          130          135          140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
          145          150          155          160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
          165          170          175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
          180          185          190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
          195          200          205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
          210          215          220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
          225          230          235          240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
          245          250          255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
          260          265          270

Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
          275          280          285

Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile

```

290 295 300

Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320

Ile Glu Met Met Arg Lys Glu His
 325

<210> 555
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1084)
 <223> FRXA02246

<400> 555
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caacaaggcg atccaggagt tgcgagcact cgcgacagtaa atg gat gtt gcg cac 115
 Met Asp Val Ala His
 1 5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50

gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala
 55 60 65

gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat 403
 Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn
 90 95 100

gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag 451
 Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu
 105 110 115

gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag 499
 Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu
 120 125 130

ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag 547
 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys
 135 140 145

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ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc 595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser
150                      155                      160                      165

cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga 643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg
170                      175                      180

agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat 691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp
185                      190                      195

aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa 739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln
200                      205                      210

ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac 787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn
215                      220                      225

ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta 835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu
230                      235                      240                      245

tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc 883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly
250                      255                      260

cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg 931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val
265                      270                      275

cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att 979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile
280                      285                      290

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc 1027
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
295                      300                      305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga 1075
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
310                      315                      320                      325

aag gaa cac taaatgttca caggtattgt cga 1107
Lys Glu His

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<210> 556

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

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Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
1                      5                      10                      15

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Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
20                      25                      30

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Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
 35 40 45
 Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
 50 55 60
 Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
 65 70 75 80
 Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
 85 90 95
 Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
 100 105 110
 Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
 115 120 125
 Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
 130 135 140
 His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
 145 150 155 160
 Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
 165 170 175
 Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
 180 185 190
 Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
 195 200 205
 Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 557

<211> 756

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(733)

<223> RXA02247

<400> 557

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ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa	atg ttc aca ggt att	115
	Met Phe Thr Gly Ile	
	1 5	

gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc	163
Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser	
10 15 20	

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg	211
Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu	
25 30 35	

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt	259
Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe	
40 45 50	

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc	307
Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg	
55 60 65	

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc	355
Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg	
70 75 80 85	

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat	403
Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His	
90 95 100	

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg	451
Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp	
105 110 115	

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg	499
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val	
120 125 130	

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct	547
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser	
135 140 145	

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc	595
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg	
150 155 160 165	

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag	643
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu	
170 175 180	

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg	691
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val	

185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733
 Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp
 200 205 210

taggttagac aacgtgagtg aac 756

<210> 558
 <211> 211
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 558
 Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu
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His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu
 20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu
 35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln
 50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys
 65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His
 85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr
 100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu
 115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser
 130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile
 145 150 155 160

Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp
 165 170 175

Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met
 180 185 190

Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe
 195 200 205

Thr Arg Asp
 210

<210> 559
 <211> 1389
 <212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1366)

<223> RXN02248

<400> 559

gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca cgcatttcac gagagactag gttagacaac	gtg agt gaa cat gag	115
	Val Ser Glu His Glu	
	1 5	

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc	163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile	
10 15 20	

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat	211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn	
25 30 35	

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc	259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val	
40 45 50	

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc	307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr	
55 60 65	

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat	355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn	
70 75 80 85	

cag gat gcc cgc gcc acc gct tac acc gtg acc gtt gat gcc aac acc	403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr	
90 95 100	

ggc acc aca gcc att tct gca aca gac cgc gcc cac act ttg cgc ttg	451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu	
105 110 115	

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac	499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His	
120 125 130	

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga	547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly	
135 140 145	

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca	595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro	
150 155 160 165	

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg	643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met	
170 175 180	

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag	691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys	
185 190 195	

BGI-121CP
 -775-
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXN02248
 <400> 559
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 aatgactaca cgcatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu
 1 5
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
 70 75 80 85
 cag gat gcc cgc gcc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
 90 95 100
 ggc acc aca gcc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
 105 110 115
 ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130
 gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145
 cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165
 gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180
 gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg 1171
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt 1219
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct 1267
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg 1315
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa 1363
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

aac taaggagcac aacaatggct aaa 1389
 Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val	Ser	Glu	His	Glu	Gln	Ala	His	Ser	Gln	Leu	Asp	Ser	Val	Glu	Glu
1				5					10					15	
Ala	Ile	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Ala	Val	Val	Val	Val	Asp	Asp
			20					25					30		
Glu	Asp	Arg	Glu	Asn	Glu	Gly	Asp	Ile	Ile	Phe	Ala	Ala	Glu	Leu	Ala
		35					40					45			
Thr	Pro	Glu	Leu	Val	Ala	Phe	Met	Val	Arg	Tyr	Ser	Ser	Gly	Tyr	Ile
	50					55					60				
Cys	Ala	Pro	Leu	Thr	Ala	Lys	Asp	Ala	Asp	Arg	Leu	Asp	Leu	Pro	Pro
65					70					75					80
Met	Thr	Ala	His	Asn	Gln	Asp	Ala	Arg	Gly	Thr	Ala	Tyr	Thr	Val	Thr
				85					90					95	
Val	Asp	Ala	Asn	Thr	Gly	Thr	Thr	Gly	Ile	Ser	Ala	Thr	Asp	Arg	Ala
			100					105					110		
His	Thr	Leu	Arg	Leu	Leu	Ala	Asp	Pro	Glu	Ala	Asp	Arg	Thr	Asp	Phe
		115					120					125			
Thr	Arg	Pro	Gly	His	Val	Val	Pro	Leu	Arg	Ala	Arg	Glu	Gly	Gly	Val
	130					135					140				
Leu	Val	Arg	Ala	Gly	His	Thr	Glu	Ala	Ala	Val	Asp	Leu	Ala	Arg	Ala
145					150					155					160
Ala	Gly	Leu	Arg	Pro	Ala	Gly	Val	Ile	Cys	Glu	Val	Val	Ser	Glu	Glu
				165					170					175	
Asp	Pro	Thr	Gly	Met	Ala	Arg	Val	Pro	Glu	Leu	Arg	Arg	Phe	Cys	Asp
			180					185					190		
Glu	His	Asp	Leu	Lys	Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg
	195						200					205			
Arg	Lys	Asn	Glu	Ile	Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro
	210					215					220				
Thr	Asp	Phe	Gly	Thr	Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp
225					230					235					240
Gly	Thr	Glu	Leu	Val	Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly
				245					250					255	
Gly	Glu	Asn	Val	Leu	Val	Arg	Val	His	Ser	Glu	Cys	Leu	Thr	Gly	Asp
			260					265					270		
Val	Phe	Gly	Ser	Arg	Arg	Cys	Asp	Cys	Gly	Gln	Gln	Leu	His	Glu	Ser
		275					280					285			

Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
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<210> 561

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> FRXA02248

<400> 561

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 Val Ser Glu His Glu
 1 5
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat	355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn	
70 75 80 85	
cag gat gcc cgc gcc acc gct tac acc gtg acc gtt gat gcc aac acc	403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr	
90 95 100	
ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg	451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu	
105 110 115	
ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac	499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His	
120 125 130	
gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga	547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly	
135 140 145	
cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca	595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro	
150 155 160 165	
gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg	643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met	
170 175 180	
gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag	691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys	
185 190 195	
ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att	739
Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile	
200 205 210	
ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg	787
Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr	
215 220 225	
ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt	835
Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val	
230 235 240 245	
gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg	883
Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu	
250 255 260	
gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg	931
Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg	
265 270 275	
cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag	979
Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln	
280 285 290	
gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga	1027
Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg	
295 300 305	
ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa	1075

Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

 ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

 gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg 1171
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

 cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt 1219
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

 gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct 1267
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

 gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg 1315
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

 gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa 1363
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

 aac taaggagcac aacaatggct aaa 1389
 Asn

 <210> 562
 <211> 422
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 562
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 Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
 35 40 45

 Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
 50 55 60

 Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
 65 70 75 80

 Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
 85 90 95

 Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
 100 105 110

 His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
 130 135 140
 Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
 145 150 155 160
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
 165 170 175
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
 180 185 190
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
 195 200 205
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
 210 215 220
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
 225 230 235 240
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
 245 250 255
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
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<210> 563

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> RXN02249

<400> 563

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tgtgggaaca agagcaccca gaaaactaag gagcacaaca	atg gct aaa gaa gga	115
	Met Ala Lys Glu Gly	
	1 5	

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta	163
Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val	
10 15 20	

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac	211
Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His	
25 30 35	

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc	259
Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg	
40 45 50	

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc	307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg	
55 60 65	

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc	355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr	
70 75 80 85	

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc	403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg	
90 95 100	

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc	451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr	
105 110 115	

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta	499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val	
120 125 130	

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc	547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu	
135 140 145	

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt	597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly	
150 155	

ttg	600
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<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
 20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(577)

<223> FRXA02249

<400> 565

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 Met Ala Lys Glu Gly
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg

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      40      45      50
gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
      55      60      65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
      70      75      80      85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
      90      95     100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
      105     110     115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
      120     125     130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu
      135     140     145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
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ttg 600

<210> 566
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<212> PRT
<213> Corynebacterium glutamicum

<400> 566
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
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Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
      35      40      45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
      50      55      60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
      65      70      75      80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
      85      90      95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
      100     105     110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly

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      115              120              125
Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
   130              135              140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
   145              150              155

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<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(679)
<223> RXA02250

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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115
              Val Thr Thr Asn Ala
              1              5

ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc 163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val
              10              15              20

ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc 211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr
              25              30              35

gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg 259
Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val
              40              45              50

acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc 307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile
              55              60              65

atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc 355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr
              70              75              80              85

ggg gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc 403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly
              90              95              100

atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg 451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val
              105              110              115

cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt 499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg
              120              125              130

ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc 547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser
              135              140              145

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BGI-121CP
 -785-
 Corynebacterium glutamicum
 RXA02250
 (101)..(679)
 CDS
 DNA
 567
 702

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<210> 568
<211> 193
<212> PRT
<213> Corynebacterium glutamicum
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1				5					10					15	
His	Ser	Gly	Ala	Val	Gly	Lys	Pro	Lys	Val	Gln	Leu	Ser	Asp	Ala	Glu
			20					25					30		
Ile	Gln	Glu	Tyr	Thr	Ala	Ala	Phe	Ala	Gly	Thr	Thr	Thr	Thr	Lys	Pro
		35					40					45			
Trp	Glu	Leu	Glu	Val	Thr	Thr	Lys	Phe	Leu	Lys	Lys	Ile	Ala	Trp	Val
	50						55				60				
Ala	Val	Val	Val	Ile	Met	Ala	Val	His	Ile	Phe	Met	Gly	Ala	Val	Val
65					70					75					80
Asp	Val	Asp	Phe	Thr	Gly	Ala	Ala	Val	Thr	Phe	Val	Asp	Thr	Leu	Ala
				85					90					95	
Phe	Pro	Ala	Leu	Gly	Ile	Ile	Phe	Ser	Val	Leu	Val	Phe	Leu	Gly	Leu
			100					105					110		
Thr	Arg	Pro	Arg	Val	Arg	Ala	Asn	Glu	Asp	Gly	Val	Glu	Val	Arg	Asn
		115					120					125			
Phe	Ile	Gly	Thr	Arg	Phe	Tyr	Pro	Trp	Val	Val	Ile	Tyr	Gly	Met	Ser
	130					135					140				
Phe	Pro	Lys	Gly	Ser	Ser	Val	Ala	Arg	Leu	Glu	Leu	Pro	Asp	Phe	Glu
145					150					155					160
Phe	Val	Pro	Met	Trp	Ala	Phe	Gln	Ser	Arg	Asp	Gly	Glu	Asp	Val	Val
				165					170					175	
Arg	Ala	Val	Ala	Thr	Phe	Arg	Asp	Leu	Glu	Asn	Lys	Tyr	Met	Pro	Glu
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Asp															

<210> 569
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1123)
 <223> RXA01489

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 Val Asp Ile Trp Ser
 1 5
 gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
 Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
 10 15 20
 ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
 Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu
 25 30 35
 gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc 259
 Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr
 40 45 50
 ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc 307
 Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr
 55 60 65
 cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc 355
 Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly
 70 75 80 85
 gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg 403
 Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu
 90 95 100
 agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg 451
 Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala
 105 110 115
 cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct 499
 Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala
 120 125 130
 ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat 547
 Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn
 135 140 145
 gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc 595
 Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser
 150 155 160 165
 acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac 643
 Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn
 170 175 180

tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt 691
 Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly
 185 190 195

gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac 739
 Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr
 200 205 210

ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg 787
 Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp
 215 220 225

ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat 835
 Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp
 230 235 240 245

atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc 883
 Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser
 250 255 260

gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931
 Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala
 265 270 275

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340

taaggccggt caccggccat caa 1146

<210> 570

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

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 20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80
 Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90
 Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110
 Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125
 Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
 130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu
 165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
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 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
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 Thr Gln Pro Ser Ala
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<210> 571

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 571

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                                         Met Val Pro Ala Glu
                                         1 5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
                        10 15 20

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
                        25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg 259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro
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cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac 307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His
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ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg 355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu
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cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att 403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile
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gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac 451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp
                        105 110 115

cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc 499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile
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gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag 547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys
                        135 140 145

atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att 595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile
150 155 160 165

tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc 643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala
                        170 175 180

ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc 691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg
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ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc 739

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Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile
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 cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc 787
 Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala
 215 220 225
 atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc 835
 Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe
 230 235 240 245
 att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt 883
 Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val
 250 255 260
 gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc 931
 Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala
 265 270 275
 agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc 979
 Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
 280 285 290
 gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg 1027
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
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 tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag 1075
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
 310 315 320 325
 att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc 1123
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
 330 335 340
 gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg 1171
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
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 gag taactttcta agcgatgtcc ggc 1197
 Glu

<210> 572

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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 Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
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 Pro Glu Gln Asn Thr Glu
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<210> 573

<211> 1146

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1123)

<223> RXA01489

<400> 573

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agcattcatg	tctgttgagt	ctatgccgta	gtctaaaaca	gtg	gat	att	tgg	agt	115
				Val	Asp	Ile	Trp	Ser	
				1				5	

gga	cta	gac	agc	gtt	ccg	gct	gat	ctt	caa	gga	tca	gta	gtc	acc	att	163
Gly	Leu	Asp	Ser	Val	Pro	Ala	Asp	Leu	Gln	Gly	Ser	Val	Val	Thr	Ile	
				10					15					20		

ggt	gtg	ttt	gat	ggg	ctc	cac	cgg	ggg	cat	caa	agt	tta	atc	ggc	gag	211
Gly	Val	Phe	Asp	Gly	Leu	His	Arg	Gly	His	Gln	Ser	Leu	Ile	Gly	Glu	
			25					30						35		

gcc	aag	aag	cag	gcc	gag	gag	ctg	ggt	gtg	cct	tgt	gtc	atg	gtg	acc	259
Ala	Lys	Lys	Gln	Ala	Glu	Glu	Leu	Gly	Val	Pro	Cys	Val	Met	Val	Thr	
			40				45					50				

ttt	gac	ccg	cat	ccg	atc	gct	gtg	ttt	ttg	cca	ggt	aaa	gag	cca	acc	307
Phe	Asp	Pro	His	Pro	Ile	Ala	Val	Phe	Leu	Pro	Gly	Lys	Glu	Pro	Thr	
		55				60					65					

cgt	ttg	gct	cct	ttg	gat	tat	cgc	ctt	aat	ttg	gct	gcg	gaa	tgt	ggc	355
Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu	Ala	Ala	Glu	Cys	Gly	
	70				75				80						85	

gtc	gat	gct	gcg	ttg	gtt	att	gat	ttc	act	aaa	gaa	ctc	gca	ggt	ctg	403
Val	Asp	Ala	Ala	Leu	Val	Ile	Asp	Phe	Thr	Lys	Glu	Leu	Ala	Gly	Leu	
				90					95					100		

agc	gct	gaa	gag	tat	ttc	aca	acc	atg	atc	gtg	gat	acg	ctg	cat	gcg	451
Ser	Ala	Glu	Glu	Tyr	Phe	Thr	Thr	Met	Ile	Val	Asp	Thr	Leu	His	Ala	
			105					110					115			

cgt	tca	gtt	gtg	gtg	ggg	gag	aac	ttc	acc	ttc	ggt	gtc	aat	ggc	gct	499
Arg	Ser	Val	Val	Val	Gly	Glu	Asn	Phe	Thr	Phe	Gly	Val	Asn	Gly	Ala	
		120				125						130				

ggc	act	gag	tcc	acg	atg	cgg	gaa	ttg	gga	caa	aag	ttt	ggc	gtg	aat	547
Gly	Thr	Glu	Ser	Thr	Met	Arg	Glu	Leu	Gly	Gln	Lys	Phe	Gly	Val	Asn	
		135				140					145					

gtc	acg	att	gct	ccg	ctg	ctg	cat	gat	gat	gac	cag	cgt	att	tgc	tcc	595
Val	Thr	Ile	Ala	Pro	Leu	Leu	His	Asp	Asp	Asp	Gln	Arg	Ile	Cys	Ser	
		150			155				160					165		

acc	ttg	gtg	cgc	gat	tac	ttg	gat	cag	ggc	gag	gtt	gag	cgc	gcg	aac	643
Thr	Leu	Val	Arg	Asp	Tyr	Leu	Asp	Gln	Gly	Glu	Val	Glu	Arg	Ala	Asn	
			170					175						180		

tgg	gcg	ctt	ggt	cga	cgc	tat	gcc	gtg	cgc	ggc	gaa	gtt	gtc	cgt	ggt	691
Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly	Glu	Val	Val	Arg	Gly	

185										190										195										
gct	ggc	cgt	ggc	ggc	aaa	gaa	ttg	ggc	tat	ccc	acc	gcg	aat	ctc	tac	739														
Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro	Thr	Ala	Asn	Leu	Tyr															
					200						205						210													
ctg	ccg	acc	tct	gtg	gcg	ctg	ccc	gcc	gat	ggc	gtg	tat	gca	ggc	tgg	787														
Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly	Val	Tyr	Ala	Gly	Trp															
					215						220						225													
ttc	acc	atc	acc	gat	gac	cgc	gaa	atc	gac	aag	gaa	atc	tcc	cgc	gat	835														
Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys	Glu	Ile	Ser	Arg	Asp															
					230						235						240	245												
atc	gac	ggc	acc	atg	gtt	cca	ggc	gtg	cgt	tac	caa	act	gcc	att	tcc	883														
Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr	Gln	Thr	Ala	Ile	Ser															
					250						255						260													
gtg	ggc	acc	aat	ccc	acc	ttc	ggc	gat	gag	cga	cgc	agc	gtc	gag	gca	931														
Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg	Arg	Ser	Val	Glu	Ala															
					265						270						275													
ttc	atc	ctc	gac	cag	gaa	gcc	gac	ctg	tac	ggg	cac	cat	gtc	atg	gtg	979														
Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly	His	His	Val	Met	Val															
					280						285						290													
gaa	ttc	gtg	gga	cac	ttg	cgc	gac	atg	gtc	aaa	ttc	aac	ggc	gtc	gac	1027														
Glu	Phe	Val	Gly	His	Leu	Arg	Asp	Met	Val	Lys	Phe	Asn	Gly	Val	Asp															
					295						300						305													
gag	cta	cta	gac	gcc	atg	gcc	cga	gat	gtc	acc	aac	gcc	cgc	gac	atc	1075														
Glu	Leu	Leu	Asp	Ala	Met	Ala	Arg	Asp	Val	Thr	Asn	Ala	Arg	Asp	Ile															
					310						315						320	325												
ctt	gcc	aaa	gac	aaa	ttg	ctt	ctc	gac	gcc	gac	acc	cag	ccc	agc	gct	1123														
Leu	Ala	Lys	Asp	Lys	Leu	Leu	Leu	Asp	Ala	Asp	Thr	Gln	Pro	Ser	Ala															
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<210> 574

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 574

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Ser	Val	Val	Thr	Ile	Gly	Val	Phe	Asp	Gly	Leu	His	Arg	Gly	His	Gln
		20						25					30		

Ser	Leu	Ile	Gly	Glu	Ala	Lys	Lys	Gln	Ala	Glu	Glu	Leu	Gly	Val	Pro
		35					40					45			

Cys	Val	Met	Val	Thr	Phe	Asp	Pro	His	Pro	Ile	Ala	Val	Phe	Leu	Pro
	50					55					60				

Gly	Lys	Glu	Pro	Thr	Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu
65					70					75					80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95
 Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110
 Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125
 Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
 130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu
 165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
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 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
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<210> 575

<211> 805

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (87)..(782)

<223> RXN01712

<400> 575

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			Met	Val	Asp	Ile	Leu	Glu	Leu	Ile	Gly
			1				5				

ccc	cta	cct	ttt	gtg	tct	acg	cca	gag	tta	agg	gca	att	gtc	gtg	act	161
Pro	Leu	Pro	Phe	Val	Ser	Thr	Pro	Glu	Leu	Arg	Ala	Ile	Val	Val	Thr	
10					15				20						25	

gcc	att	aat	ggg	tcc	acc	act	att	aat	ggc	acg	tct	ggg	cag	ctt	gga	209
Ala	Ile	Asn	Gly	Ser	Thr	Thr	Ile	Asn	Gly	Thr	Ser	Gly	Gln	Leu	Gly	
				30					35					40		

aat	tcc	acg	gat	acg	gaa	ctt	ctg	ttg	gcg	ctt	cgc	agg	tgg	tcg	gac	257
Asn	Ser	Thr	Asp	Thr	Glu	Leu	Leu	Leu	Ala	Leu	Arg	Arg	Trp	Ser	Asp	
			45					50					55			

gtg	gtg	ttg	ggt	ggg	tcg	agc	acg	gtg	aag	gct	gaa	aat	tat	ggg	ggc	305
Val	Val	Leu	Val	Gly	Ser	Ser	Thr	Val	Lys	Ala	Glu	Asn	Tyr	Gly	Gly	
		60					65						70			

gtg	gag	ggt	tcg	cct	gaa	atc	cag	aag	caa	cgc	cag	gag	ttg	ggg	cag	353
Val	Glu	Val	Ser	Pro	Glu	Ile	Gln	Lys	Gln	Arg	Gln	Glu	Leu	Gly	Gln	
	75					80					85					

gaa	gag	att	ccg	ccg	att	gag	gtg	atg	tca	ggg	tcg	ttg	aat	ttt	gat	401
Glu	Ala	Ile	Pro	Pro	Ile	Ala	Val	Met	Ser	Gly	Ser	Leu	Asn	Phe	Asp	
90					95					100					105	

gtg	gat	act	cgc	ttt	ttc	ctt	gag	gcc	gaa	gtg	ccg	ccg	atc	atc	atc	449
Val	Asp	Thr	Arg	Phe	Phe	Leu	Glu	Ala	Glu	Val	Pro	Pro	Ile	Ile	Ile	
				110					115					120		

acg	gat	aat	tcc	gat	caa	gca	aag	cag	cag	cgg	ctt	gtg	gat	gct	ggg	497
Thr	Asp	Asn	Ser	Asp	Gln	Ala	Lys	Gln	Gln	Arg	Leu	Val	Asp	Ala	Gly	
			125					130						135		

gct	cag	ggt	att	gag	gtg	gag	acg	ttg	acg	gag	gag	ggt	ggc	gtc	gaa	545
Ala	Gln	Val	Ile	Glu	Val	Glu	Thr	Leu	Thr	Ala	Glu	Val	Gly	Val	Glu	
		140					145					150				

aag	ctt	agg	tct	ttg	ggg	tac	gcc	cgc	att	gat	tgt	gag	ggc	ggg	gca	593
Lys	Leu	Arg	Ser	Leu	Gly	Tyr	Ala	Arg	Ile	Asp	Cys	Glu	Gly	Gly	Ala	
	155					160					165					

acg	ttg	tat	ggg	cag	atg	ttg	gcc	gcc	gat	ctt	ggt	gat	gtg	tgg	cat	641
Thr	Leu	Tyr	Gly	Gln	Met	Leu	Ala	Ala	Asp	Leu	Val	Asp	Val	Trp	His	
170					175					180					185	

cac	acg	att	gat	ccg	acg	ttg	tcg	ggc	agc	gtg	gag	cgc	ccc	acg	gtg	689
His	Thr	Ile	Asp	Pro	Thr	Leu	Ser	Gly	Ser	Val	Glu	Arg	Pro	Thr	Val	
				190					195					200		

aag	ggc	ggc	gat	gat	gag	ccg	cgc	cga	ttc	gag	ttg	gag	cac	gtc	ttt	737
Lys	Gly	Gly	Asp	Asp	Ala	Pro	Arg	Arg	Phe	Ala	Leu	Glu	His	Val	Phe	
			205					210					215			

gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag 782
 Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys
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tgagtgttgg actctccgga tct 805

<210> 576

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

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Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys
 225 230

<210> 577

<211> 578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (55)..(555)

<223> FRXA01712

<400> 577

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Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
      5                                10                                15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg      153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
      20                                25                                30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc      201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
      35                                40                                45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag      249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
      50                                55                                60                                65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg      297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
      70                                75                                80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc      345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
      85                                90                                95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc      393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
      100                               105                               110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc      441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
      115                               120                               125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga      489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
      130                               135                               140                               145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg      537
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu
      150                               155                               160

cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct      578
Arg Tyr Lys Arg Ala Lys
      165

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<210> 578

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 578

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Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
 1             5             10             15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val
          20             25             30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
          35             40             45

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys
          50             55             60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr
 65             70             75             80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala
          85             90             95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala
          100            105            110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser
          115            120            125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg
          130            135            140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe
 145            150            155            160

Leu Arg Tyr Lys Arg Ala Lys
          165

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<210> 579

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXN02384

<400> 579

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ctgatgaggc ggatatccgc aacatcgaca gcattgatga actcccacct ttgccagctg 60

aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115
                               Val Thr Arg Arg Leu
                               1             5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163
Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met
          10             15             20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211
Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala
          25             30             35

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gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259
Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe
      40                      45                      50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307
Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala
      55                      60                      65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355
Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His
      70                      75                      80                      85

ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat 403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr
      90                      95                      100

cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc 451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro
      105                      110                      115

ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc 499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val
      120                      125                      130

gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc 547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu
      135                      140                      145

atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg 595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu
      150                      155                      160                      165

gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc 643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr
      170                      175                      180

tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag 691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu
      185                      190                      195

aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct 739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro
      200                      205                      210

cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc 787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly
      215                      220                      225

tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg 831
Trp Asn Met Gly Val Thr Gln
      230                      235

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<210> 580

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn

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      1             5             10             15
Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu
      20             25             30
Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn
      35             40             45
Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala
      50             55             60
Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg
      65             70             75             80
Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu
      85             90             95
Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro
      100            105            110
Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg
      115            120            125
Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp
      130            135            140
Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu
      145            150            155            160
Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser
      165            170            175
Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr
      180            185            190
Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala
      195            200            205
Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln
      210            215            220
Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln
      225            230            235

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<210> 581

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXN01560

<400> 581

atgggagcaa ggctcattta gctacttcga cgtggaagcg cacatcggtg agttgattcc 60

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tgcatcagta agcgatgcgt ttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115
                Val Gly Val Ser Tyr
                        1             5

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atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
 10 15 20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
 25 30 35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser
 40 45 50

atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg 307
 Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
 55 60 65

ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca 355
 Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
 70 75 80 85

ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac 403
 Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
 90 95 100

ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc 450
 Gly Val Asn Gly Pro Val Asp Ala Asn
 105 110

ttt 453

<210> 582

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
 1 5 10 15

Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
 20 25 30

Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
 35 40 45

Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60

His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80

Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 583

<211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXN00667

<400> 583
 ggcacatcagtg tttgaaggga aaagcagggtc aaacaagggtg cggctgattt gagcgatcac 60
 agcaccgaga tctgtgctga agaattcaat gattggggttg atg att gcg ttg aag 115
 Met Ile Ala Leu Lys
 1 5
 tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta 163
 Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu
 10 15 20
 ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac 211
 Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp
 25 30 35
 gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg 259
 Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr
 40 45 50
 cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt 307
 Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg
 55 60 65
 ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc 355
 Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
 70 75 80 85
 gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc 403
 Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
 90 95 100
 gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac 451
 Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
 105 110 115
 gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct 499
 Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
 120 125 130
 cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg 547
 Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
 135 140 145
 act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act 595
 Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
 150 155 160 165
 tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac 643
 Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
 170 175 180
 caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag gca atc 691

Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu Ala Ile
 185 190 195

gca gaa ttc gtt cca ggg cta ctt gat gat ggt ccc gcg att tgg gaa 739
 Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly Pro Ala Ile Trp Glu
 200 205 210

tcc cgc atc gaa aaa gaa cgc ggc atc gtg caa gcc ttc gtc gtg gaa 787
 Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln Ala Phe Val Val Glu
 215 220 225

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg 1027
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag 1075
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt 1124
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu
 330 335

agacatcacc cag 1137

<210> 584

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 584

Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
 1 5 10 15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly

65	70	75	80
Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp	85	90	95
Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His	100	105	110
Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr	115	120	125
Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val	130	135	140
Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg	145	150	155
Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu	165	170	175
Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys	180	185	190
Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly	195	200	205
Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln	210	215	220
Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser	225	230	235
Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His	245	250	255
Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly	260	265	270
Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile	275	280	285
Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp	290	295	300
Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp	305	310	315
Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly	325	330	335

Ser Leu

<210> 585

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga 787
 Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly
 215 220 225

 atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg 835
 Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met
 230 235 240 245

 gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca 883
 Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
 250 255 260

 tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc 931
 Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
 265 270 275

 ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct 979
 Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
 280 285 290

 atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt 1027
 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
 295 300 305

 gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc 1075
 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
 310 315 320 325

 cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc 1123
 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
 330 335 340

 gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc 1171
 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
 345 350 355

 tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att 1219
 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
 360 365 370

 acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt 1268
 Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
 375 380 385

 caaactcatc agc 1281

<210> 586

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
 1 5 10 15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
 20 25 30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His

35					40					45					
Tyr	Leu	Tyr	Asn	Pro	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr
50						55					60				
Ile	Thr	His	Phe	Thr	Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu
65					70					75					80
Leu	Ala	Ile	Val	Leu	Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp
				85					90					95	
Ala	Leu	Arg	Ser	Met	Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu
			100					105					110		
Thr	Glu	Thr	Val	Gln	Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile
		115					120					125			
Leu	Leu	Leu	Met	Leu	Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys
130						135					140				
Ser	Trp	Leu	Gly	Gly	Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro
145					150					155					160
Met	Phe	Leu	Pro	Leu	Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly
				165					170					175	
Ser	Leu	Ile	Leu	Gly	Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala
			180					185					190		
Trp	Phe	Leu	Val	Pro	Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro
			195				200					205			
Tyr	Leu	Gly	Glu	Thr	Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu
210						215					220				
Ala	Ile	Tyr	Phe	Gly	Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu
225					230					235					240
Ile	Phe	Gly	Ala	Met	Val	Gly	Leu	Ala	Val	Leu	Ala	Leu	Leu	Arg	Phe
				245					250					255	
Arg	Asn	Thr	Glu	Pro	Tyr	Phe	Trp	Ala	Ala	Thr	Thr	Thr	Gly	Val	Leu
			260					265					270		
Leu	Thr	Gly	Val	Phe	Phe	Leu	Ser	Ser	Leu	Gly	Gln	Met	Tyr	Tyr	Ser
		275					280					285			
Met	Met	Ile	Phe	Pro	Met	Ile	Phe	Thr	Leu	Leu	Gly	Ser	Arg	Ser	Val
290						295					300				
Phe	His	Asn	Trp	Val	Ala	Trp	Val	Ala	Ala	Tyr	Phe	Leu	Leu	Ser	Pro
305					310					315					320
Asp	Thr	Phe	Thr	Ser	Gln	Arg	Leu	Pro	Asp	Val	Ala	Arg	Trp	Met	Glu
				325					330					335	
Phe	Phe	Ser	Ala	Thr	Val	Gly	Trp	Gly	Leu	Leu	Ile	Val	Val	Thr	Phe
			340					345					350		
Val	Ser	Ala	Leu	Ile	Trp	Phe	Ile	Gly	Asp	Ile	Arg	Ala	Lys	Gly	Thr
		355					360					365			

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
 370 375 380

Thr Ala
 385

<210> 587

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> RXC02380

<400> 587

gcagattttt gacgaagtcg catcgtggat tgaagctgcc taaaaactcg cgaggacgca 60

tgetcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115
 Met Thr Thr Thr Val
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145

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att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
150                      155                      160                      165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
                      170                      175                      180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
                      185                      190                      195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
                      200                      205                      210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777
Gly Gln Asn Gln Ala
215

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<210> 588
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

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<400> 588
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Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
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Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
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Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
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Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
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Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
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Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
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Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
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Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
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Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

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Met Thr Thr Thr Val
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Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
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His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
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Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
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Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
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Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
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Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
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Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
120 125 130

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His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
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 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
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 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
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Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
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Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
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Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
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Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
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Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val
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Val Ser Ala Leu Glu
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Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
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Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
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acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259
Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
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Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
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Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
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Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
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Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
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Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
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Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

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 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
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 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65 70 75 80
 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
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 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
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Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp	
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Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu	
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Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys	
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Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
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Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
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Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
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 Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp
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Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu	Ile	Pro	Ile	Val	Val	
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Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn	Gly	Leu	Phe	Ala	Tyr	
		280					285					290				
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Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu	Gly	Trp	Thr	Leu	Ser	
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Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu	Val	Leu	Leu	His	Leu	
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Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr	Pro	Thr	Phe	Ile	Ile	
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Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser	Leu	Leu	Ala	Pro	Leu	
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Leu	Ser	Ser	Ser	Pro	Glu	Arg	Val	Val	Val	Leu	Leu	Gly	Ala	Ala	Asn	
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Gly	Phe	Ser	Phe	Ile	Thr	Gly	Ala	Val	Ile	Gly	Ala	Tyr	Leu	Leu	Arg	
	375					380					385					
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Asn	Lys	Leu	Gly	Leu	Leu	Gly	Met	Arg	Ser	Leu	Ala	Lys	Thr	Ser	Leu	
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Trp	Ala	Leu	Gly	Ser	Ala	Ala	Val	Gly	Ala	Ala	Ala	Ala	Trp	Ala	Leu	
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Gly	Trp	Leu	Ile	Gln	Ala	Val	Val	Gly	Asp	Phe	Leu	Leu	Gly	Thr	Leu	
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Ile	Phe	Val	Thr	Gly	Ile	Val	Leu	Ser	Arg	Ser	Gly	Leu	Pro	Glu	Val	
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Gln	Asn	Leu	Gly	Gln	Ala	Leu	Thr	Arg	Ile	Pro	Gly	Leu	Ser	Arg	Phe	
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Pro	Val	Pro	Pro	Pro	Met	Ser	Ala	Gly	Ile	Val	Arg	Gly	Pro	Arg	Leu			
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Val	Pro	Gly	Ala	Pro	Val	Gly	Asp	Gly	Arg	Phe	Arg	Leu	Leu	Ala	Asp			
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Thr	Gly	Lys	Glu	Val	Ala	Leu	Ile	Phe	Val	Asp	Thr	Ser	Gly	Asn	Ala			
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cca	ttt	gcg	cca	ctg	tct	tcg	gca	gcc	gca	gcg	ggc	atc	gcc	tac	gag	1891		
Pro	Phe	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Ala	Ala	Gly	Ile	Ala	Tyr	Glu			
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gtg	cag	cgc	cgc	acc	aag	aag	ctg	gcc	agc	ttg	ggc	agc	ttg	gcg	gta	1939		
Val	Gln	Arg	Arg	Thr	Lys	Lys	Leu	Ala	Ser	Leu	Gly	Ser	Leu	Ala	Val			
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Ala	Pro	Asn	Ile	His	Ser	Glu	Ala	Tyr	Arg	Asn	Gly	Cys	Leu	Ile	Val			
615				620				625										
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Ala	Asp	Trp	Val	Pro	Gly	Ser	Ser	Leu	Ser	Ala	Val	Ala	Glu	Ser	Gly			
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Ala	Asp	Pro	Arg	Ala	Ala	Ala	Phe	Ala	Leu	Ala	Glu	Leu	Thr	Glu	Thr			
650				655				660										
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Ile	Gly	Glu	Ala	His	Glu	Met	Gly	Ile	Pro	Ala	Gly	Leu	Asp	Asn	Lys			
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Cys	Arg	Ile	Arg	Ile	Asn	Thr	Asp	Gly	His	Ala	Val	Leu	Ala	Leu	Pro			
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Ser	Ala	Ala	Glu	Met	Leu	Ile	Asp	Ala	Thr	Leu	Ala	Pro	Ser	Asp	Val			
710				715				720				725						
aag	gca	atg	gtc	act	gaa	gcc	cag	ggg	cta	gct	aca	gaa	gac	aat	ccc	2323		
Lys	Ala	Met	Val	Thr	Glu	Ala	Gln	Gly	Leu	Ala	Thr	Glu	Asp	Asn	Pro			
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Asp	Tyr	Ala	Ser	Leu	Ala	Met	Ala	Met	Arg	Thr	Cys	Gly	Leu	Phe	Thr	
			745					750					755			
gag	gaa	cca	acc	cac	ctt	gtg	gtg	aag	aag	gaa	aag	aca	cca	aag	cct	2419
Glu	Glu	Pro	Thr	His	Leu	Val	Val	Lys	Lys	Glu	Lys	Thr	Pro	Lys	Pro	
		760					765					770				
gcg	aca	cgt	gat	ggc	ttc	ggc	gcc	tcc	gac	tac	acc	gtc	aag	ggc	atg	2467
Ala	Thr	Arg	Asp	Gly	Phe	Gly	Ala	Ser	Asp	Tyr	Thr	Val	Lys	Gly	Met	
	775					780					785					
gca	gcc	atc	gcc	gct	gtg	gtg	atc	atc	ttg	gtt	tcc	ctg	gtg	gcc	gcc	2515
Ala	Ala	Ile	Ala	Ala	Val	Val	Ile	Ile	Leu	Val	Ser	Leu	Val	Ala	Ala	
	790				795				800						805	
ggc	acc	gcg	ttc	ctc	acc	agc	ttc	ttc	ggc	agc	agc	acc	aac	gaa	caa	2563
Gly	Thr	Ala	Phe	Leu	Thr	Ser	Phe	Phe	Gly	Ser	Ser	Thr	Asn	Glu	Gln	
			810						815					820		
tcc	cgc	ttg	gcc	tct	gtt	gaa	gcc	acc	acc	tct	gca	aca	cca	gaa	cct	2611
Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser	Ala	Thr	Pro	Glu	Pro	
			825					830					835			
gtg	ggg	cca	ccg	gtc	tac	ctg	gat	ctg	gat	caa	gcc	cgc	acg	tgg	gat	2659
Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln	Ala	Arg	Thr	Trp	Asp	
		840					845					850				
gac	ggc	gca	gga	aca	gat	gtc	acc	gac	gtc	acc	gac	ggc	aac	acc	tcc	2707
Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr	Asp	Gly	Asn	Thr	Ser	
	855					860					865					
acc	gca	tgg	acc	tcc	acc	ggc	ggc	gac	ggc	ctc	cta	gtt	gac	ctg	tcc	2755
Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu	Leu	Val	Asp	Leu	Ser	
	870				875					880					885	
acg	cct	gcc	cgc	ctc	gac	cgc	gtc	atc	ttg	acc	acc	ggc	acc	ggc	tcc	2803
Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr	Thr	Gly	Thr	Gly	Ser	
			890						895					900		
gac	agc	aac	gtg	acc	tcg	acc	gtg	aag	atc	tac	gca	ttc	aac	gac	gcc	2851
Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr	Ala	Phe	Asn	Asp	Ala	
			905					910					915			
tca	cca	cac	tcc	ctg	tcg	gaa	ggc	atc	gag	atc	ggc	acc	gtg	gat	tat	2899
Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile	Gly	Thr	Val	Asp	Tyr	
		920					925					930				
tcc	ggc	cgc	agt	ctc	agc	cac	agc	atc	cgc	gat	tcc	tcc	aag	ctt	ccg	2947
Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp	Ser	Ser	Lys	Leu	Pro	
	935					940					945					
ggc	cag	gtg	gaa	tcc	gtg	gtg	att	ctg	gtc	gat	gag	gtt	cgt	tcc	tca	2995
Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp	Glu	Val	Arg	Ser	Ser	
	950				955					960					965	
caa	acc	tca	gac	acc	aat	cca	cag	atg	cag	atc	gct	gaa	gta	caa	ctt	3043
Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile	Ala	Glu	Val	Gln	Leu	
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Val Gly Trp

3075

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<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg
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20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
165 170 175

Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
180 185 190

Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
195 200 205

Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
210 215 220

Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
225 230 235 240

Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
245 250 255

Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
260 265 270

Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590

Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile

915	920	925
Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp		
930	935	940
Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp		
945	950	955
Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile		
	965	970
		975
Ala Glu Val Gln Leu Val Gly Trp		
980		

<210> 595

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXA01807

<400> 595

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				Met	Pro	Ser	Ala	Gly	
				1				5	

gag	gag	att	tta	gag	cag	cgc	gca	cag	ctg	gag	ttt	gat	cag	cgc	cgc	163
Glu	Glu	Ile	Leu	Glu	Gln	Arg	Ala	Gln	Leu	Glu	Phe	Asp	Gln	Arg	Arg	
			10						15					20		

gcc	gat	gtg	gtg	atg	atc	ggc	agc	cag	gtg	gtt	tat	ggc	tcc	gtg	ggg	211
Ala	Asp	Val	Val	Met	Ile	Gly	Ser	Gln	Val	Val	Tyr	Gly	Ser	Val	Gly	
		25						30					35			

ctc	agt	gct	gcc	att	ccg	gtg	atg	cac	aac	gaa	ggc	ctc	cgc	gtg	gtc	259
Leu	Ser	Ala	Ala	Ile	Pro	Val	Met	His	Asn	Glu	Gly	Leu	Arg	Val	Val	
		40					45					50				

gct	gtc	ccc	acc	gtg	gtg	tta	agt	tcc	atg	ccg	cgt	tat	gca	agt	tct	307
Ala	Val	Pro	Thr	Val	Val	Leu	Ser	Ser	Met	Pro	Arg	Tyr	Ala	Ser	Ser	
	55					60					65					

cac	cgc	cag	ccg	atg	tcg	gac	caa	tgg	ctc	gcc	gac	gcg	ctg	caa	gac	355
His	Arg	Gln	Pro	Met	Ser	Asp	Gln	Trp	Leu	Ala	Asp	Ala	Leu	Gln	Asp	
	70				75				80					85		

ctg	gtg	gat	ctg	ggg	att	atc	gat	gag	gtt	tcc	acc	att	tcc	acc	ggc	403
Leu	Val	Asp	Leu	Gly	Ile	Ile	Asp	Glu	Val	Ser	Thr	Ile	Ser	Thr	Gly	
			90					95						100		

tat	ttt	acc	tcc	gct	tct	cag	gtg	cgt	gtg	gtc	gct	gcg	tgg	ctg	cag	451
Tyr	Phe	Thr	Ser	Ala	Ser	Gln	Val	Arg	Val	Val	Ala	Ala	Trp	Leu	Gln	
			105					110					115			

aaa	atc	cgc	gaa	acc	cat	ccg	cat	gtg	cgc	atc	gtg	gtg	gat	ccc	atc	499
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Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile
 120 125 130
 atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547
 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr
 135 140 145
 gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595
 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn
 150 155 160 165
 gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu
 170 175 180
 ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr
 185 190 195
 gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
 200 205 210
 atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
 215 220 225
 tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
 230 235 240 245
 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
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 aaa gcg ctt taggtttcgt ccgtctctga cag 915
 Lys Ala Leu

<210> 596

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 596

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
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 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
 20 25 30
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80

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<222> (101)..(1438)  
<223> RXN02754
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                                         Val Asn Thr Asn Pro
                                           1                    5

tct gaa ttc tcc tca aac cgt tca aca gct ctg ctt act gat aaa tat      163
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
                      10                        15                20

gag ctg acc atg ctt caa gca gcg ctg gct gat ggt tct gca gaa cgc      211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
                      25                        30                35
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ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga	259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg	
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tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac	307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp	
55 60 65	
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac	355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
70 75 80 85	
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat	403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
90 95 100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
105 110 115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
120 125 130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
250 255 260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg	
265 270 275	

aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser
280 285 290

tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt 1027
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
295 300 305

gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca 1075
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
310 315 320 325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg 1123
Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct 1171
Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac 1219
Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc 1267
Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct 1315
Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta 1363
Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act 1411
Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
425 430 435

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Arg Phe Val Gly Phe Pro Pro Ala Ala
440 445

aac 1461

<210> 598

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 598

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Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60
 Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365

Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
 385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
 405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
 420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
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<210> 599

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> FRXA02405

<400> 599

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 Val Asn Thr Asn Pro
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp
 90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451
 Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr
 105 110 115

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gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu
120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg 547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met
135 140 145

gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg
150 155 160 165

acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct 643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala
170 175 180

gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att 691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile
185 190 195

cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn
200 205 210

gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu
215 220 225

tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr
230 235 240 245

caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca 871
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro
250 255

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<210> 600

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

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Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
85 90 95

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Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255

Pro

<210> 601
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(486)
 <223> FRXA02754

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 1 5 10 15
 atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
 20 25 30
 tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
 35 40 45
 atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60


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gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240
Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
65 70 75 80

ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
85 90 95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
100 105 110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
115 120 125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
130 135 140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
145 150 155 160

gcc gct tagacaattc ggtctcacca aac 509
Ala Ala

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<210> 602

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 602

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Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
1 5 10 15

Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
20 25 30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
35 40 45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
50 55 60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
65 70 75 80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
85 90 95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
100 105 110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
115 120 125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
130 135 140

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<400> 603																
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agctcctgtt	actcctagct	cctcgaagga	tgcgtaattt	atg	act	acc	cat	att	115							
				Met	Thr	Thr	His	Ile	5							
				1												
gac	cgc	atc	gtt	ggc	gca	gcg	tta	tcc	gag	gat	gcg	cca	tgg	ggc	gac	163
Asp	Arg	Ile	Val	Gly	Ala	Ala	Leu	Ser	Glu	Asp	Ala	Pro	Trp	Gly	Asp	
			10						15					20		
att	acc	tcc	gac	act	ttt	atc	cca	gga	tcg	gcg	cag	ctg	agc	gcc	aag	211
Ile	Thr	Ser	Asp	Thr	Phe	Ile	Pro	Gly	Ser	Ala	Gln	Leu	Ser	Ala	Lys	
			25					30					35			
gtt	gtt	gcc	cgg	gag	cca	ggg	gtg	ttc	agc	ggg	cag	gcg	ctt	tta	gac	259
Val	Val	Ala	Arg	Glu	Pro	Gly	Val	Phe	Ser	Gly	Gln	Ala	Leu	Leu	Asp	
		40					45					50				
gcc	tcc	ttc	cgg	ctc	gtc	gat	cct	agg	ata	aac	gca	tcc	ctt	aag	gtg	307
Ala	Ser	Phe	Arg	Leu	Val	Asp	Pro	Arg	Ile	Asn	Ala	Ser	Leu	Lys	Val	
	55					60					65					
gct	gat	ggg	gac	agc	ttt	gaa	acc	ggg	gac	atc	cta	gga	aca	att	acc	355
Ala	Asp	Gly	Asp	Ser	Phe	Glu	Thr	Gly	Asp	Ile	Leu	Gly	Thr	Ile	Thr	
70					75				80						85	
ggc	agt	gct	aga	agc	atc	ctc	cgt	tca	gag	gcg	att	gct	ctc	aac	ttc	403
Gly	Ser	Ala	Arg	Ser	Ile	Leu	Arg	Ser	Glu	Arg	Ile	Ala	Leu	Asn	Phe	
				90				95						100		
att	cag	agg	acg	tcc	ggc	atc	gct	aca	ttg	aca	tcg	tgc	tat	gtt	gca	451
Ile	Gln	Arg	Thr	Ser	Gly	Ile	Ala	Thr	Leu	Thr	Ser	Cys	Tyr	Val	Ala	
			105				110						115			
gag	gtt	aaa	ggc	acc	aaa	gcc	cgc	att	gtt	gat	acc	cgg	aaa	acc	aca	499
Glu	Val	Lys	Gly	Thr	Lys	Ala	Arg	Ile	Val	Asp	Thr	Arg	Lys	Thr	Thr	
		120				125					130					
ccc	ggc	ctg	cgc	atc	att	gaa	cgc	caa	gct	gtc	cgt	gac	ggg	ggc	gga	547
Pro	Gly	Leu	Arg	Ile	Ile	Glu	Arg	Gln	Ala	Val	Arg	Asp	Gly	Gly	Gly	
	135					140				145						

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ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595
Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn
150                      155                      160                      165

cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643
His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
                      170                      175                      180

tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
                      185                      190                      195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
                200                      205                      210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
                215                      220                      225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
230                      235                      240                      245

ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
                      250                      255                      260

gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931
Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
                265                      270                      275

att ttc taatgctcta ccttgataat gca 960
Ile Phe

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<210> 604

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

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Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
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Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
                20                      25                      30

Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
                35                      40                      45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
                50                      55                      60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
                65                      70                      75                      80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
                85                      90                      95

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Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
 100 105 110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp
 115 120 125

Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val
 130 135 140

Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val
 145 150 155 160

Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser
 165 170 175

Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
 180 185 190

His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
 195 200 205

Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
 210 215 220

Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala
 225 230 235 240

Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
 245 250 255

Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu
 260 265 270

Asp Leu Gly Leu Asp Ile Phe
 275

<210> 605
 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1384)
 <223> RXA02111

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gctcattcca gccaccggt tagaagaaaa gaccccaatc atg acc acc tca atc 115
 Met Thr Thr Ser Ile
 1 5

acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
 10 15 20

gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
 25 30 35

gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct	259
Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala	
40 45 50	
ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac	307
Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp	
55 60 65	
gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa	355
Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys	
70 75 80 85	
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac	403
Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His	
90 95 100	
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc	451
Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr	
105 110 115	
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct	499
Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala	
120 125 130	
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc	547
Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro	
135 140 145	
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc	595
Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser	
150 155 160 165	
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc	643
Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr	
170 175 180	
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc	691
Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe	
185 190 195	
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc	739
Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser	
200 205 210	
gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc	787
Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro	
215 220 225	
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc	835
Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile	
230 235 240 245	
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc	883
Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr	
250 255 260	
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc	931
Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys	
265 270 275	

tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc 979
 Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala
 280 285 290

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca 1027
 Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro
 295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa 1075
 Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
 310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa 1123
 Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
 330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc 1171
 Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
 345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att 1219
 Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
 360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac 1267
 His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
 375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga 1315
 Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
 390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act 1363
 Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
 410 415 420

cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga 1407
 Pro Ser Ser Ser Lys Asp Ala
 425

<210> 606

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala
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Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln
 20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
 35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
 50 55 60

Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80

Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
 115 120 125
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
 130 135 140
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
 145 150 155 160
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
 180 185 190
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
 195 200 205
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
 245 250 255
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
 290 295 300
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
 305 310 315 320
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
 325 330 335
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
 340 345 350
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
 355 360 365
 Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
 370 375 380
 Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
 385 390 395 400

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
420 425

<210> 607
<211> 954
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(931)
<223> RXA01073
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ccaagacacc accgcgccat gtttgcctag gattaggtac atg aca aac act caa 115
Met Thr Asn Thr Gln
1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163
Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala
10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211
Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala
25 30 35

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tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc    259
Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser
          40                      45                      50
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act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307
Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala
55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355
Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr
70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403
Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile
90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451
Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala
105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499
Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp
120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547
Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr
135 140 145

gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595

Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala
 150 155 160 165

gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala
 170 175 180

gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile
 185 190 195

ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr
 200 205 210

gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu
 215 220 225

ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp
 230 235 240 245

gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly
 250 255 260

cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg
 265 270 275

taatccaaca gtttgagtgt cgc 954

<210> 608

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro
 1 5 10 15

Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val
 20 25 30

Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser
 35 40 45

Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val
 50 55 60

Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
 65 70 75 80

Val Arg Leu Pro Tyr Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val
 85 90 95

Ala Leu Glu Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys
 100 105 110

Asp Ala Thr Asp Ala Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu
 115 120 125
 Pro Glu Leu Thr Asp Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg
 130 135 140
 Met Val Ala Gln Tyr Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile
 145 150 155 160
 Gly Thr Asp His Ala Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe
 165 170 175
 Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg
 180 185 190
 Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp
 195 200 205
 Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro
 210 215 220
 Asp Glu Glu Ala Leu Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu
 225 230 235 240
 Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His
 245 250 255
 Leu Trp Lys Val Gly Gln His Lys Arg His Leu Pro Ala Thr Pro Gln
 260 265 270
 Glu Asn Trp Trp Arg
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<210> 609

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXN02754

<400> 609

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agttcactgt agctcccgtt gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg

40	45	50	
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac			307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp			
55	60	65	
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac			355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp			
70	75	80	85
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat			403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp			
	90	95	100
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act			451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr			
	105	110	115
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg			499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu			
	120	125	130
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg			547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met			
	135	140	145
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc			595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg			
150	155	160	165
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct			643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala			
	170	175	180
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att			691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile			
	185	190	195
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac			739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn			
	200	205	210
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa			787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu			
	215	220	225
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc			835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr			
230	235	240	245
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc			883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly			
	250	255	260
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc			931
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg			
	265	270	275
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc			979
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser			
	280	285	290

tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt 1027
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
 295 300 305

gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca 1075
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
 310 315 320 325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg 1123
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct 1171
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac 1219
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc 1267
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct 1315
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta 1363
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act 1411
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
 425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca 1458
 Arg Phe Val Gly Phe Pro Pro Ala Ala
 440 445

aac 1461

<210> 610

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 610

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
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 20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
 385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
 405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
 420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
 435 440 445

<210> 611

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02299

<400> 611

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taaaacttgc aggacaaccc ccataaggac accacaggac atg ctg cgc acc atc 115
 Met Leu Arg Thr Ile
 1 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163
 Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
 10 15 20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211
 Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
 25 30 35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259
 Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
 40 45 50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307
 Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile
 55 60 65

tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
 Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
 70 75 80 85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
 Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
 90 95 100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
 Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
 105 110 115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
 Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
 120 125 130

aga agc att tagcgtttta gctcgccaat att
Arg Ser Ile
135

531

<210> 612

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
1 5 10 15

Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
20 25 30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
35 40 45

Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
50 55 60

Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
65 70 75 80

Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
85 90 95

Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
100 105 110

Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
115 120 125

Gly Leu Leu Thr Ser Arg Ser Ile
130 135

<210> 613

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXA01928

<400> 613

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tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
Met Gln Val Ala Thr
1 5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
10 15 20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt	211
Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val	
25 30 35	
aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc	259
Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val	
40 45 50	
aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac	307
Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn	
55 60 65	
tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt	355
Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly	
70 75 80 85	
gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc	403
Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly	
90 95 100	
ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag	451
Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu	
105 110 115	
ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg	499
Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala	
120 125 130	
aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa	547
Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys	
135 140 145	
gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac	595
Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp	
150 155 160 165	
att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc	643
Ile Pro Val Glu Ile Arg Pro Val Pro Ile Arg Gly Ala Asp Gly	
170 175 180	
tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg	691
Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala	
185 190 195	
caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa	739
Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys	
200 205 210	
gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc	787
Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala	
215 220 225	
agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc	835
Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala	
230 235 240 245	
acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg	883
Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu	
250 255 260	
gtg gtc ggc gcg att ttc gtg ggg ccg gtg ccg ttg atc gac aat atc	931

Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
 265 270 275

gag ctc tagtaccaac cctgcgttgc agc
 Glu Leu

960

<210> 614

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
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His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
 20 25 30

His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
 35 40 45

Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
 50 55 60

Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
 65 70 75 80

Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
 85 90 95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
 100 105 110

Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
 115 120 125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
 130 135 140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu
 245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg
 260 265 270

Leu Ile Asp Asn Ile Glu Leu
 275

<210> 615

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXN01929

<400> 615

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ggaattttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115
 Met Pro Met Ser Gly
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
 135 140 145

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ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
150                      155                      160                      165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643
Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
170                      175                      180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
185                      190                      195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
200                      205                      210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
215                      220                      225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
230                      235                      240                      245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
250                      255                      260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
265                      270

aag 936

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<210> 616

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
20                      25                      30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
35                      40                      45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
50                      55                      60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
65                      70                      75                      80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
85                      90                      95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
100                      105                      110

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Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly
130 135 140

His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
145 150 155 160

Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
165 170 175

Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
180 185 190

Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
195 200 205

Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
210 215 220

Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
225 230 235 240

Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
245 250 255

Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
260 265 270

<210> 617

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 617

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Met Ser Gly Ile Asp
1 5

gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc 163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly
10 15 20

cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att 211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile
25 30 35

ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc 259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala
40 45 50

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aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag 307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu
    55                      60                      65

atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt 355
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu
    70                      75                      80                      85

gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag 403
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln
                      90                      95                      100

gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg 451
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala
                      105                      110                      115

gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att 499
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile
                      120                      125                      130

gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag 547
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln
                      135                      140                      145

tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt 595
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser
    150                      155                      160                      165

tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg 643
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala
                      170                      175                      180

ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt 691
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val
                      185                      190                      195

acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc 739
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly
                      200                      205                      210

aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc 787
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg
                      215                      220                      225

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
    230                      235                      240                      245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
                      250                      255                      260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
Phe Pro Gly Glu Ala Glu Ser Phe
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<210> 618

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

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Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
          20           25           30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
          35           40           45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
          50           55           60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
          65           70           75           80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
          85           90           95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
          100          105          110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
          115          120          125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
          130          135          140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
          145          150          155          160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
          165          170          175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
          180          185          190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
          195          200          205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
          210          215          220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
          225          230          235          240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
          245          250          255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
          260          265

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<210> 619

<211> 921

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

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cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115
                                   Leu Ser Phe Thr His
                                   1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163
Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly
                                   10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211
Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly
                                   25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259
Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg
                                   40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307
Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp
                                   55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355
His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn
                                   70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403
Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly
                                   90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451
Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu
                                   105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499
Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr
                                   120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547
Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro
                                   135 140 145

gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc 595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala
                                   150 155 160 165

att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca 643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala
                                   170 175 180

ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac 691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His
                                   185 190 195

ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca 739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala
                                   200 205 210

```

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ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca 787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro
    215                220                225

gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc 835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly
    230                235                240                245

gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc 883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe
    250                255                260

aaa aac atc gaa ggc tgatcccggt ttaccagtt cgc 921
Lys Asn Ile Glu Gly
    265

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<210> 620

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

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Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln
  1                5                10                15

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Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val
    20                25                30

```

```

Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile
    35                40                45

```

```

Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala
    50                55                60

```

```

Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala
    65                70                75                80

```

```

Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val
    85                90                95

```

```

Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr
    100                105                110

```

```

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
    115                120                125

```

```

Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn
    130                135                140

```

```

Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
    145                150                155                160

```

```

Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp
    165                170                175

```

```

Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala
    180                185                190

```

```

His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln

```


195	200	205
Val Leu Lys Ala Ala Gly	Val Thr Pro Asp Tyr	Val Glu Ile Arg Gly
210	215	220
Leu Asp Leu Gly Pro Ala	Pro Glu Ile Gly Asp	Ala Arg Leu Phe Ala
225	230	235
Ala Ile Thr Leu Gly Asp	Val Gln Leu His Asp	Asn Val Gly Leu Pro
245	250	255
Leu Gly Ile Gly Phe Lys	Asn Ile Glu Gly	
260	265	

<210> 621

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 621

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cttttcacca aaatttttac gaaaggcgag attttctccc	atg gct att gaa ctg	115
	Met Ala Ile Glu Leu	
	1 5	

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt	163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val	
10 15 20	

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc	211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu	
25 30 35	

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag	259
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys	
40 45 50	

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
---	-----

Ile	Lys	Pro	Ala	Asp	Asp	Ile	Ile	Val	Gly	Met	Val	Ala	Pro	Lys	Gly		
		120					125					130					
cca	ggc	cac	ttg	gtt	cgc	cgt	cag	ttc	gtt	gat	ggc	aag	ggt	gtt	cct	547	
Pro	Gly	His	Leu	Val	Arg	Arg	Gln	Phe	Val	Asp	Gly	Lys	Gly	Val	Pro		
	135					140					145						
tgc	ctc	atc	gca	gtc	gac	cag	gac	cca	acc	gga	acc	gca	cag	gct	ctg	595	
Cys	Leu	Ile	Ala	Val	Asp	Gln	Asp	Pro	Thr	Gly	Thr	Ala	Gln	Ala	Leu		
150					155					160					165		
acc	ctg	tcc	tac	gca	gca	gca	atc	ggg	ggc	gca	cgc	gca	ggc	gtt	atc	643	
Thr	Leu	Ser	Tyr	Ala	Ala	Ala	Ile	Gly	Gly	Ala	Arg	Ala	Gly	Val	Ile		
				170					175					180			
cca	acc	acc	ttc	gaa	gct	gag	acc	gtc	acc	gac	ctc	ttc	ggc	gag	cag	691	
Pro	Thr	Thr	Phe	Glu	Ala	Glu	Thr	Val	Thr	Asp	Leu	Phe	Gly	Glu	Gln		
			185					190					195				
gct	gtt	ctc	tgc	ggg	ggc	acc	gag	gaa	ctg	gtc	aag	gtt	ggc	ttc	gag	739	
Ala	Val	Leu	Cys	Gly	Gly	Thr	Glu	Glu	Leu	Val	Lys	Val	Gly	Phe	Glu		
		200					205					210					
gtt	ctc	acc	gaa	gct	ggc	tac	gag	cca	gag	atg	gca	tac	ttc	gag	gtt	787	
Val	Leu	Thr	Glu	Ala	Gly	Tyr	Glu	Pro	Glu	Met	Ala	Tyr	Phe	Glu	Val		
	215					220					225						
ctt	cac	gag	ctc	aag	ctc	atc	gtt	gac	ctc	atg	ttc	gaa	ggg	ggc	atc	835	
Leu	His	Glu	Leu	Lys	Leu	Ile	Val	Asp	Leu	Met	Phe	Glu	Gly	Gly	Ile		
230					235				240						245		
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Ser	Asn	Met	Asn	Tyr	Ser	Val	Ser	Asp	Thr	Ala	Glu	Phe	Gly	Gly	Tyr		
				250					255					260			
ctc	tcc	ggc	cca	cgc	gtc	atc	gat	gca	gac	acc	aag	tcc	cgc	atg	aag	931	
Leu	Ser	Gly	Pro	Arg	Val	Ile	Asp	Ala	Asp	Thr	Lys	Ser	Arg	Met	Lys		
			265					270					275				
gac	atc	ctg	acc	gat	atc	cag	gac	ggc	acc	ttc	acc	aag	cgc	ctc	atc	979	
Asp	Ile	Leu	Thr	Asp	Ile	Gln	Asp	Gly	Thr	Phe	Thr	Lys	Arg	Leu	Ile		
		280				285						290					
gca	aac	gtt	gag	aac	ggc	aac	acc	gag	ctt	gag	ggc	ctt	cgt	gct	tcc	1027	
Ala	Asn	Val	Glu	Asn	Gly	Asn	Thr	Glu	Leu	Glu	Gly	Leu	Arg	Ala	Ser		
	295					300					305						
tac	aac	aac	cac	cca	atc	gag	gag	acc	ggc	gct	aag	ctc	cgc	gac	ctc	1075	
Tyr	Asn	Asn	His	Pro	Ile	Glu	Glu	Thr	Gly	Ala	Lys	Leu	Arg	Asp	Leu		
310					315					320					325		
atg	agc	tgg	gtc	aag	gtt	gac	gct	cgc	gca	gaa	acc	gct	taagttttcac			1124	
Met	Ser	Trp	Val	Lys	Val	Asp	Ala	Arg	Ala	Glu	Thr	Ala					
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<210> 622

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 622

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Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
      20           25           30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
      35           40           45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
      50           55           60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
      65           70           75           80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
      85           90           95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
      100          105          110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
      115          120          125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
      130          135          140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145          150          155          160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
      165          170          175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
      180          185          190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
      195          200          205

Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
      210          215          220

Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
      225          230          235          240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
      245          250          255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
      260          265          270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
      275          280          285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
      290          295          300

Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala

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<400> 623																
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Met Ala Ile Glu Leu 1 5																
ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163																
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val 10 15 20																
gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211																
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu 25 30 35																
cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259																
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys 40 45 50																
tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307																
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala 55 60 65																
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355																
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr 70 75 80 85																
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Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala 90 95 100																
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451																
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu 105 110 115																
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499																
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly 120 125 130																
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547																
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro 135 140 145																

556

tgc ctc atc
Cys Leu Ile
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<210> 624
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 624
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His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45
Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60
Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80
Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95
Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110
Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
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Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140
Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 625
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA02239

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Val Pro Met Thr His
1 5
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163

Val	Ser	Ser	Pro	Ser	Ala	Pro	Arg	Asn	Val	Val	Val	Gly	Val	Ala	Gly		
				10					15					20			
gga	atc	gca	gcg	tac	aag	gcg	tgt	cac	atc	gtg	cg	g	ttt	aaa	gaa	211	
Gly	Ile	Ala	Ala	Tyr	Lys	Ala	Cys	His	Ile	Val	Arg	Ala	Phe	Lys	Glu		
			25					30					35				
gcg	ggc	gat	aat	gtg	cg	gtg	gtt	cct	acg	gaa	tcc	g	ttg	aag	ttt	259	
Ala	Gly	Asp	Asn	Val	Arg	Val	Val	Pro	Thr	Glu	Ser	Ala	Leu	Lys	Phe		
		40					45				50						
gtg	ggg	aag	g	acg	ttt	gaa	g	ttg	tct	ggc	aat	ccg	gtg	tct	aca	307	
Val	Gly	Lys	Ala	Thr	Phe	Glu	Ala	Leu	Ser	Gly	Asn	Pro	Val	Ser	Thr		
	55					60					65						
acg	gtg	ttt	gat	g	gtg	gat	tcg	gtg	cag	cat	gtg	aaa	gtt	ggc	cag	355	
Thr	Val	Phe	Asp	Ala	Val	Asp	Ser	Val	Gln	His	Val	Lys	Val	Gly	Gln		
	70					75				80					85		
gaa	gct	gat	ttg	atc	gtg	att	g	ccg	g	aca	gcc	gat	ttg	atg	g	403	
Glu	Ala	Asp	Leu	Ile	Val	Ile	Ala	Pro	Ala	Thr	Ala	Asp	Leu	Met	Ala		
			90					95						100			
cgt	gtg	gtg	gca	gg	ctc	gg	gac	gat	ctg	ttg	g	g	acg	ctg	ctg	451	
Arg	Val	Val	Ala	Gly	Leu	Gly	Asp	Asp	Leu	Leu	Ala	Ala	Thr	Leu	Leu		
			105					110						115			
gtg	gca	acg	tgc	ccc	gtg	gtt	att	g	ccg	gcc	atg	cat	acg	gag	atg	499	
Val	Ala	Thr	Cys	Pro	Val	Val	Ile	Ala	Pro	Ala	Met	His	Thr	Glu	Met		
		120					125					130					
tgg	ttt	aat	ccg	gct	acc	gta	gcc	aat	gtg	gca	acg	ctg	agg	cag	cg	547	
Trp	Phe	Asn	Pro	Ala	Thr	Val	Ala	Asn	Val	Ala	Thr	Leu	Arg	Gln	Arg		
	135					140					145						
ggg	att	acc	gtg	att	gag	cct	g	cat	gg	cga	ctc	acc	gg	aaa	gat	595	
Gly	Ile	Thr	Val	Ile	Glu	Pro	Ala	His	Gly	Arg	Leu	Thr	Gly	Lys	Asp		
	150				155				160					165			
aca	ggc	cct	ggc	cg	ctg	ccg	gat	cca	gag	cag	att	gtt	gat	tta	gcc	643	
Thr	Gly	Pro	Gly	Arg	Leu	Pro	Asp	Pro	Glu	Gln	Ile	Val	Asp	Leu	Ala		
			170					175						180			
aat	g	gtg	cac	gcc	ggg	g	agg	ttg	cct	cag	gat	ttg	g	ggc	aag	691	
Asn	Ala	Val	His	Ala	Gly	Ala	Arg	Leu	Pro	Gln	Asp	Leu	Ala	Gly	Lys		
			185					190						195			
aaa	gtg	ctg	atc	act	gct	gg	ggc	acg	cat	gag	cat	att	gat	cct	gtg	739	
Lys	Val	Leu	Ile	Thr	Ala	Gly	Gly	Thr	His	Glu	His	Ile	Asp	Pro	Val		
		200					205					210					
cg	ttt	att	ggc	aat	agt	tcc	tcg	ggc	cgt	caa	gg	ttt	g	ttg	gg	787	
Arg	Phe	Ile	Gly	Asn	Ser	Ser	Ser	Gly	Arg	Gln	Gly	Phe	Ala	Leu	Gly		
	215					220					225						
gaa	atc	gca	gca	cag	cga	gg	gct	cat	gtc	agc	atc	gtg	g	gga	aat	835	
Glu	Ile	Ala	Ala	Gln	Arg	Gly	Ala	His	Val	Ser	Ile	Val	Ala	Gly	Asn		
	230				235					240				245			
gct	g	gag	ctg	ccc	act	ccg	gca	ggc	gca	gag	atc	gtg	ccg	gtg	gtg	883	
Ala	Ala	Glu	Leu	Pro	Thr	Pro	Ala	Gly	Ala	Glu	Ile	Val	Pro	Val	Val		

250	255	260	
tcc aca caa gac atg ttt gat gca gtc	cag gaa cga gct ggc caa tct	931	
Ser Thr Gln Asp Met Phe Asp Ala Val	Gln Glu Arg Ala Gly Gln Ser		
265	270 275		
gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg	979		
Asp Phe Ile Val Met Ala Ala Ala Val	Ala Asp Phe Thr Pro Ala Ser		
280	285 290		
cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca	1027		
Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala			
295	300 305		
ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg	1075		
Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr			
310	315 320 325		
gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg	1123		
Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val			
330	335 340		
ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat	1171		
Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr			
345	350 355		
gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat	1219		
Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn			
360	365 370		
gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg	1267		
Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp			
375	380 385		
att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa	1315		
Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys			
390	395 400 405		
atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa	1363		
Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu			
410	415 420		
gtc tagaaaaatc cagctagacc act	1389		
Val			

<210> 626

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 626

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Val	Gly	Val	Ala	Gly	Gly	Ile	Ala	Ala	Tyr	Lys	Ala	Cys	His	Ile	Val
			20					25					30		

Arg	Ala	Phe	Lys	Glu	Ala	Gly	Asp	Asn	Val	Arg	Val	Val	Pro	Thr	Glu
			35				40						45		

Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly
 50 55 60
 Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His
 65 70 75 80
 Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr
 85 90 95
 Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu
 100 105 110
 Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala
 115 120 125
 Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala
 130 135 140
 Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg
 145 150 155 160
 Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln
 165 170 175
 Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln
 180 185 190
 Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu
 195 200 205
 His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210 215 220
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
 225 230 235 240
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
 245 250 255
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
 260 265 270
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
 275 280 285
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290 295 300
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
 305 310 315 320
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
 325 330 335
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
 340 345 350
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
 355 360 365

Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370 375 380
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
 385 390 395 400
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
 405 410 415
 Leu Ala Tyr Arg Glu Val
 420

<210> 627
 <211> 1092
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1069)
 <223> RXA00581

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 cgatcacact agtggagtag ctaaggtgca caatggattc atg gca gag caa aac 115
 Met Ala Glu Gln Asn
 1 5
 gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc 163
 Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe
 10 15 20
 agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac 211
 Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn
 25 30 35
 tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc 259
 Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly
 40 45 50
 atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg 307
 Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro
 55 60 65
 ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act 355
 Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr
 70 75 80 85
 gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg 403
 Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro
 90 95 100
 ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc 451
 Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr
 105 110 115
 gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc 499
 Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg
 120 125 130

gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta 547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu
135 140 145

atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac 595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp
150 155 160 165

caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc 643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu
170 175 180

gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca 691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro
185 190 195

ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc 739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly
200 205 210

tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc 787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe
215 220 225

gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg 835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp
230 235 240 245

tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc 883
Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro
250 255 260

ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931
Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile
265 270 275

gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979
Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val
280 285 290

gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa 1027
Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys
295 300 305

ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc 1069
Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile
310 315 320

taggggttct tgctggtttt gag 1092

<210> 628

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 628

Met Ala Glu Gln Asn Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro
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Arg Thr Pro Asp Phe Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp
 20 25 30
 Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val
 35 40 45
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala
 50 55 60
 Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala
 65 70 75 80
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro
 85 90 95
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val
 100 105 110
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp
 115 120 125
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr
 130 135 140
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe
 145 150 155 160
 Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val
 165 170 175
 Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala
 180 185 190
 Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile
 195 200 205
 Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met
 210 215 220
 Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu
 225 230 235 240
 Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr
 245 250 255
 Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala
 260 265 270
 Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn
 275 280 285
 Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser
 290 295 300
 Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met
 305 310 315 320
 Arg Lys Ile

<210> 629
 <211> 1023
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> RXS00838

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 tgcttataaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
 Met Lys Ile Ala Ile
 1 5
 gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
 10 15 20
 tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
 25 30 35
 ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr
 40 45 50
 gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307
 Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp
 55 60 65
 gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct 355
 Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala
 70 75 80 85
 gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403
 Glu Leu Leu Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln
 90 95 100
 aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451
 Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp
 105 110 115
 cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499
 Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro
 120 125 130
 gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547
 Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp
 135 140 145
 tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
 150 155 160 165
 att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
 170 175 180

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gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg 1023
Lys Glu Glu Glu Asn Ser Leu
295 300

<210> 630
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 630
Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe

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115              120              125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
130              135              140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
145              150              155              160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
165              170              175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
180              185              190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
195              200              205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
210              215              220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
225              230              235              240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
245              250              255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
260              265              270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
275              280              285

Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu
290              295              300

<210> 631
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXC02238

<400> 631
ggcgcttagc caaaacatag agcggtaggg tatgcttata cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
Val Thr Asn Val Ser
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
25 30 35

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acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaattg tagagctcat 60

gccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
                               Val Ser Lys Leu Lys
                               1           5
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ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
                10                15                20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
                25                30                35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
                40                45                50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
                55                60                65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
                70                75                80                85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
                90                95                100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
                105                110                115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
                120                125                130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
                135                140                145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
150                155                160

tataaaccaa aaa 606

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<210> 634

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 634

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Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
  1                5                10                15

```

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Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
  20                25                30

```

```

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
  35                40                45

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Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
  50                55                60

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Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
 145 150 155 160

Pro

<210> 635
 <211> 606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(583)
 <223> FRXA02903

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gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
 Val Ser Lys Leu Lys
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu

	90	95	100	
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa				451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln				
	105	110	115	
atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata				499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile				
	120	125	130	
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga				547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly				
	135	140	145	
atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc				593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro				
	150	155	160	
tataaaccaa aaa				606
<210>	636			
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<212>	PRT			
<213>	Corynebacterium glutamicum			
<400>	636			
Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly				
1 5 10 15				
Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp				
20 25 30				
Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr				
35 40 45				
Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn				
50 55 60				
Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly				
65 70 75 80				
Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp				
85 90 95				
Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile				
100 105 110				
Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu				
115 120 125				
Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg				
130 135 140				
Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys				
145 150 155 160				
Pro				

<210> 637
 <211> 783
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(760)
 <223> RXA00166

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 gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115
 Val Glu Leu Ala Arg
 1 5
 ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
 10 15 20
 agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
 25 30 35
 atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259
 Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
 40 45 50
 gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307
 Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
 55 60 65
 acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355
 Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
 70 75 80 85
 gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403
 Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
 90 95 100
 aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451
 Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
 105 110 115
 atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca 499
 Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
 120 125 130
 gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547
 Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
 135 140 145
 ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595
 Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
 150 155 160 165
 tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag 643
 Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
 170 175 180

tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691
 Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
 185 190 195

ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739
 Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
 200 205 210

gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg 783
 Ala Gly Arg Ser Ser Asn Leu
 215 220

<210> 638

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 638

Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly
 1 5 10 15

Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu
 20 25 30

Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala
 35 40 45

Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn
 50 55 60

Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val
 65 70 75 80

Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala
 85 90 95

Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His
 100 105 110

Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe
 115 120 125

Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr
 130 135 140

Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His
 145 150 155 160

Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val
 165 170 175

Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro
 180 185 190

Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser
 195 200 205

Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu
 210 215 220

<210> 639
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1369)
 <223> RXA00633

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 tacactgcag atatacatcc aaaccaagtg acggaggaaa atg gaa aac ccc agc 115
 Met Glu Asn Pro Ser
 1 5
 ttg cgc gag ctt gat cac cga aac atc tgg cac ccg tat gcc gcg ccg 163
 Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro
 10 15 20
 ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg 211
 Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr
 25 30 35
 ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg 259
 Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser
 40 45 50
 gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa 307
 Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys
 55 60 65
 caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag 355
 Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu
 70 75 80 85
 ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc 403
 Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser
 90 95 100
 ttt gac cac gtc ttt tat tcc gat tcg ggc tcg gtc tca gtg gag gtc 451
 Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val
 105 110 115
 gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa 499
 Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu
 120 125 130
 cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac cac gga gac aca ttc 547
 Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe
 135 140 145
 acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg 595
 Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp
 150 155 160 165
 aaa ggc aca ctc ccc gag cag att ttc gcc ccc gcc cca cca gtt cgg 643
 Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg
 170 175 180

ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg 691
 Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu
 185 190 195

ctt atc gac gag gcg gtc tcc gca atc atc atc gaa ccg atc gtc caa 739
 Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln
 200 205 210

ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc 787
 Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val
 215 220 225

gcc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att 835
 Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu Ile Val Asp Glu Ile
 230 235 240 245

gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat 883
 Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn
 250 255 260

ggc cta caa cca gac atc atg tgt gtg ggc aag gcc ctc acc ggt gga 931
 Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly
 265 270 275

ttc atg tcc ttc gcc gct act tta tgc acg gac aag gtg gct caa tta 979
 Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu
 280 285 290

atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt 1027
 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe
 295 300 305

atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc 1075
 Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile
 310 315 320 325

att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa 1123
 Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu
 330 335 340

ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat 1171
 Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp
 345 350 355

gtc egg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc 1219
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val
 360 365 370

aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc 1267
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile
 375 380 385

cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg 1315
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr
 390 395 400 405

tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa 1363
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys
 410 415 420

ggg aaa taaaccatgc catttttatt tgt
Gly Lys

1392

<210> 640

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His
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Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp
20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met
35 40 45

Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys
50 55 60

Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly
65 70 75 80

Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn
85 90 95

Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser
100 105 110

Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly
115 120 125

Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr
130 135 140

His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly
145 150 155 160

Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro
165 170 175

Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu
180 185 190

Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile
195 200 205

Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala
210 215 220

Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu
225 230 235 240

Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe
245 250 255

Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys
260 265 270

Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp
 275 280 285

Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met
 290 295 300

His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His
 305 310 315 320

Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys
 325 330 335

Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu
 340 345 350

Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu
 355 360 365

Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp
 370 375 380

His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro
 385 390 395 400

Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu
 405 410 415

His Ala Ala Val Lys Gly Lys
 420

<210> 641
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> RXA00632

<400> 641
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ctgcactgcg cttcatgctg cagttaaagg gaaataaacc atg cca ttt tta ttt 115
 Met Pro Phe Leu Phe
 1 5

gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163
 Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val
 10 15 20

ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211
 Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys
 25 30 35

cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259
 Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile
 40 45 50

gaa cgc ttg act gga att gct gga gag gaa ttt gct cgt ttc aaa gac 307
 Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp
 55 60 65
 cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355
 Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile
 70 75 80 85
 cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403
 Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp
 90 95 100
 cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451
 Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly
 105 110 115
 gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499
 Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
 120 125 130
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
 135 140 145
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
 150 155 160 165
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
 170 175 180
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
 185 190 195
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro
 200 205 210
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 215 220
 tcg 795

<210> 642

<211> 224

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 642

Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr
 1 5 10 15

Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp
 20 25 30

Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly
 35 40 45

Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe
 50 55 60
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu
 65 70 75 80
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly
 85 90 95
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu
 100 105 110
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala
 115 120 125
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu
 130 135 140
 Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr
 145 150 155 160
 Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala
 165 170 175
 Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe
 180 185 190
 Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu
 195 200 205
 Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 210 215 220

<210> 643
 <211> 1125
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1102)
 <223> RXA00295

<400> 643
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 ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115
 Met Thr Ile Pro Gly
 1 5
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly
 10 15 20
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln

25										30										35										
atc	cca	gac	ttg	atg	gaa	tta	gcc	cac	cag	gtt	cgg	ttg	aag	tgg	tgt		259													
Ile	Pro	Asp	Leu	Met	Glu	Leu	Ala	His	Gln	Val	Arg	Leu	Lys	Trp	Cys															
40					45					50																				
ggg	gaa	gaa	atc	gag	gtc	gag	ggc	att	att	tcc	ctc	aaa	act	ggc	ggt		307													
Gly	Glu	Glu	Ile	Glu	Val	Glu	Gly	Ile	Ile	Ser	Leu	Lys	Thr	Gly	Gly															
55					60					65																				
tgc	cct	gaa	gat	tgt	cat	ttc	tgc	tca	cag	tct	ggg	ttg	ttt	gaa	tcg		355													
Cys	Pro	Glu	Asp	Cys	His	Phe	Cys	Ser	Gln	Ser	Gly	Leu	Phe	Glu	Ser															
70					75					80					85															
ccg	gtg	cgt	tcg	gtg	tgg	ctg	gat	att	ccg	aat	ctg	gtt	gaa	gcc	gct		403													
Pro	Val	Arg	Ser	Val	Trp	Leu	Asp	Ile	Pro	Asn	Leu	Val	Glu	Ala	Ala															
90					95					100																				
aaa	cag	acc	gca	aaa	act	ggc	gct	acc	gaa	ttc	tgt	atc	gtc	gcc	gca		451													
Lys	Gln	Thr	Ala	Lys	Thr	Gly	Ala	Thr	Glu	Phe	Cys	Ile	Val	Ala	Ala															
105					110					115																				
gtc	aag	ggg	cct	gat	gag	agg	ctc	atg	acc	cag	ctg	gag	gaa	gca	gtc		499													
Val	Lys	Gly	Pro	Asp	Glu	Arg	Leu	Met	Thr	Gln	Leu	Glu	Glu	Ala	Val															
120					125					130																				
ctc	gcg	att	cac	tct	gaa	gtt	gaa	att	gaa	gtc	gca	gca	tcg	atc	gga		547													
Leu	Ala	Ile	His	Ser	Glu	Val	Glu	Ile	Glu	Val	Ala	Ala	Ser	Ile	Gly															
135					140					145																				
acg	tta	aat	aag	gaa	cag	gtg	gat	cgc	ctc	gct	gct	gcc	ggc	gtg	cac		595													
Thr	Leu	Asn	Lys	Glu	Gln	Val	Asp	Arg	Leu	Ala	Ala	Ala	Gly	Val	His															
150					155					160					165															
cgc	tac	aac	cat	aat	ttg	gaa	act	gcg	cgt	tcc	tat	ttc	cct	gaa	gtt		643													
Arg	Tyr	Asn	His	Asn	Leu	Glu	Thr	Ala	Arg	Ser	Tyr	Phe	Pro	Glu	Val															
170					175					180																				
gtc	acc	act	cat	aca	tgg	gaa	gag	cgc	cgc	gaa	act	ttg	cgc	ctg	gtg		691													
Val	Thr	Thr	His	Thr	Trp	Glu	Glu	Arg	Arg	Glu	Thr	Leu	Arg	Leu	Val															
185					190					195																				
gca	gaa	gct	gga	atg	gaa	gtc	tgt	tcc	ggc	gga	atc	tta	gga	atg	ggc		739													
Ala	Glu	Ala	Gly	Met	Glu	Val	Cys	Ser	Gly	Gly	Ile	Leu	Gly	Met	Gly															
200					205					210																				
gaa	act	tta	gag	cag	cgc	gcc	gag	ttt	gcc	gtg	cag	ctg	gcg	gag	ctt		787													
Glu	Thr	Leu	Glu	Gln	Arg	Ala	Glu	Phe	Ala	Val	Gln	Leu	Ala	Glu	Leu															
215					220					225																				
gat	ccg	cac	gaa	gtc	ccc	atg	aac	ttc	ctt	gat	cct	cgc	ccg	ggc	acc		835													
Asp	Pro	His	Glu	Val	Pro	Met	Asn	Phe	Leu	Asp	Pro	Arg	Pro	Gly	Thr															
230					235					240					245															
cca	ttt	gcc	gat	agg	gaa	ttg	atg	gac	agc	cgt	gac	gct	ctg	cgc	tct		883													
Pro	Phe	Ala	Asp	Arg	Glu	Leu	Met	Asp	Ser	Arg	Asp	Ala	Leu	Arg	Ser															
250					255					260																				
att	ggt	gcg	ttc	cgc	ctt	gcg	atg	cct	cac	acc	atg	ctt	cgt	ttt	gct		931													
Ile	Gly	Ala	Phe	Arg	Leu	Ala	Met	Pro	His	Thr	Met	Leu	Arg	Phe	Ala															
265					270					275																				

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
 Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
 280 285 290

 ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc 1027
 Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
 295 300 305

 ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg 1075
 Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
 310 315 320 325

 ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac 1122
 Pro Ile Lys Val Leu Asn Lys Val Ile
 330

 gac 1125

<210> 644

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 644

Met Thr Ile Pro Gly Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu
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Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr
 20 25 30

Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val
 35 40 45

Arg Leu Lys Trp Cys Gly Glu Ile Glu Val Glu Gly Ile Ile Ser
 50 55 60

Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser
 65 70 75 80

Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn
 85 90 95

Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe
 100 105 110

Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln
 115 120 125

Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val
 130 135 140

Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala
 145 150 155 160

Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser
 165 170 175

Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu
 180 185 190

Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly
195 200 205

Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val
210 215 220

Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp
225 230 235 240

Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg
245 250 255

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr
260 265 270

Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly
275 280 285

Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn
290 295 300

Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met
305 310 315 320

Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile
325 330

<210> 645

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00223

<400> 645

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tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115
Met Arg Glu Val Ala
1 5

gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163
Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln
10 15 20

tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211
Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu
25 30 35

gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259
Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr
40 45 50

gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307
Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His
55 60 65

gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly
 70 75 80 85

att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu
 90 95 100

ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Thr Ala Ala Ala
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac 1027
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc 1075
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala
 310 315 320 325

 cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc 1123
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser
 330 335 340

 atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt 1171
 Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg
 345 350 355

 act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg 1212
 Thr Ala Gly Met Ala Phe
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu
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 Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala
 20 25 30

 Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile
 35 40 45

 Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val
 50 55 60

 Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro
 65 70 75 80

 Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly
 85 90 95

 Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser
 100 105 110

 Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp
 115 120 125

 Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala
 130 135 140

 Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val
 145 150 155 160

 Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu
 165 170 175

 Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu
 180 185 190

 Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu
 245 250 255

His Thr Ile Pro Asn Val Leu Val His Thr Thr Glu Pro Ser Leu Pro
 260 265 270

Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile
 275 280 285

Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys
 290 295 300

Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile
 305 310 315 320

Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr
 325 330 335

Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val
 340 345 350

Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe
 355 360

<210> 647
 <211> 1197
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1174)
 <223> RXN00262

<400> 647
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attctgtgca tgcacttgac ctaggactcg atatttttcta atg ctc tac ctt gat 115
 Met Leu Tyr Leu Asp
 1 5

aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg 163
 Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp
 10 15 20

cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg 211
 Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val
 25 30 35

gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc 259
 Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala
 40 45 50

cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga	307
Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly	
55 60 65	
tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct	355
Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro	
70 75 80 85	
cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta	403
Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu	
90 95 100	
gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac	451
Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr	
105 110 115	
cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	499
Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys	
120 125 130	
gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat	547
Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn	
135 140 145	
gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt	595
Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser	
150 155 160 165	
acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac	643
Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp	
170 175 180	
ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct	691
Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro	
185 190 195	
aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc	739
Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile	
200 205 210	
cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt	787
His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val	
215 220 225	
gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa	835
Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu	
230 235 240 245	
tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	883
Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro	
250 255 260	
gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca	931
Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala	
265 270 275	
tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	979
Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu	
280 285 290	
gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga	1027

Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 295 300 305
 gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca 1075
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 310 315 320 325
 cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat 1123
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 330 335 340
 gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga 1171
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 345 350 355
 ggg tgacgctagt cagaggttta cgg 1197
 Gly

<210> 648

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala
 1 5 10 15

Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser
 20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala
 35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr
 50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala
 65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu
 85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
 130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
 145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
 165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
 180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
 195 200 205
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 210 215 220
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 225 230 235 240
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 245 250 255
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 260 265 270
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 275 280 285
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 290 295 300
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 305 310 315 320
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 325 330 335
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 340 345 350
 Val Ala Leu Ile Arg Gly
 355

<210> 649

<211> 920

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (79)..(897)

<223> FRXA00262

<400> 649

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cgtgcttagc taatcctagtg gcc ggg cac ctc atc acc acc ccg atc gag 111
 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu
 1 5 10

cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 15 20 25

ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 30 35 40

gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
 45 50 55
 ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
 60 65 70 75
 gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
 80 85 90
 cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
 95 100 105
 aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
 110 115 120
 ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt 495
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 125 130 135
 ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 140 145 150 155
 ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 160 165 170
 gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 175 180 185
 att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 190 195 200
 gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 205 210 215
 gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 220 225 230 235
 gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 240 245 250
 cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 255 260 265
 gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
 Val Ala Leu Ile Arg Gly
 270

<210> 650

<211> 273

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 650

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu
 1 5 10 15
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 20 25 30
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 35 40 45
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 50 55 60
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 65 70 75 80
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 85 90 95
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 100 105 110
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 115 120 125
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 130 135 140
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 145 150 155 160
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 165 170 175
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 180 185 190
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 195 200 205
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 210 215 220
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 225 230 235 240
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 245 250 255
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 260 265 270
 Gly

<210> 651

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<220>  
<221> CDS  
<222> (101)..(1273)  
<223> RXN00435
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Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
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ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739
Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly
      200                      205                      210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787
Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser
      215                      220                      225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835
Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser
      230                      235                      240                      245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883
Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His
      250                      255                      260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg 931
Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly
      265                      270                      275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979
Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser
      280                      285                      290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc 1027
Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala
      295                      300                      305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc 1075
Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe
      310                      315                      320                      325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac 1123
Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp
      330                      335                      340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca 1171
Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala
      345                      350                      355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg 1219
Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro
      360                      365                      370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg 1267
Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser
      375                      380                      385

ctt gcc taaaccgcaa gcacgagctt gcc 1296
Leu Ala
      390

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<210> 652

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 652

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
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 Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30
 Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140
 Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala
 145 150 155 160
 His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys
 165 170 175
 Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr
 180 185 190
 Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val
 195 200 205
 Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile
 210 215 220
 Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu
 225 230 235 240
 Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro
 245 250 255
 Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val
 260 265 270
 Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu
 275 280 285
 His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly
 290 295 300
 Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val
 305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr
 325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp
 340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr
 355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr
 370 375 380

Arg Val Leu Ala Ser Leu Ala
 385 390

<210> 653

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA00435

<400> 653

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Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu	
1 5 10 15	
tgg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg	96
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
20 25 30	
cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg	144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg	192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat	240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc	288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac	336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc	384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	
115 120 125	
ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc acc atg gaa ggc gtg	432
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val	

130 135 140
 ccc gca gat atg gtg tac cgc cga ttg gtg gac aat cgt ttg atc act 480
 Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr
 145 150 155 160
 acc gtc agc cct gct gac ccg ctg ctc gaa gca atg ggt gtg act gaa 528
 Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
 165 170 175
 gct ggc gga tcg atc act atc gga cta agc ccg ttt agc acc tac tat 576
 Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr
 180 185 190
 gaa gtg gat cag ctg acc agg gtg ctg gca tcg ctt gcc taaaccgcaa 625
 Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala
 195 200 205
 gcacgagctt gcc 638

 <210> 654
 <211> 205
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 654
 Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu
 1 5 10 15
 Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro
 20 25 30
 Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu
 35 40 45
 Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly
 50 55 60
 Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp
 65 70 75 80
 Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe
 85 90 95
 His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His
 100 105 110
 Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala
 115 120 125
 Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val
 130 135 140
 Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr
 145 150 155 160
 Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
 165 170 175
 Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr

180	185	190
Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala		
195	200	205
<210> 655		
<211> 535		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(535)		
<223> FRXA02801		
<400> 655		
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gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc	gtg ggt ttt gat gtg	115
	Val Gly Phe Asp Val	
	1 5	
gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac		163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr		
	10 15 20	
ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga		211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly		
	25 30 35	
gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg		259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser		
	40 45 50	
cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg		307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala		
	55 60 65	
tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg		355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg		
	70 75 80 85	
cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt		403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg		
	90 95 100	
cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc		451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr		
	105 110 115	
gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat		499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp		
	120 125 130	
ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag		535
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln		
	135 140 145	

<210> 656

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 656

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
 1 5 10 15

Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30

Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140

Gln
 145

<210> 657

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXA02516

<400> 657

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aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc 115
 Met Ser Asp Phe Leu
 1 5

aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
 10 15 20

atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac 211
 Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp
 25 30 35

tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag	259
Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu	
40 45 50	
cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa	307
His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln	
55 60 65	
ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc	355
Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile	
70 75 80 85	
gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat	403
Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn	
90 95 100	
gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt	451
Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg	
105 110 115	
tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag	499
Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu	
120 125 130	
cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga	547
Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg	
135 140 145	
acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att	595
Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile	
150 155 160 165	
gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc	643
Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe	
170 175 180	
act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg	691
Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu	
185 190 195	
gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc	739
Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys	
200 205 210	
cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat	787
Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp	
215 220 225	
ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc	835
Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly	
230 235 240 245	
gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg	883
Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu	
250 255 260	
act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac	931
Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr	
265 270 275	
gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag	979

Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln
280 285 290

gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg 1027
Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met
295 300 305

gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa 1075
Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu
310 315 320 325

aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca 1123
Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala
330 335 340

gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca 1171
Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro
345 350 355

cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc 1219
His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val
360 365 370

ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg 1267
Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser
375 380 385

aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac 1315
Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp
390 395 400 405

cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag 1363
Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu
410 415 420

taatgaacct tgagcagatg tac 1386

<210> 658
<211> 421
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 658
Met Ser Asp Phe Leu Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val
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Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro
20 25 30

Leu Ala Tyr Leu Asp Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val
35 40 45

Trp Arg Ala Glu Glu His Phe Val Leu His Thr Asn Ala Pro Val His
50 55 60

Arg Gly Ala Tyr Gln Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly
65 70 75 80

Ala Arg Glu Lys Ile Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile
85 90 95

Ala Phe Thr Lys Asn Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr
 100 105 110
 Leu Gly Asp Asp Arg Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr
 115 120 125
 Val Val Ile Thr Glu Leu Glu His His Ala Asn Leu Val Pro Trp Gln
 130 135 140
 Glu Leu Cys Arg Arg Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr
 145 150 155 160
 Glu Asp Gly Arg Ile Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val
 165 170 175
 Lys Val Val Ala Phe Thr His Gln Ser Asn Val Thr Gly Ala Val Ala
 180 185 190
 Asp Val Pro Glu Leu Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr
 195 200 205
 Val Leu Asp Ala Cys Gln Ser Val Pro His Met Pro Val Asn Phe His
 210 215 220
 Glu Leu Asp Val Asp Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly
 225 230 235 240
 Pro Ala Gly Val Gly Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu
 245 250 255
 Leu Pro Pro Phe Leu Thr Gly Gly Ser Met Ile Glu Val Val Thr Met
 260 265 270
 Glu Gly Ser Thr Tyr Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr
 275 280 285
 Gln Met Thr Ser Gln Val Val Gly Leu Gly Ala Ala Val Asp Met Leu
 290 295 300
 Asn Glu Ile Gly Met Glu Ala Ile Ala Ala His Glu His Ala Leu Thr
 305 310 315 320
 Ala Tyr Ala Leu Glu Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala
 325 330 335
 Gly Pro Leu Thr Ala Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val
 340 345 350
 Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly
 355 360 365
 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser
 370 375 380
 Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr
 385 390 395 400
 Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln
 405 410 415

Phe Phe Gly Val Glu
420

<210> 659
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXA02517

<400> 659
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cagcgatcga gaaggccaag caattctttg gagttgagta atg aac ctt gag cag 115
Met Asn Leu Glu Gln
1 5
atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163
Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys
10 15 20
ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211
Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser
25 30 35
tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc 259
Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser
40 45 50
acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307
Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln
55 60 65
gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355
Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp
70 75 80 85
aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403
Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg
90 95 100
ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451
Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe
105 110 115
tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499
Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly
120 125 130
tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547
Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His
135 140 145
tagcccgctg tattaattgg agg 570

<210> 660

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Met Asn Leu Glu Gln Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys
 1 5 10 15

Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His
 20 25 30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu
 35 40 45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly
 50 55 60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val
 65 70 75 80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys
 85 90 95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly
 100 105 110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys
 115 120 125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala
 130 135 140

Val Ala His Ala His
 145

<210> 661

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

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ctaaaaatat cactaactcg aaagatgtaa ggttgcat ttt gtg act atc gca cct 115
 Val Thr Ile Ala Pro
 1 5

gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg 163
 Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro
 10 15 20

att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct 211
 Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro
 25 30 35

gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr	
40 45 50	
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser	
55 60 65	
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys	
70 75 80 85	
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly	
90 95 100	
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr	
105 110 115	
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala	
120 125 130	
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His	
135 140 145	
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu	
150 155 160 165	
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val	
170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr	
185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val	
200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile	
215 220 225	
acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc	835
Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr	
230 235 240 245	
atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt	883
Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg	
250 255 260	
tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa	931
Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Lys Glu	
265 270 275	
atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac	979

Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa 1027
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
 295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc 1075
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
 310 315 320 325

gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac 1123
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
 330 335 340

acc cca gtg gtg tcc ttc aac taagcccgaa gttttttaac cgc 1167
 Thr Pro Val Val Ser Phe Asn
 345

<210> 662

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg
 1 5 10 15

Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln
 20 25 30

Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
 35 40 45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
 100 105 110

Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
 115 120 125

Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
 130 135 140

Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
 145 150 155 160

Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
 165 170 175

Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
 180 185 190

Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
195 200 205

Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
210 215 220

Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
225 230 235 240

Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
245 250 255

His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
260 265 270

Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
275 280 285

Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
290 295 300

Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
305 310 315 320

Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
325 330 335

Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
340 345

<210> 663

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(853)

<223> RXA01746

<400> 663

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tgacttatca accttgtag ggctaggggtg gatattctatc atg act gca cca aga 115
Met Thr Ala Pro Arg
1 5

gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc 163
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro
10 15 20

att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat 211
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp
25 30 35

tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat 259
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp
40 45 50

cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc 307
 Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
 55 60 65

acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct 355
 Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala
 70 75 80 85

gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc 403
 Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile
 90 95 100

tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta 451
 Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val
 105 110 115

aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt 499
 Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val
 120 125 130

gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct 547
 Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
 135 140 145

cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata 595
 His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile
 150 155 160 165

act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg 643
 Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr
 170 175 180

ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc 691
 Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly
 185 190 195

ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa 739
 Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu
 200 205 210

tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg 787
 Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg
 215 220 225

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
 230 235 240 245

aat ctc cct aaa ccg ggg tagtacgagg aattttgtcg gtg 876
 Asn Leu Pro Lys Arg Gly
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<210> 664

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

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 Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
 35 40 45
 Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60
 Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80
 Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95
 Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110
 Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125
 Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140
 Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160
 Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175
 Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190
 Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205
 Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
 210 215 220
 Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
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 Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly
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<211> 1179

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1156)

<223> RXA02106

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aagcaaaatc tctttagcaa attcggttac tgtggggcgc atg aat aac cat ttt 115

	Met	Asn	Asn	His	Phe	
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gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc						163
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr						
	10				20	
gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc						211
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu						
	25				35	
gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg						259
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala						
	40				50	
tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gca gcg						307
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala						
	55				65	
ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat						355
Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp						
	70				80	85
att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc						403
Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr						
	90				95	100
gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt						451
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu						
	105				115	
aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag						499
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln						
	120				130	
cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg						547
Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val						
	135				145	
atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt						595
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val						
	150				160	165
aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca						643
Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala						
	170				175	180
atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg						691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro						
	185				190	195
gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg						739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu						
	200				210	
gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg						787
Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp						
	215				225	
tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc						835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly						

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230          235          240          245
gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg 883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
          250          255          260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga 931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
          265          270          275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt 979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
          280          285          290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac 1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
          295          300          305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag 1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
          310          315          320          325

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa 1123
Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
          330          335          340

tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac 1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
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aag 1179

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<212> PRT
<213> Corynebacterium glutamicum

<400> 666
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          20          25          30

Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
          35          40          45

Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
          50          55          60

Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
          65          70          75          80

Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
          85          90          95

Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
          100          105          110

Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln

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115	120	125
Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp 130 135 140		
Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile 145 150 155 160		
Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met 165 170 175		
Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr 180 185 190		
Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln 195 200 205		
Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His 210 215 220		
Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly 225 230 235 240		
Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu 245 250 255		
His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln 260 265 270		
Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser 275 280 285		
Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg 290 295 300		
Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly 305 310 315 320		
Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp 325 330 335		
Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln 340 345 350		

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<211> 403

<212> DNA

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<220>

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<222> (101)..(403)

<223> RXS01183

<400> 667

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                                   Met Ala Phe Ser Val
                                   1                               5

gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163
Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln
                                   10                               20

tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211
Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu
                                   25                               30                               35

gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259
Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala
                                   40                               45                               50

ggg gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307
Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val
                                   55                               60                               65

ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355
Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn
                                   70                               75                               80                               85

gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403
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Asp Glu Pro Leu Leu Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile
 35                               40                               45

Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp
 50                               55                               60

Asp Thr Val Asp Val Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp
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Glu Glu Glu Glu Pro
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Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
25 30 35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
 40 45 50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
55 60 65

tcg	gta	gtc	aac	acc	ctc	cgt	ggc	gtt	gac	ttc	tca	gag	aac	gtt	gtg	355
Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe	Ser	Glu	Asn	Val	Val	
70					75					80					85	

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
90 95 100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
105 110 115

aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
120 125 130

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
135 140 145

aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150 155 160 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac 643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
170 175 180

aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc 691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe
185 190 195

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 Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
 200 205 210

acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc 787
 Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val
 215 220 225

gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct 835
 Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
 230 235 240 245

cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt 883
 His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
 250 255 260

gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc 931
 Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
 265 270 275

ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc 979
 Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala
 280 285 290

aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc 1027
 Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
 295 300 305

tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca 1075
 Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
 310 315 320 325

aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg 1123
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 330 335 340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag 1171
 Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
 345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac 1219
 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
 360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga 1267
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<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

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 35 40 45
 Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
 50 55 60
 Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
 65 70 75 80
 Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
 85 90 95
 Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
 100 105 110
 Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
 115 120 125
 Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
 130 135 140
 Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
 145 150 155 160
 Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
 165 170 175
 Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met
 180 185 190
 Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn
 195 200 205
 Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr
 210 215 220
 Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala
 225 230 235 240
 Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala
 245 250 255
 Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met
 260 265 270
 Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr
 275 280 285
 Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val
 290 295 300
 Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
 305 310 315 320
 Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
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 50 55 60
 Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
 65 70 75 80
 Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
 85 90 95
 Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
 100 105 110
 Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
 115 120 125
 Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
 130 135 140
 Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
 145 150 155 160
 Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
 165 170 175
 Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met
 180 185 190
 Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn
 195 200 205
 Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr
 210 215 220
 Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala
 225 230 235 240
 Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala
 245 250 255
 Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met
 260 265 270
 Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr
 275 280 285
 Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val
 290 295 300
 Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
 305 310 315 320
 Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
 325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
 340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
 355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
 370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe
 385 390

<210> 671
 <211> 294
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(271)
 <223> RXS01261

<400> 671
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 atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
 Val Thr Glu His Tyr
 1 5
 gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
 Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
 10 15 20
 cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
 Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
 25 30 35
 tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
 Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
 40 45 50
 gat caa aaa cgc tgaagttgcc cataccttta ccc 294
 Asp Gln Lys Arg
 55

<210> 672
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 672
 Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45

Pro Ser Lys Val Ser Asp Gln Lys Arg
50 55

<210> 673
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA02717

<400> 673
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gcgtccttca cccggccgag tacctttttc tgtcgagttt atg cca ccc cgc gac 115
Met Pro Pro Arg Asp
1 5
gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac 163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp
10 15 20
ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc 211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr
25 30 35
cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg 259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu
40 45 50
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg 307
Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met
55 60 65
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg 355
Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu
70 75 80 85
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc 403
Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser
90 95 100
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag 451
Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys
105 110 115
tcc act cct gag ttc cgg gaa ttc gac ctc ggt atc gcc tcc ttc ccc 499
Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro
120 125 130
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act 547
Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr
135 140 145
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc 595
Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe
150 155 160 165

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ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca 643
Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala
170 175 180

gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att 691
Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile
185 190 195

acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctc tct ggt gct caa 739
Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln
200 205 210

ttg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat 787
Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn
215 220 225

gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc 835
Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser
230 235 240 245

acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac 883
Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His
250 255 260

ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac 931
Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn
265 270 275

ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg 979
Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val
280 285 290

cgt taagccctct taggaatcat gaa 1005
Arg

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<210> 674

<211> 294

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 674

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Met Pro Pro Arg Asp Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala
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Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
20 25 30

Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu
35 40 45

Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His
50 55 60

Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly
65 70 75 80

Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu
85 90 95

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Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu
 100 105 110
 Ile Asp Leu Ile Lys Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly
 115 120 125
 Ile Ala Ser Phe Pro Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu
 130 135 140
 Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser
 145 150 155 160
 Ile Thr Gln Met Phe Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp
 165 170 175
 Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro
 180 185 190
 Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu
 195 200 205
 Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg
 210 215 220
 Ala Ala Asn Gly Asn Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val
 225 230 235 240
 Gly Ile Glu Tyr Ser Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly
 245 250 255
 Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
 260 265 270
 Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
 275 280 285
 Gly Gln Asp Ala Val Arg
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<210> 675

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02027

<400> 675

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tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

gat atc 601
 Asp Ile

<210> 676

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 676

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45

Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60

Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu

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<210> 677
<211> 595
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(595)
<223> FRXA02027
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				Met	Ser	Gln	Thr	Lys	5									
				1														
cag	gaa	ctg	cgc	acg	aag	ctt	cgg	gaa	gcg	cgc	acc	aat	atg	gat	gag	163		
Gln	Glu	Leu	Arg	Thr	Lys	Leu	Arg	Glu	Ala	Arg	Thr	Asn	Met	Asp	Glu			
				10													20	
gct	tct	cgc	acg	cga	gaa	aac	gca	gcc	atc	att	gcc	aac	gtt	tct	tat	211		
Ala	Ser	Arg	Thr	Arg	Glu	Asn	Ala	Ala	Ile	Ile	Ala	Asn	Val	Ser	Tyr			
			25													30	35	
tac	atc	cgc	tca	aag	cag	cca	aaa	agg	att	gcc	gct	tac	gtg	ccg	gtg	259		
Tyr	Ile	Arg	Ser	Lys	Gln	Pro	Lys	Arg	Ile	Ala	Ala	Tyr	Val	Pro	Val			
		40													45	50		
cgt	acc	gaa	cct	ggt	ggg	cga	ttg	ctt	ctt	gac	gcc	ctc	cac	gcc	gaa	307		
Arg	Thr	Glu	Pro	Gly	Gly	Arg	Leu	Leu	Leu	Asp	Ala	Leu	His	Ala	Glu			
	55													60	65			
act	tcc	gcg	ctt	att	ttg	cca	gtc	tcc	ctc	gag	gat	cga	cgc	ctc	gac	355		
Thr	Ser	Ala	Leu	Ile	Leu	Pro	Val	Ser	Leu	Glu	Asp	Arg	Arg	Leu	Asp			
	70													75	80	85		
tgg	gct	ctt	tat	gaa	ggc	cca	acc	agc	ctt	gtt	cct	ggc	gca	ttt	ggc	403		
Trp	Ala	Leu	Tyr	Glu	Gly	Pro	Thr	Ser	Leu	Val	Pro	Gly	Ala	Phe	Gly			
				90													95	100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

<210> 678

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
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Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45

Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60

Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80

Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95

Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110

Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125

Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140

Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160

Gly Glu Ile Arg Asp
 165

<210> 679

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 679

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				Met	Ile	Gly	Ala	Ile	
				1				5	

tgg	gca	caa	ggc	cgt	gac	ggc	atc	atc	ggc	gac	ggc	acc	gac	atg	ccc	163
Trp	Ala	Gln	Gly	Arg	Asp	Gly	Ile	Ile	Gly	Asp	Gly	Thr	Asp	Met	Pro	
			10					15						20		

tgg	cac	atc	ccg	gaa	gac	ctc	aaa	cac	ttc	aag	aaa	acc	acc	atg	ggc	211
Trp	His	Ile	Pro	Glu	Asp	Leu	Lys	His	Phe	Lys	Lys	Thr	Thr	Met	Gly	
			25					30						35		

cag	ccg	gtc	atc	atg	ggt	cgt	cgc	acg	tgg	gag	tct	ttg	ccg	ttc	aag	259
Gln	Pro	Val	Ile	Met	Gly	Arg	Arg	Thr	Trp	Glu	Ser	Leu	Pro	Phe	Lys	
		40					45					50				

ccg	ctt	ccc	ggc	cgc	gag	aac	ttc	att	ctc	tcc	tca	cgc	gag	ccc	ggc	307
Pro	Leu	Pro	Gly	Arg	Glu	Asn	Phe	Ile	Leu	Ser	Ser	Arg	Glu	Pro	Gly	
	55					60					65					

gac	tgg	tcc	gcc	ggc	ggc	aca	gtg	gtc	acc	gaa	atc	cct	aaa	agc	ggc	355
Asp	Trp	Ser	Ala	Gly	Gly	Thr	Val	Val	Thr	Glu	Ile	Pro	Lys	Ser	Gly	
	70				75				80						85	

tgg	atc	atg	ggc	ggc	ggc	gag	gtc	tac	aag	gcc	acc	gtc	ggc	agc	gcc	403
Trp	Ile	Met	Gly	Gly	Gly	Glu	Val	Tyr	Lys	Ala	Thr	Val	Gly	Ser	Ala	
			90					95						100		

gac	gtt	tta	gaa	ata	acg	ctt	atc	gac	gcc	acc	ttc	gat	gtt	tcc	act	451
Asp	Val	Leu	Glu	Ile	Thr	Leu	Ile	Asp	Ala	Thr	Phe	Asp	Val	Ser	Thr	
		105						110						115		

ccc	gtc	tac	gca	ccc	gaa	atc	ccg	gcg	aac	ttc	aac	ctc	gat	gac	gaa	499
Pro	Val	Tyr	Ala	Pro	Glu	Ile	Pro	Ala	Asn	Phe	Asn	Leu	Asp	Asp	Glu	
		120					125					130				

tcc	gag	tgg	ttt	acc	tca	ggc	gag	tat	cgt	tac	aag	ttc	cag	cgc	tac	547
Ser	Glu	Trp	Phe	Thr	Ser	Gly	Glu	Tyr	Arg	Tyr	Lys	Phe	Gln	Arg	Tyr	
	135					140					145					

atc	aag	gtt	taaggagcaa	acaacatgag	caa											579
Ile	Lys	Val														
150																

<210> 680

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

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Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
          20             25             30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
          35             40             45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
          50             55             60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
          65             70             75             80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
          85             90             95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
          100            105            110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
          115            120            125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
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Lys Phe Gln Arg Tyr Ile Lys Val
145             150

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<210> 681
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> RXN01321

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<400> 681
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                               Met Gln Arg Met Thr
                               1             5

ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163
Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu
          10             15             20

cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val
          25             30             35

gcg aag ttg tcg tcg ttc cta gct gag cgt ggg ggt tgg att act gag 259
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu
          40             45             50

gct gga tat ttc acg gat cct gat tcg aat tgg ttc ttt act cgt cag 307

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Ala	Gly	Tyr	Phe	Thr	Asp	Pro	Asp	Ser	Asn	Trp	Phe	Phe	Thr	Arg	Gln		
55						60					65						
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Ala	Ile	Arg	Ala	Glu	Ser	Ile	Asp	Thr	Thr	Ile	Glu	Gln	Leu	Arg	Glu		
70					75					80					85		
gag	ttc	gct	ccg	ctt	gcg	gag	gag	ttc	ggc	ccg	agg	gct	aag	tgg	agt	403	
Glu	Phe	Ala	Pro	Leu	Ala	Glu	Glu	Phe	Gly	Pro	Arg	Ala	Lys	Trp	Ser		
				90					95					100			
ttc	act	gac	act	gcg	cag	gtg	aag	aag	gct	gtg	ttg	ttg	gtg	tct	aag	451	
Phe	Thr	Asp	Thr	Ala	Gln	Val	Lys	Lys	Ala	Val	Leu	Leu	Val	Ser	Lys		
			105					110					115				
gag	ggc	cac	tgc	ttg	cac	gat	ttg	tta	ggc	cgt	gtg	gct	gag	aat	gat	499	
Glu	Gly	His	Cys	Leu	His	Asp	Leu	Leu	Gly	Arg	Val	Ala	Glu	Asn	Asp		
		120					125					130					
tat	ccg	atg	gaa	gtt	gtt	gcg	gtt	gtg	ggc	aac	cat	gag	aac	ttg	cgt	547	
Tyr	Pro	Met	Glu	Val	Val	Ala	Val	Val	Gly	Asn	His	Glu	Asn	Leu	Arg		
		135				140						145					
tat	att	gcg	gag	aac	cat	aat	gtt	ccg	ttt	ttc	cat	gtg	ccg	ttt	cct	595	
Tyr	Ile	Ala	Glu	Asn	His	Asn	Val	Pro	Phe	Phe	His	Val	Pro	Phe	Pro		
150					155					160					165		
aag	gat	gcg	gtt	ggc	aag	cgg	aag	gcg	ttt	gac	cag	gtc	gct	gag	att	643	
Lys	Asp	Ala	Val	Gly	Lys	Arg	Lys	Ala	Phe	Asp	Gln	Val	Ala	Glu	Ile		
				170					175					180			
gtg	aat	ggc	tat	gat	ccg	gat	gcg	att	gtt	ttg	gct	cgt	ttt	atg	cag	691	
Val	Asn	Gly	Tyr	Asp	Pro	Asp	Ala	Ile	Val	Leu	Ala	Arg	Phe	Met	Gln		
			185					190					195				
att	ttg	ccg	ccg	gat	ttg	tgt	gag	atg	tgg	gct	ggc	cgt	gtg	ttg	aat	739	
Ile	Leu	Pro	Pro	Asp	Leu	Cys	Glu	Met	Trp	Ala	Gly	Arg	Val	Leu	Asn		
		200					205					210					
att	cat	cac	agt	ttc	ttg	ccg	tcg	ttt	atg	ggc	gcg	cgc	ccg	tat	cat	787	
Ile	His	His	Ser	Phe	Leu	Pro	Ser	Phe	Met	Gly	Ala	Arg	Pro	Tyr	His		
		215				220					225						
cag	gcg	tat	agc	cgt	ggc	gtg	aag	ttg	att	ggc	gcg	acc	tgc	cat	tat	835	
Gln	Ala	Tyr	Ser	Arg	Gly	Val	Lys	Leu	Ile	Gly	Ala	Thr	Cys	His	Tyr		
230					235					240				245			
gcg	act	ggg	gat	ctg	gat	gat	ggc	ccg	atc	att	gag	cag	gat	gtt	att	883	
Ala	Thr	Gly	Asp	Leu	Asp	Asp	Gly	Pro	Ile	Ile	Glu	Gln	Asp	Val	Ile		
				250					255					260			
cgt	gtg	acg	cat	aag	gat	acg	ccg	act	gag	atg	cag	cgt	ttg	ggc	cgc	931	
Arg	Val	Thr	His	Lys	Asp	Thr	Pro	Thr	Glu	Met	Gln	Arg	Leu	Gly	Arg		
			265				270						275				
gat	gcg	gag	aag	cag	gtg	ctg	gct	cgc	ggc	ttg	cgt	ttc	cac	ttg	gag	979	
Asp	Ala	Glu	Lys	Gln	Val	Leu	Ala	Arg	Gly	Leu	Arg	Phe	His	Leu	Glu		
		280					285					290					
gac	cgg	gtg	ctg	gtt	tac	ggc	aac	cgc	acg	gtt	gtc	ttt	gat			1021	
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 <211> 307
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
 50 55 60
 Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
 65 70 75 80
 Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
 85 90 95
 Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
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Val Phe Asp
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<210> 683

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (23)..(559)

<223> FRXA01321

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Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn	
15 20 25	
cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt	148
His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly	
30 35 40	
aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat	196
Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp	
45 50 55	
ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat	244
Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp	
60 65 70	
ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc	292
Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe	
75 80 85 90	
ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt	340
Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg	
95 100 105	
ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg	388
Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu	
110 115 120	
gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag	436
Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys	
125 130 135	
gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag	484
Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln	
140 145 150	

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
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tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
 Tyr Gly Asn Arg Thr Val Val Phe Asp
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cgc 582

<210> 684

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
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His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 20 25 30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 35 40 45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 165 170 175

Val Phe Asp

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<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

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 <222> (101)..(952)
 <223> RXA00461

<400> 685

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                               Val Thr Ala Ile Lys
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ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln
                               10                               15                               20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr
                               25                               30                               35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys
                               40                               45                               50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu
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Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu
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aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct 403
Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro
                               90                               95                               100

aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag 451
Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys
                               105                               110                               115

gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac 499
Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn
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gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg 547
Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu
                               135                               140                               145

cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc 595
Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly
                               150                               155                               160                               165

cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt 643
Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg
                               170                               175                               180

tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg 691
Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu
                               185                               190                               195

gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag 739
Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln

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ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc			787
Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu			
215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac			835
Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His			
230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc			883
Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly			
	250	255	260
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc			931
Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg			
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gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg			975
Ala Glu Lys Leu Ala Gly Leu			
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<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

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Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
35 40 45

Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
50 55 60

Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
65 70 75 80

Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
85 90 95

Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
100 105 110

Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
115 120 125

Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
130 135 140

Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
145 150 155 160

Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
165 170 175

Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190

Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205

Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220

Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240

Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
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Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
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Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
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 <211> 711
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01514

<400> 687
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 Val Asp Asn His Ala
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gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
 Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
 10 15 20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
 Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
 25 30 35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
 Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
 40 45 50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
 His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
 55 60 65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
 Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
 70 75 80 85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403

His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
 90 95 100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
 Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
 105 110 115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
 Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
 120 125 130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
 Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
 135 140 145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
 Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
 150 155 160 165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
 Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
 170 175 180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
 Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
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<210> 688

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 688

Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr
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 20 25 30

Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
 35 40 45

Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
 50 55 60

Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
 65 70 75 80

Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
 85 90 95

Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
 100 105 110

Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
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<211> 513
<212> DNA
<213> *Corynebacterium glutamicum*

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												Met	Ala	Asp	Arg	Ile	5						
												1											
gaa								ctt	aaa	ggc	ctt	gaa	tgc	ttc	gga	cac	cac	ggt	gtg	ttc	gac	ttt	163
Glu	Leu	Lys	Gly	Leu	Glu	Cys	Phe	Gly	His	His	Gly	Val	Phe	Asp	Phe								
												10						15	20				
gaa								aaa	gag	caa	ggc	cag	ccc	ttc	att	gtg	gat	gtc	acc	tgc	tgg	atg	211
Glu	Lys	Glu	Gln	Gly	Gln	Pro	Phe	Ile	Val	Asp	Val	Thr	Cys	Trp	Met								
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Asp	Phe	Asp	Ala	Ala	Gly	Ala	Ser	Asp	Asp	Leu	Ser	Asp	Thr	Val	Asp								
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tac								ggc	gcg	ttg	gca	ttg	ttg	gtt	gct	gaa	atc	gtg	gaa	ggc	cca	tcc	307
Tyr	Gly	Ala	Leu	Ala	Leu	Leu	Val	Ala	Glu	Ile	Val	Glu	Gly	Pro	Ser								
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agg								gat	ttg	atc	gag	acg	gtg	gcc	acg	gaa	tct	gcg	gat	gct	gtg	atg	355
Arg	Asp	Leu	Ile	Glu	Thr	Val	Ala	Thr	Glu	Ser	Ala	Asp	Ala	Val	Met								
												70						75	80			85	
gct								aaa	ttt	gat	gcg	ctt	cat	gcg	gtg	gaa	gta	acc	atc	cat	aag	ccc	403
Ala	Lys	Phe	Asp	Ala	Leu	His	Ala	Val	Glu	Val	Thr	Ile	His	Lys	Pro								
												90						95	100				
aaa								gca	ccg	atc	cca	cgt	act	ttt	gct	gac	gtc	gcg	gtg	gtt	gcc	cga	451
Lys	Ala	Pro	Ile	Pro	Arg	Thr	Phe	Ala	Asp	Val	Ala	Val	Ala	Arg									
												105						110	115				
cgt								tcc	agg	aaa	tcc	atg	gct	gct	gga	agg	agc	aac	gcc	taatgcatgc	500		

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513

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 690
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 35 40 45
 Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
 50 55 60
 Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
 65 70 75 80
 Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
 85 90 95
 Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
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 Asn Ala
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<210> 691
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 <213> Corynebacterium glutamicum

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 <222> (101)..(952)
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 Met Asn Val Ser Ser
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 ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
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gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
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atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

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 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
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gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
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tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
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gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931

Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
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 Ser Gly Gly Thr His His Gly
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975

<210> 692

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 692

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Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45

Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60

Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
 195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
 210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
 225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
 245 250 255

Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
 260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
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<211> 859

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(859)

<223> RXA02024

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 Met Ser Ser Leu Pro
 1 5
 gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
 Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
 10 15 20
 ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc 211
 Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val
 25 30 35
 att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc 259
 Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly
 40 45 50
 ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca 307
 Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro
 55 60 65
 atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt 355
 Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val
 70 75 80 85
 gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca 403
 Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala
 90 95 100
 acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag 451
 Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln
 105 110 115
 gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg 499
 Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly
 120 125 130
 gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg 547
 Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val
 135 140 145

gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt 595
 Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg
 150 155 160 165

gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc 643
 Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe
 170 175 180

ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag 691
 Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu
 185 190 195

gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat 739
 Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp
 200 205 210

ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc 787
 Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly
 215 220 225

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe
 230 235 240 245

cgc gtg cat gaa gtt gcg gaa acc 859
 Arg Val His Glu Val Ala Glu Thr
 250

<210> 694

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
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Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160
 Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190
 Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205
 Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240
 Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr
 245 250

<210> 695
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> RXA00106

<400> 695
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 gctacgatcc acaccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
 Met Ile Gly Ala Ile
 1 5
 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
 10 15 20
 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
 25 30 35
 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
 40 45 50
 ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
 55 60 65
 gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
 Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403

Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150

<210> 696

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
 1 5 10 15

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 697

<211> 1556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (1533)

<223> RXA00989

<400> 697

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Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn	
1 5 10 15	
gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct	96
Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser	
20 25 30	
ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag	144
Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu	
35 40 45	
atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg	192
Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu	
50 55 60	
gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg	240
Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met	
65 70 75 80	
agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca	288
Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala	
85 90 95	
att cac gtg gct ggc acc aac ggt aag acc tcc acc acc cgc atg atc	336
Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile	
100 105 110	
gag tcg ttg ctg cgc gca ttc cac cgc cgc acc ggc cgg acc acc agc	384
Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser	
115 120 125	
ccg cac ctg cag ctg gta acc gaa cgc atc gcg att gat ggc aag ccc	432
Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro	
130 135 140	
atc cac ccg cgt gat ttc gtg cgg atc tac gaa gag att aag ccc tac	480
Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr	
145 150 155 160	
atg gag atg acc gac gcc tgg tca gag gcc gag ggc gga ccg aag atg	528
Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met	
165 170 175	
agc aag ttt gag gca ctc gtg gcc ctc gct tac gca ggt ttt gcc gac	576
Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp	
180 185 190	
gct cct gtt gac gtc gcc gtc gtt gag gtt ggt ctt ggc gga cgc tgg	624
Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp	
195 200 205	
gat gcc act aac gtg atc aac gca gct gtt tcc gtg atc acc ccg gtg	672
Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val	

210	215	220	
ggc atg gac cac gtg gat cgc ctg ggc aac acc att ggt gaa atc gct			720
Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala			
225	230	235	240
ggg gaa aag gcc ggc atc atc aag gct cgt cct gca tct gag gat ggc			768
Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly			
	245	250	255
acc gag cct gag ggc aac gtt gtc atc gtg ggc aag cag gag cca gaa			816
Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu			
	260	265	270
gca atg aac gtg att ctg cag caa gcc gtg gac gtg gac gca gct gtt			864
Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val			
	275	280	285
gct cgt ttg aac atg gaa ttc ggc gtg gtg gaa tcc gcc att gcc gtt			912
Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val			
	290	295	300
ggg gga cag cag ctc acc ctg aag ggt ttg ggc ggc gaa tac acc gac			960
Gly Gly Gln Gln Leu Thr Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp			
305	310	315	320
atc ttc ctc cca ctg tct ggc gcg cac caa gca gat aat gcc gcg gtt			1008
Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Ala Val			
	325	330	335
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca			1056
Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro			
	340	345	350
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca			1104
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro			
	355	360	365
ggg cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca			1152
Gly Arg Leu Glu Arg Leu Ser Ala Pro Thr Val Phe Ile Asp Ala			
	370	375	380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt			1200
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg			
385	390	395	400
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac			1248
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp			
	405	410	415
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa			1296
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu			
	420	425	430
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat			1344
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp			
	435	440	445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc			1392
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val			
	450	455	460

caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa 1440
 Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu
 465 470 475 480
 gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc 1488
 Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile
 485 490 495
 gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca 1533
 Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala
 500 505 510
 tgagcaagcg tgaagaatca att 1556

<210> 698

<211> 511

<212> PRT

<213> Corynebacterium glutamicum

<400> 698

Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn
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 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala
 85 90 95
 Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile
 100 105 110
 Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser
 115 120 125
 Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro
 130 135 140
 Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr
 145 150 155 160
 Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met
 165 170 175
 Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp
 180 185 190
 Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp
 195 200 205

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Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val
210                      215                      220

Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala
225                      230                      235                      240

Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly
245                      250                      255

Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu
260                      265                      270

Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val
275                      280                      285

Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val
290                      295                      300

Gly Gly Gln Gln Leu Thr Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp
305                      310                      315                      320

Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Ala Val
325                      330                      335

Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro
340                      345                      350

Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro
355                      360                      365

Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala
370                      375                      380

Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg
385                      390                      395                      400

Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp
405                      410                      415

Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu
420                      425                      430

Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp
435                      440                      445

Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val
450                      455                      460

Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu
465                      470                      475                      480

Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile
485                      490                      495

Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala
500                      505                      510

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<210> 699

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> RXA01517

<400> 699

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gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg 115
                               Met His Ala Val Leu
                               1 5

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val
          10          15          20

atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca 211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser
          25          30          35

acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg 259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val
          40          45          50

ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc 307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly
          55          60          65

caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg 355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly
          70          75          80          85

cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa 403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu
          90          95          100

gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct 451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala
          105          110          115

tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat 499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp
          120          125          130

gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat 547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp
          135          140          145

ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat 597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
          150          155

gca 600

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<210> 700

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala
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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 701

<211> 1983

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 701

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gtgctttttct cgttgttttg tggttttgtc agaggatgtc atg cgc gtt tta att 115
 Met Arg Val Leu Ile
 1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
 Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
 10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
 Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
 25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
 Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
 40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt	307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg	
55 60 65	
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg	355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala	
70 75 80 85	
ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt	403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly	
90 95 100	
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc	451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile	
105 110 115	
cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc	499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg	
120 125 130	
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc	547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile	
135 140 145	
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat	595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His	
150 155 160 165	
ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	1027
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	1075
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	1123
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	
gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat	1171
Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr	
345 350 355	
ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg	1219
Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser	
360 365 370	
tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc	1267
Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala	
375 380 385	
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat	1315
Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr	
390 395 400 405	
ggg gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg	1363
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro	
410 415 420	
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc	1411
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro	
425 430 435	
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Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu	
440 445 450	
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg	1507
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu	
455 460 465	
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc	1555
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro	
470 475 480 485	
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca	1603
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr	
490 495 500	
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt	1651
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser	
505 510 515	
ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt	1699
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly	
520 525 530	
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct	1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg 1891
His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat 1939
Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

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<211> 620
<212> PRT
<213> Corynebacterium glutamicum

<400> 702
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Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln

165																170																175															
Ile	Ile	Lys	Asn	Phe	Leu	Asn	Leu	Ala	Arg	Thr	Tyr	Arg	Trp	Gln	Leu																																
			180						185						190																																
Thr	Glu	Lys	Thr	Ile	Pro	Leu	Ser	Val	Asp	Ser	Ala	Ala	Val	Phe	Glu																																
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Thr	Phe	Phe	Ala	His	Ser	Ser	His	Ala	Phe	Trp	Leu	Asp	Asp	Ala	Gln																																
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Gly	Thr	Ser	Tyr	Leu	Gly	Asp	Ala	Ser	Gly	Pro	Leu	Ala	Arg	Thr	Lys																																
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Thr	His	Asn	Val	Gly	Glu	Gly	Asp	Phe	Phe	Thr	Trp	Leu	Lys	Glu	Asp																																
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Leu	Ala	Ala	Asn	Ser	Val	Ala	Pro	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Trp																																
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Val	Gly	Tyr	Val	Gly	Tyr	Glu	Leu	Lys	Ala	Glu	Ala	Gly	Ala	Arg	Ala																																
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Ala	His	Thr	Ser	Ser	Leu	Pro	Asp	Ala	His	Leu	Ile	Phe	Ala	Asp	Arg																																
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Ala	Ile	Ala	Val	Glu	Ser	Asp	Gln	Val	Arg	Leu	Leu	Ala	Leu	Gly	Glu																																
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Gln	Asp	Glu	Trp	Phe	Glu	Glu	Thr	Ile	Lys	Lys	Leu	His	Asn	Leu	Val																																
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Ala	Pro	Arg	Ile	Pro	Ala	Ser	Gly	His	Leu	Ala	Leu	Gln	Val	Arg	Asp																																
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Ser	Lys	Asp	Glu	Tyr	Leu	Asp	Lys	Ile	Arg	Arg	Ala	Gln	Glu	Leu	Ile																																
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Thr	Arg	Gly	Glu	Ser	Tyr	Glu	Ile	Cys	Leu	Thr	Thr	Lys	Leu	Gln	Gly																																
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Thr	Thr	Asp	Val	Ala	Pro	Leu	Ala	Ala	Tyr	Leu	Ala	Leu	Arg	Gly	Ala																																
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Asn	Pro	Thr	Ala	Tyr	Gly	Ala	Tyr	Leu	Gln	Leu	Gly	Asp	Thr	Ser	Ile																																
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Leu	Ser	Ser	Ser	Pro	Glu	Arg	Phe	Ile	Thr	Ile	Asp	Ser	Ala	Gly	Tyr																																
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Val	Glu	Ser	Lys	Pro	Ile	Lys	Gly	Thr	Arg	Pro	Arg	Gly	Arg	Thr	Ala																																
			435						440						445																																
Gln	Glu	Asp	Gln	Glu	Ile	Ile	Ala	Glu	Leu	Arg	Ser	Asn	Pro	Lys	Asp																																
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Arg	Ala	Glu	Asn	Leu	Met	Ile	Val	Asp	Leu	Val	Arg	Asn	Asp	Leu	Ala																																
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Arg	Gly	Ala	Leu	Pro	Thr	Thr	Val	Lys	Thr	Ser	Lys	Leu	Phe	Asp	Val																																
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Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
500 505 510

Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
610 615 620

<210> 703

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

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ccattgcgct tgctgctggt tccactttgg aggtcatccg atg aca cac gtt gtt 115
Met Thr His Val Val
1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala

70	75	80	85	
ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac				403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His				
	90	95	100	
ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct				451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro				
	105	110	115	
gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc				499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile				
	120	125	130	
cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg				547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val				
	135	140	145	
gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att				595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile				
	150	155	160	165
ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc				643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly				
	170	175	180	
ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att				691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile				
	185	190	195	
ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat				744
Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn				
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tca				747
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Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg				
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Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile				
35	40	45		
Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met				
50	55	60		
Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys				
65	70	75	80	
Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro				
85	90	95		

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
 130 135 140
 Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
 145 150 155 160
 Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
 165 170 175
 Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
 180 185 190
 Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 195 200 205

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1243)
 <223> RXA02790

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 Met Glu Pro Val Tyr
 1 5
 gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
 10 15 20
 ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
 25 30 35
 acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
 Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
 40 45 50
 gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307
 Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu
 55 60 65
 gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355
 Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
 70 75 80 85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac	451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac	499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
120 125 130	
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag	595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc	643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag	691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc	931
Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	
tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc	1027
Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr	
295 300 305	
cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc	1075
Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala	
310 315 320 325	

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga 1123
 Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
 330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc 1171
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
 345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac 1219
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
 360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg 1266
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<210> 706

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

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Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
 35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
 50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
 65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
 85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala
 100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
 115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220
 Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240
 Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255
 Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270
 Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285
 Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320
 Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335
 Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350
 Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365
 Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

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 Met Ile Gly Ala Ile
 1 5

 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
 10 15 20

 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
 25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259

Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
 40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
 55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
 Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150

<210> 708

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 709

<211> 2599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2599)

<223> RXN02198

<400> 709

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 Met Ser Thr Ser Val
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
 105 110 115

gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt 499
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
 120 125 130

tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat 547
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
 135 140 145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac 595
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
 150 155 160 165

ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag 643
 Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln
 170 175 180

gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat 691
 Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp
 185 190 195

aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc 739
 Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr
 200 205 210

atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca 787
 Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro
 215 220 225

ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag 835
 Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu
 230 235 240 245

atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg 883
 Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val
 250 255 260

tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca 931
 Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala
 265 270 275

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979
 Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe
 280 285 290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca 1027
 Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr
 295 300 305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag 1075
 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu
 310 315 320 325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag 1123
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc 1171
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc 1219
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc 1267
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt 1315

Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	390	395	400	405	
gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc	1363				
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr		410	415	420	
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg	1411				
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu		425	430	435	
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt	1459				
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu		440	445	450	
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	1507				
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp		455	460	465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555				
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys		470	475	480	485
cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag	1603				
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln		490	495	500	
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651				
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp		505	510	515	
gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac	1699				
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp		520	525	530	
tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat	1747				
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp		535	540	545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca	1795				
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro		550	555	560	565
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac	1843				
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn		570	575	580	
cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att	1891				
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile		585	590	595	
gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg	1939				
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro		600	605	610	
atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc	1987				
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val		615	620	625	
tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag	2035				
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln					

630	635	640	645	
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa				2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu	650	655	660	
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc				2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile	665	670	675	
gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag				2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys	680	685	690	
gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg				2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met	695	700	705	
aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc				2275
Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe	710	715	720	725
gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa				2323
Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu	730	735	740	
ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag				2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu	745	750	755	
ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat				2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp	760	765	770	
atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac				2467
Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp	775	780	785	
gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca				2515
Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala	790	795	800	805
gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg				2563
Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val	810	815	820	
aag tcc acc gtg gtg atg aag caa acc atc agc gac				2599
Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp	825	830		

<210> 710

<211> 833

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

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Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala

20										25					30					
Met	Gly	Thr	Gln	Leu	Gln	Gly	Phe	Asp	Leu	Asp	Val	Glu	Lys	Asp	Phe					
35										40					45					
Leu	Asp	Leu	Glu	Gly	Cys	Asn	Glu	Ile	Leu	Asn	Asp	Thr	Arg	Pro	Asp					
50										55					60					
Val	Leu	Arg	Gln	Ile	His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu					
65										70					75					80
Val	Glu	Thr	Asn	Thr	Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr					
										85					90					95
Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val					
100										105					110					
Ala	Arg	Glu	Val	Ala	Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg					
115										120					125					
Arg	Phe	Val	Val	Gly	Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu					
130										135					140					
Gly	His	Ala	Pro	Tyr	Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala					
145										150					155					160
Leu	Gly	Ile	Ile	Asp	Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala					
										165					170					175
Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala					
180										185					190					
Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val					
195										200					205					
Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu					
210										215					220					
Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala					
225										230					235					240
Thr	Gly	Pro	Asp	Glu	Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His					
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Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu					
260										265					270					
Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln					
275										280					285					
Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly					
290										295					300					
Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val					
305										310					315					320
Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala					
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Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val					
340										345					350					

Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
690 695 700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser
820 825 830

Asp

<210> 711

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2578)

<223> FRXA02198

<400> 711

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Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly

40	45	50	
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att			307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile			
55	60	65	
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act			355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr			
70	75	80	85
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt			403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg			
90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct			451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala			
105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt			499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly			
120	125	130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat			547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr			
135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac			595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp			
150	155	160	165
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag			643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln			
170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat			691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp			
185	190	195	
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Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr			
200	205	210	
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Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro			
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Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu			
230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg			883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val			
250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca			931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala			
265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc			979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe			
280	285	290	

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Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
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Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
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Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
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Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
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Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
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Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
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Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
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ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555
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Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
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gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
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Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
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Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val	
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Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln	
630 635 640 645	
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa	2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu	
650 655 660	
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc	2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile	
665 670 675	
gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag	2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys	
680 685 690	
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Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met	
695 700 705	
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Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe	
710 715 720 725	
gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa	2323
Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu	
730 735 740	
ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag	2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu	
745 750 755	
ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat	2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp	
760 765 770	
atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac	2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515
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 790 795 800 805

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Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
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Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
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Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
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Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
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Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
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Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
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Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
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Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
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Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
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Glu 210	Thr 215	Gly 220	Thr 225	Met 230	Leu 235	Met 240	Gly 245	Ser 250	Glu 255	Ile 260	Gly 265	Ala 270	Ala 275	Leu 280
Thr 225	Ala 230	Leu 235	Gln 240	Pro 245	Leu 250	Gly 255	Ile 260	Asp 265	Met 270	Ile 275	Gly 280	Leu 285	Asn 290	Cys 295
Thr 230	Gly 235	Pro 240	Asp 245	Glu 250	Met 255	Ser 260	Glu 265	His 270	Leu 275	Arg 280	Tyr 285	Leu 290	Ser 295	Lys 300
Ala 235	Asp 240	Ile 245	Pro 250	Val 255	Ser 260	Val 265	Met 270	Pro 275	Asn 280	Ala 285	Gly 290	Leu 295	Pro 300	Val 305
Gly 240	Lys 245	Asn 250	Gly 255	Ala 260	Glu 265	Tyr 270	Pro 275	Leu 280	Glu 285	Ala 290	Glu 295	Asp 300	Leu 305	Ala 310
Ala 245	Leu 250	Ala 255	Gly 260	Phe 265	Val 270	Ser 275	Glu 280	Tyr 285	Gly 290	Leu 295	Ser 300	Met 305	Val 310	Gly 315
Cys 250	Cys 255	Gly 260	Thr 265	Thr 270	Pro 275	Glu 280	His 285	Ile 290	Arg 295	Ala 300	Val 305	Arg 310	Asp 315	Ala 320
Val 255	Gly 260	Val 265	Pro 270	Glu 275	Gln 280	Glu 285	Thr 290	Ser 295	Thr 300	Leu 305	Thr 310	Lys 315	Ile 320	Pro 325
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Met 270	Ile 275	Gly 280	Glu 285	Arg 290	Thr 295	Asn 300	Ser 305	Asn 310	Gly 315	Ser 320	Lys 325	Ala 330	Phe 335	Arg 340
Ala 275	Met 280	Leu 285	Ser 290	Gly 295	Asp 300	Trp 305	Glu 310	Lys 315	Cys 320	Val 325	Asp 330	Ile 335	Ala 340	Lys 345
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Lys 315	Arg 320	Leu 325	Ile 330	Asp 335	Asp 340	Ile 345	Thr 350	Gly 355	Ser 360	Tyr 365	Gly 370	Leu 375	Asp 380	Ile 385
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530	535	540
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Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile 565	570	575
Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe 580	585	590
Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser 595	600	605
Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val 610	615	620
Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu 625	630	635 640
Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys 645	650	655
Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu 660	665	670
Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu 675	680	685
Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp 690	695	700
Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln 705	710	715 720
Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala 725	730	735
Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly 740	745	750
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys 755	760	765
Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser 770	775	780
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser 785	790	795 800
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<212> DNA

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Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
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Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
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Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
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Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
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His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser	
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Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	
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Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met	
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Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp	
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Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala			
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Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile			
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<213> Corynebacterium glutamicum

<400> 714

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr			
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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg			
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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu			
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Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro			
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Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu			
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Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu			
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Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala			
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Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg			
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Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr			
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Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr			
	180	185	190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
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 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
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 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
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 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
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 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
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 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
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 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
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 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
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Leu	Leu	Pro	Leu	Arg	Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln	Trp	Ser
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Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	Ser	Val	Asp	Pro
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705					710					715					720
Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val	Leu	Val	Glu	Ser	Ala	Lys	Gln
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Met Thr Ser Asn Phe

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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc	1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta	1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att	1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc	1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat	1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp	
440 445 450	
ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac	1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His	
455 460 465	
ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc	1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu	
470 475 480 485	
gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc	1603

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Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
      490                               495                               500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg 1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
      505                               510                               515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag 1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
      520                               525                               530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
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ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
      550                               555                               560

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
      570                               575                               580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg 1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
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Arg Arg Arg
      600

<210> 716
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<212> PRT
<213> Corynebacterium glutamicum

<400> 716
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Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
      35              40              45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
      50              55              60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
      65              70              75              80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
      85              90              95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
      100             105             110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
      115             120             125

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Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
450 455 460

Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
465 470 475 480

Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
530 535 540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Ala Thr Arg Arg Arg
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<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(580)

<223> FRXA02086

<400> 717

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aacgatctca tcgaggctgg cgccaagatc atccaggtgg atg agc ctg cga ttc 115
Met Ser Leu Arg Phe
1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307

Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
 55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
 70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
 90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
 105 110 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
 120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
 135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
 Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
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aac 603

<210> 718

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

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 20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
 35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val

130 135 140

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<220>
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 <222> (101)..(1303)
 <223> RXN02648

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 Met Ser Gln Asn Arg
 1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu	
150 155 160 165	
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca	643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala	
170 175 180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp	
185 190 195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu	
200 205 210	
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Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro	
215 220 225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag	835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys	
230 235 240 245	
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala	
250 255 260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly	
265 270 275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile	
280 285 290	
ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca	1027
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala	
295 300 305	
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt	1075
Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu	
310 315 320 325	
cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac	1123
Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn	
330 335 340	
gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc	1171
Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala	
345 350 355	
aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg	1219
Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu	
360 365 370	
ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta	1267
Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu	
375 380 385	

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
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<210> 720

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

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 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320

Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
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Phe

<210> 721
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(525)
 <223> FRXA02648

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agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 723

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(784)

<223> FRXA02658

<400> 723

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 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595

Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
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<210> 724

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

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 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
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<210> 725

<211> 551

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(528)

<223> RXS02197

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ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac	96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp	
20 25 30	
ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct	144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro	
35 40 45	
att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag	192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu	
50 55 60	
tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc	240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala	
65 70 75 80	
gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt	288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly	
85 90 95	
gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac	336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp	
100 105 110	
ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct	384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro	
115 120 125	
gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt	432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Pro Gly Arg	
130 135 140	
atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc	480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser	
145 150 155 160	

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

taacaccttt gagagggaaa act 551

<210> 726

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

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 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

<210> 727

<211> 546

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(523)

<223> RXC00988

<400> 727

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ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa 115
 Met Ser Lys Arg Glu
 1 5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85

atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
 90 95 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
 105 110 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
 120 125 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 728

<211> 141

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 728

Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
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His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
 20 25 30

Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

<210> 729

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(574)

<223> RXC01518

<400> 729

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 Val Ala Phe Met Gln
 1 5
 aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20
 gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211
 Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35
 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
 40 45 50
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
 55 60 65
 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
 70 75 80 85
 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
 90 95 100
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
 105 110 115

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gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
      120              125              130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
      135              140              145

cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc 594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150              155

aag 597

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<210> 730

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 730

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Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
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Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
              20              25              30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
      35              40              45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
      50              55              60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
      65              70              75              80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
              85              90              95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
      100              105              110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
      115              120              125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
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Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
145              150              155

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<210> 731

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXC01942

<400> 731

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gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
                                         Met Leu Arg Ile Gly
                                         1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
                        10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
                        25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
                        40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
                        55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
                        70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
                        90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
                        105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp
                        120 125 130

gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc 547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu
                        135 140 145

aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac 595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp
                        150 155 160 165

gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta 643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu
                        170 175 180

gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt 691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser
                        185 190 195

cgc gtg aat tagcactaaa acatcgtcaa agt 723
Arg Val Asn
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<210> 732
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 732
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 20 25 30
 Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu
 35 40 45
 Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu
 50 55 60
 Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr
 65 70 75 80
 Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala
 85 90 95
 Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr
 100 105 110
 Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu
 115 120 125
 Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val
 130 135 140
 Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser
 145 150 155 160
 Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp
 165 170 175
 Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
 180 185 190
 Ala Glu Ile Leu Ser Arg Val Asn
 195 200

<210> 733
 <211> 1194
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1171)
 <223> RXN02802

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	Val	Lys	Asn	Leu	Asp	
	1				5	
atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa						163
Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln						
	10			15	20	
aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc						211
Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly						
	25		30		35	
ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc						259
Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly						
	40		45		50	
cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac						307
His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His						
	55		60		65	
cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag						355
Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu						
	70		75		80	85
tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg						403
Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr						
	90		95		100	
gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca						451
Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala						
	105		110		115	
gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac						499
Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His						
	120		125		130	
ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca						547
Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala						
	135		140		145	
tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac						595
Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His						
	150		155		160	165
ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc						643
Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Pro Gly Ser						
	170		175		180	
gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta						691
Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val						
	185		190		195	
atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg						739
Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val						
	200		205		210	
ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc						787
Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly						
	215		220		225	
acc tgg gaa tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg						835
Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg						

230					235					240					245					
gtg	ctt	ggg	tct	gct	ggg	gtt	tct	ggg	att	tct	ggc	ggt	ttt	ggt	gag	883				
Val	Leu	Gly	Ser	Ala	Gly	Val	Ser	Gly	Ile	Ser	Gly	Gly	Phe	Gly	Glu					
250					255					260										
gtg	ctc	gat	gtt	cct	cga	gtt	tcc	gcg	ctg	ggt	gac	ggc	gtt	tct	ctc	931				
Val	Leu	Asp	Val	Pro	Arg	Val	Ser	Ala	Leu	Val	Asp	Gly	Val	Ser	Leu					
265					270					275										
atc	gac	gtc	cgc	gaa	ccc	tcc	gaa	ttc	tcc	gcc	tac	tcc	atc	ccc	ggc	979				
Ile	Asp	Val	Arg	Glu	Pro	Ser	Glu	Phe	Ser	Ala	Tyr	Ser	Ile	Pro	Gly					
280					285					290										
gcg	cac	aac	acc	cca	ctg	tcc	gcc	atc	cgc	gaa	ggc	gcc	atc	cca	ccc	1027				
Ala	His	Asn	Thr	Pro	Leu	Ser	Ala	Ile	Arg	Glu	Gly	Ala	Ile	Pro	Pro					
295					300					305										
tcc	gtt	tcc	gca	ggg	aaa	gag	gtt	atc	gtc	tac	tgc	gca	gct	ggg	gtc	1075				
Ser	Val	Ser	Ala	Gly	Lys	Glu	Val	Ile	Val	Tyr	Cys	Ala	Ala	Gly	Val					
310					315					320					325					
cgc	tcc	gca	caa	gcc	atc	gca	att	tta	gaa	tcc	gca	ggc	tac	acc	gga	1123				
Arg	Ser	Ala	Gln	Ala	Ile	Ala	Ile	Leu	Glu	Ser	Ala	Gly	Tyr	Thr	Gly					
330					335					340										
atg	agc	agc	ctc	gac	ggc	gga	atc	gaa	ggc	tgg	cta	gat	tcc	cta	ggg	1171				
Met	Ser	Ser	Leu	Asp	Gly	Gly	Ile	Glu	Gly	Trp	Leu	Asp	Ser	Leu	Gly					
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taaaaccaag gcgttggtgcc acc															1194					
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Glu	Ile	Gly	Gln	Gln	Lys	Gln	Gln	Ser	Leu	Phe	Asp	Ala	Lys	Val	Ser					
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Val	Ile	Gly	Ala	Gly	Gly	Leu	Gly	Ser	Pro	Ala	Leu	Leu	Tyr	Leu	Ala					
35					40					45										
Gly	Ala	Gly	Val	Gly	His	Ile	His	Ile	Ile	Asp	Asp	Asp	Leu	Val	Asp					
50					55					60										
Leu	Ser	Asn	Leu	His	Arg	Gln	Val	Ile	His	Thr	Thr	Ala	Gly	Val	Gly					
65				70					75					80						
Thr	Pro	Lys	Ala	Glu	Ser	Ala	Arg	Glu	Ala	Met	Leu	Ala	Leu	Asn	Pro					
85					90					95										
Ser	Val	Lys	Val	Thr	Val	Ser	Val	Arg	Arg	Leu	Asp	Trp	Ser	Asn	Ala					
100					105					110										
Leu	Ser	Glu	Leu	Ala	Asp	Ser	Asp	Val	Ile	Leu	Asp	Gly	Ser	Asp	Asn					


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Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
  130              135              140

Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val
  145              150              155              160

Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro
              165              170              175

Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly
              180              185              190

Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys
              195              200              205

Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr
  210              215              220

Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro
  225              230              235              240

Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser
              245              250              255

Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val
              260              265              270

Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala
  275              280              285

Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu
  290              295              300

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr
  305              310              315              320

Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser
              325              330              335

Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp
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Leu Asp Ser Leu Gly
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<210> 735

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(474)

<223> FRXA02802

<400> 735

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ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa				99
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu	20	25	30	
tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg				147
Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly	35	40	45	
tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat				195
Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp	50	55	60	
gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc				243
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val	65	70	75	
cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac				291
Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn	80	85	90	95
acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc				339
Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser	100	105	110	
gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca				387
Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala	115	120	125	
caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc				435
Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser	130	135	140	
ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag				484
Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly	145	150	155	
gcgttgtgcc acc				497

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<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu	1	5	10	15
Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu Tyr	20	25	30	
Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser	35	40	45	
Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val	50	55	60	
Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg	65	70	75	80

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
 Leu Ala Ser Trp Ala Ala Lys Leu Gly Ile Pro
 135 140 145

<210> 738

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro

145

<210> 739

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00437

<400> 739

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ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140
 Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741

<211> 383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(360)

<223> FRXA00437

<400> 741

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 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15
 ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30
 tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45
 tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60
 acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80
 tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95
 gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110
 ggc tcc acc gat tgg gtc ggc ctg tgaaaaacct cgacatcgcc cgc 383
 Gly Ser Thr Asp Trp Val Gly Leu

115

120

<210> 742

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 742

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110

Gly Ser Thr Asp Trp Val Gly Leu
 115 120

<210> 743

<211> 591

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(568)

<223> RXN00439

<400> 743

ctgccaccgc agactgtctg atcaggatcc cggcgcgggac tacggtggag gaaaacgaca 60

tcgttaagat ttaccatttc aactaacagg agttaattta atg agc gag ctc acc 115
 Met Ser Glu Leu Thr
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp

40	45	50	
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg			307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr			
55	60	65	
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act			355
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr			
70	75	80	85
gtg gat ttt ttt gag ctt act gat ggt gtt ccg att gag gct tcg gtg			403
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val			
90	95	100	
aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg			451
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val			
105	110	115	
agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag			499
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys			
120	125	130	
atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa			547
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys			
135	140	145	
tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg			591
Ser Gly Asp Trp Ser Val Gln			
150	155		
<210> 744			
<211> 156			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 744			
Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val			
1	5	10	15
Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly			
20	25	30	
Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly			
35	40	45	
Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met			
50	55	60	
Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro			
65	70	75	80
Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg			
85	90	95	
Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu			
100	105	110	
Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile			
115	120	125	

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
 130 135 140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
 145 150 155

<210> 745

<211> 218

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act 48
 Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1 5 10 15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg 96
 Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
 20 25 30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc 144
 Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
 35 40 45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt 192
 Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
 50 55 60

cag tgacagctct gggtatcggt gcg 218
 Gln
 65

<210> 746

<211> 65

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 746

Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
 20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
 35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
 50 55 60

Gln
 65

<210> 747
 <211> 358
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(358)
 <223> FRXA00442

<400> 747
 ctgccaccgc agactgtctg atcaggatcc cggcgcgggac tacggtggag gaaaacgaca 60
 tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115
 Met Ser Glu Leu Thr
 1 5
 cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
 10 15 20
 aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
 25 30 35
 ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
 40 45 50
 gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
 Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
 55 60 65
 ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355
 Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
 70 75 80 85
 gtg 358
 Val

<210> 748
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 748
 Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1 5 10 15
 Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
 20 25 30
 Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
 35 40 45
 Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
 50 55 60
 Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro

cac cat gaa cac tgaccccgct tacgtcgccg aac 582
His His Glu His

[illegible]

150

<210> 750

<211> 153

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
 1 5 10 15

Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30

Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45

Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60

Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80

Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95

Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110

Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125

Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr
 130 135 140

Gly Thr Leu Gln Gly His His Glu His
 145 150

<210> 751

<211> 1287

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1264)

<223> RXN00441

<400> 751

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agcgttacga ttgttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115
 Met Ser Arg Ser Pro
 1 5

gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163
 Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser
 10 15 20

acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg	211
Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala	
25 30 35	
gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat	259
Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp	
40 45 50	
ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc	307
Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val	
55 60 65	
ggg cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga	355
Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg	
70 75 80 85	
ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct	403
Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro	
90 95 100	
aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat	451
Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn	
105 110 115	
ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc	499
Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe	
120 125 130	
ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca	547
Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro	
135 140 145	
gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag	595
Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln	
150 155 160 165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc	643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile	
170 175 180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct	691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro	
185 190 195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc	739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile	
200 205 210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc	787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg	
215 220 225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc	835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile	
230 235 240 245	
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc	883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile	
250 255 260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct	931

Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro
 265 270 275
 ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca 979
 Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser
 280 285 290
 ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc 1027
 Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val
 295 300 305
 gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc 1075
 Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile
 310 315 320 325
 acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc 1123
 Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg
 330 335 340
 ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct 1171
 Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro
 345 350 355
 ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct 1219
 Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser
 360 365 370
 gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt 1264
 Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385
 taagatttac ccattcaact aac 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu
 1 5 10 15
 Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
 20 25 30
 Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45
 Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60
 Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80
 Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95
 Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125
 Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140
 Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160
 Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175
 Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190
 Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205
 Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220
 Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240
 Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255
 Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
 260 265 270
 Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
 275 280 285
 Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
 290 295 300
 Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
 305 310 315 320
 Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
 325 330 335
 Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro
 340 345 350
 Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys
 355 360 365
 His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly
 370 375 380
 Lys Arg His Arg
 385

<210> 753

<211> 815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(792)

<223> FRXA00441

<400> 753

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1 5 10 15	
att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg	96
Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser	
20 25 30	
gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc	144
Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val	
35 40 45	
gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca	192
Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser	
50 55 60	
gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt	240
Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu	
65 70 75 80	
cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac	288
Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His	
85 90 95	
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att	336
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile	
100 105 110	
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His	
115 120 125	
ggg aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser	
130 135 140	
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc	480
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser	
145 150 155 160	
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc	528
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser	
165 170 175	
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag	576
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln	
180 185 190	
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu	
195 200 205	
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn	
210 215 220	

ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct 720
 Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
 225 230 235 240

ggg tca agc tgc cac cgc aga ctg tct gat cag gat ccc ggc gcg gac 768
 Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
 245 250 255

tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac 815
 Tyr Gly Gly Gly Lys Arg His Arg
 260

<210> 754

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 754

Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp
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Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
 20 25 30

Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
 35 40 45

Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
 50 55 60

Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
 65 70 75 80

Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
 85 90 95

Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
 100 105 110

Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
 115 120 125

Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
 130 135 140

Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
 145 150 155 160

Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
 165 170 175

Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
 180 185 190

Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
 195 200 205

Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
 210 215 220

Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
225 230 235 240

Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
245 250 255

Tyr Gly Gly Gly Lys Arg His Arg
260

<210> 755

<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2335)

<223> RXN02085

<400> 755

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gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
                                         Met Thr Ser Asn Phe
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tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
                        10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
                        25 30 35

ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
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tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
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atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
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gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
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tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
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gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu

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135	140	145	
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cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct			643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro			
170	175		180
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag			691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys			
185	190		195
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc			739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr			
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act			787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr			
215	220		225
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc			835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly			
230	235		240
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc			883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly			
250	255		260
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt			931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly			
265	270		275
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc			979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg			
280	285		290
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc			1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg			
295	300		305
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac			1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr			
310	315		320
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc			1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala			
330	335		340
ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta			1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu			
345	350		355
gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att			1219
Ala Gly Asn Ile Asp Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile			
360	365		370
gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc			1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu			
375	380		385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
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cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
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 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
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ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
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 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
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cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
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 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
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ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843
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 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg
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 Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg
 600 605 610

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tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat 2035
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 665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
 680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
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 Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
 710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323
 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
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 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
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Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu

115	120	125
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130 135 140		
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145 150 155 160		
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165 170 175		
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr 180 185 190		
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu 195 200 205		
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg 210 215 220		
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr 225 230 235 240		
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly 245 250 255		
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu 260 265 270		
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly 275 280 285		
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys 290 295 300		
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu 305 310 315 320		
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val 325 330 335		
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu 340 345 350		
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala 355 360 365		
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro 370 375 380		
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg 385 390 395 400		
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr 405 410 415		
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala 420 425 430		
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met 435 440 445		

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
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 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
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 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
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<211> 1923

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 757

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                                         Met Thr Ser Asn Phe
                                         1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
                        10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
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ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
                        40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
                        55 60 65

atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
                        70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
                        90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
                        105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
                        120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
                        135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
                        150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
                        170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys

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185										190										195										
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		200					205					210																		
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Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly															
230					235					240					245															
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883														
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly															
				250					255					260																
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Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu	Ala	Ala	Trp	Lys	Gly															
			265					270					275																	
gag	gag	ctg	ctg	gtt	gcg	ggc	atc	gtt	gat	ggc	cgt	aac	att	tgg	cgc	979														
Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg															
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Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg															
		295				300					305																			
ggc	cca	atc	gca	gtg	tct	acc	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac	1075														
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				330					335					340																
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Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu															
			345					350					355																	
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gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc	1267														
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Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe															
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cca	cag	acc	cca	tcc	att	cgt	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa	1411														
Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu															
			425					430					435																	

BGI-121CP
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 1267
 1315
 1363
 1411

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Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
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Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
      455                      460                      465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc 1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
      470                      475                      480                      485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc 1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
      490                      495                      500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg 1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
      505                      510                      515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag 1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
      520                      525                      530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
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      570                      575                      580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg 1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
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<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Ala Thr Arg Arg Arg
 595 600

<210> 759

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 759

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 aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115
 Met Ser Leu Arg Phe

1

5

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gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
      10              15              20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
      25              30              35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
      40              45              50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
      55              60              65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
      70              75              80              85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
      90              95              100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
      105              110              115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
      120              125              130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
      135              140              145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
      150              155              160

aac 603

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<210> 760

<211> 160

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 760

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Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
  1              5              10              15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
      20              25              30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35              40              45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
      50              55              60

```

```

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65                      70                      75                      80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
                      85                      90                      95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
          100                      105                      110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
          115                      120                      125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
          130                      135                      140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
          145                      150                      155                      160

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<210> 761
<211> 1326
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1303)
<223> RXN02648

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<400> 761
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gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc      115
                                   Met Ser Gln Asn Arg
                                   1                      5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt      163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
                      10                      15                      20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc      211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
                      25                      30                      35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt      259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
                      40                      45                      50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc      307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
                      55                      60                      65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc      355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
          70                      75                      80                      85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa      403

```

Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu		
				90					95					100			
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451	
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
			105					110					115				
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
		120					125					130					
ggc	atc	ttc	acc	ggc	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
	135					140					145						
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
150					155					160					165		
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
				170					175					180			
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
			185					190					195				
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
		200					205					210					
tac	aag	atc	atc	acc	gat	gca	ggc	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
	215					220					225						
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
230					235					240				245			
gat	tac	ttg	gac	tgg	atc	ggc	aca	cgc	atc	gat	gcc	atc	aac	agt	gca	883	
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala		
				250					255					260			
gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	tgc	tgg	ggc	931	
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly		
			265					270					275				
tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggc	gac	atc	att	979	
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile		
		280					285					290					
ggc	gag	atc	ctg	cgc	gca	gag	gtc	ggc	ggc	ttc	tcc	ttc	gaa	ggc	gca	1027	
Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala		
	295					300					305						
tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	aac	aag	ctt	1075	
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu		
310					315					320					325		
cct	gaa	ggc	tct	gtt	atc	tac	cct	ggc	gtt	gtg	tct	cac	tcc	atc	aac	1123	
Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	Ser	Ile	Asn		

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          330          335          340
gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc 1171
Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
          345          350          355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg 1219
Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
          360          365          370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta 1267
Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
          375          380          385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          390          395          400

aacgagggtt gct 1326

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<210> 762

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
  1              5              10              15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
          20              25              30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
          35              40              45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
          50              55              60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
          65              70              75              80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
          85              90              95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
          100             105             110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
          115             120             125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
          130             135             140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
          145             150             155             160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
          165             170             175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr

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<400> 763
gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1             5             10             15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96

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```

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
      20                      25                      30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
      35                      40                      45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
      50                      55                      60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
      65                      70                      75                      80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
      85                      90                      95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
      100                      105                      110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
      115                      120                      125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
      130                      135                      140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
      145                      150                      155                      160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
      165                      170                      175

taagctagac aacgagggtt gct 548

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<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1                      5                      10                      15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
      20                      25                      30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
      35                      40                      45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
      50                      55                      60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe

```

65	70	75	80
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu	85	90	95
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His	100	105	110
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val	115	120	125
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp	130	135	140
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu	145	150	155
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe	165	170	175

<210> 765

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 765

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gagtttgata ctttctttcg acttttagat tggattttca	atg agc cag aac cgc	115
	Met Ser Gln Asn Arg	
	1 5	

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt	163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu	
10 15 20	

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc	211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe	
25 30 35	

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt	259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val	
40 45 50	

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc	307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr	
55 60 65	

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc	355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg	
70 75 80 85	

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa	403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu	
90 95 100	

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gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
215 220 225

<210> 766
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 766
Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100 105 110

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Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 767

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 gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
 Met Ala Asp Arg Ile
 1 5
 gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
 Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
 10 15 20
 gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
 Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
 25 30 35
 gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
 Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
 40 45 50
 tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
 Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
 55 60 65
 agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
 Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
 70 75 80 85

```

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
          90          95          100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
          105          110          115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
          120          125          130

agttttgtcc atc 513

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<210> 768

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 768

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Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
  1             5             10             15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
          20             25             30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
          35             40             45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
          50             55             60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
          65             70             75             80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
          85             90             95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
          100            105            110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
          115            120            125

Asn Ala
  130

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<210> 769

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 769

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ctccccgcgct gaggtgtttct ccctgattcgc ggggcactaa atg aac gta tcc tct																115
Met Asn Val Ser Ser																
1 5																
ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act																163
Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr																
10 15 20																
gag gat tcc ttt tgc gac ggt ggc aag tac att gac gtt gat cag gcg																211
Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala																
25 30 35																
atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat																259
Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp																
40 45 50																
gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc																307
Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser																
55 60 65																
gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc																355
Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala																
70 75 80 85																
ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct																403
Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala																
90 95 100																
gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg																451
Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu																
105 110 115																
gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg																499
Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val																
120 125 130																
tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag																547
Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln																
135 140 145																
gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat																595
Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp																
150 155 160 165																
gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc																643
Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile																
170 175 180																
gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg																691
Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp																
185 190 195																
cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc																739
Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile																
200 205 210																
ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac																787
Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp																
215 220 225																

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245

 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260

 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275

 agt gga gga act cac cat ggc tgcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 770

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
 1 5 10 15

 Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30

 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45

 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60

 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95

 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110

 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125

 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140

 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160

 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175

 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190

 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser

195	200	205
Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala		
210	215	220
Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp		
225	230	235 240
Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp		
	245	250 255
Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val		
	260	265 270
Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly		
275	280	

<210> 771

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 771

cactgatgac ctggatcagg ccgtcaaatt catcgctgat gcacacgctg gattggacgt 60

agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg 115
Met Ser Ser Leu Pro
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

ggg ggc aca ttt gag gac acc gct ggc cta aac agg gca ggc gag gtc 211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val
25 30 35

att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc 259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly
40 45 50

ccg ggg gat ttc gtg tcg ggc gag gaa gag atc gac cgc gtg gtg cca 307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro
55 60 65

atc atc gct ggc gtg cga gaa cgt ttt cct gac att gat att tct gtt 355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val
70 75 80 85

gat acc tgg cgg ggc tcg gtg gct gat gtc gca gtg ggc cat gga gca 403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala
90 95 100

acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag 451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln

105	110	115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg			499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly			
120	125	130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg			547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val			
135	140	145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt			595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg			
150	155	160	165
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc			643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe			
170	175	180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag			691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu			
185	190	195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat			739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp			
200	205	210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc			787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly			
215	220	225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt			835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe			
230	235	240	245
cgc gtg cat gaa gtt gcg gaa acc			859
Arg Val His Glu Val Ala Glu Thr			
250			

<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Met	Ser	Ser	Leu	Pro	Val	Ile	Met	Ala	Ile	Val	Asn	Arg	Thr	Pro	Asp
1				5					10					15	

Ser	Phe	Tyr	Asp	Lys	Gly	Ala	Thr	Phe	Glu	Asp	Thr	Ala	Ala	Leu	Asn
			20					25					30		

Arg	Ala	Ala	Glu	Val	Ile	Glu	Gln	Gly	Ala	Gly	Ile	Val	Asp	Ile	Gly
		35					40					45			

Gly	Val	Lys	Ala	Gly	Pro	Gly	Asp	Phe	Val	Ser	Ala	Glu	Glu	Glu	Ile
	50					55					60				

Asp	Arg	Val	Val	Pro	Ile	Ile	Ala	Ala	Val	Arg	Glu	Arg	Phe	Pro	Asp
65					70					75				80	

Ile	Asp	Ile	Ser	Val	Asp	Thr	Trp	Arg	Ala	Ser	Val	Ala	Asp	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<210> 773
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

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<220>  
<221> CDS  
<222> (101)..(661)  
<223> RXA01719
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<400> 773
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cgaggacggt ctggttgatg ttgtgctggg gagaatgtaa atg aat atc atc att 115
Met Asn Ile Ile Ile
1 5

ctt gct ggt ggc gag ggt aaa cgc atg ggt ggg gtg gat aag gct gct 163
Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala
10 15 20

gtg gcg gtg gat ggt cgc acg ctg ctg gat atc ctg ctt tca cag ctg 211
Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu
25 30 35

gat cca gaa gat gac gtc gtg gtg gtt tcc ccc gcg atc atc gac gga 259
Asp Pro Glu Asp Asp Val Val Val Val Ser Pro Ala Ile Ile Asp Gly
40 45 50

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atc acg act gtc tgc gag gaa cct ccg ctt ggc ggg ccg gtc gcg gga 307
Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
    55                      60                      65

atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
    70                      75                      80                      85

att ctt gcc gtg gac gcg cct tat tct gca gcg atg ctg ccc cta ctt 403
Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
                90                      95                      100

cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
                105                      110                      115

ggc tgg gta caa ccg ttg tgc gcg ctg tgg aga agt ggc agc cta gaa 499
Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu
                120                      125                      130

gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
                135                      140                      145

tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
                150                      155                      160                      165

gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643
Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val
                170                      175                      180

acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct 684
Thr Leu Pro Lys Ala His
                185

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<210> 774

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 774

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Met Asn Ile Ile Ile Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly
  1                      5                      10                      15

Val Asp Lys Ala Ala Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile
                20                      25                      30

Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro
                35                      40                      45

Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
                50                      55                      60

Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
                65                      70                      75                      80

His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
                85                      90                      95

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Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
100 105 110

Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
115 120 125

Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
130 135 140

Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
145 150 155 160

Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
165 170 175

Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
180 185

<210> 775

<211> 1332

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1309)

<223> RXA01720

<400> 775

acacccgttt gagaatctca acctcttaaa acagcgcgaa ctattgattt ggcaactacc 60

ctatatattt gagtgtttat tgtcgaaaaa ggggtttcaa gtg gca cag caa cgc 115
Val Ala Gln Gln Arg
1 5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
10 15 20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
25 30 35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
40 45 50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
55 60 65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
70 75 80 85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
90 95 100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc	451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr	
105 110 115	
aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag	499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu	
120 125 130	
cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa	547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys	
135 140 145	
gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act	595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr	
150 155 160 165	
gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct	643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro	
170 175 180	
tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga	691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly	
185 190 195	
aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag	739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu	
200 205 210	
cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat	787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp	
215 220 225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg	835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala	
230 235 240 245	
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg	883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val	
250 255 260	
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att	931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile	
265 270 275	
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca	979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala	
280 285 290	
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt	1027
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe	
295 300 305	
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg	1075
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg	
310 315 320 325	
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg	1123
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg	
330 335 340	
gcg ctg aag gcg ccg gag ggc ccc gta ttg gcg ata ccg gtg gcg att	1171

Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile
 345 350 355

gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg 1219
 Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met
 360 365 370

gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg 1267
 Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser
 375 380 385

att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg 1309
 Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met
 390 395 400

taaatgaata tcattcattct tgc 1332

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Val Ala Gln Gln Arg Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp
 1 5 10 15

Ser Val Ala Pro Leu Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His
 20 25 30

Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro
 35 40 45

Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp
 50 55 60

Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro
 65 70 75 80

Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val
 85 90 95

Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val
 100 105 110

Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu
 115 120 125

Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala
 130 135 140

Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala
 145 150 155 160

Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr
 165 170 175

Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp
 180 185 190

Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro

195	200	205
Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His 210 215 220		
Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys 225 230 235 240		
Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala 245 250 255		
Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe 260 265 270		
Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly 275 280 285		
Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala 290 295 300		
Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu 305 310 315 320		
Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala 325 330 335		
Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala 340 345 350		
Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala 355 360 365		
His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala 370 375 380		
Leu Val Thr Ser Ser Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu 385 390 395 400		
Gly Arg Met		

<210> 777

<211> 1237

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (2)..(1207)

<223> RXS03223

<400> 777

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Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys	
1 5 10 15	

gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca	97
Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala	
20 25 30	

gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag	145
Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	
35 40 45	
tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc	193
Ser Phe Ser Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	
50 55 60	
gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag	241
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln	
65 70 75 80	
cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt	289
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	
85 90 95	
gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga	337
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	
100 105 110	
gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa	385
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	
115 120 125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc	433
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val	
130 135 140	
tta ggc cct gcc caa att ggt ttg ctg gca gct gtt ggt cgc tcc aaa	481
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys	
145 150 155 160	
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct	529
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala	
165 170 175	
gaa ctt gtt gat att gat cgc cag cca ggc ctg ggc cag gtt tat gat	577
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp	
180 185 190	
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat	625
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp	
195 200 205	
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag	673
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu	
210 215 220	
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga	721
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly	
225 230 235 240	
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctg aac gag	769
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu	
245 250 255	
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc	817
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val	
260 265 270	
caa gga ttc ggt ctg ctg ggc gag aac aag att cca tgc ttc ctt ctg	865

Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu
 275 280 285

cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc 913
 Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg
 290 295 300

ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt 961
 Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val
 305 310 315 320

gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009
 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys
 325 330 335

ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057
 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
 340 345 350

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg 1105
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc 1153
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa 1201
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

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 Gly Arg

<210> 778

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

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 20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg

100					105					110					
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115					120					125			
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135					140				
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145					150					155					160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
	195						200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225					230					235					240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
	290					295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305					310					315					320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325					330					335	
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
	370					375					380				
Thr	Glu	Ile	Arg	Pro	Gly	Asp	Val	Val	Asp	Val	Ile	Phe	Leu	Ala	Gln
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Gly	Arg														

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1206)
 <223> FRXA01970

<400> 779
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 gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 96
 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30
 gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag 144
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45
 tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc 192
 Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60
 gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag 240
 Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80
 cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt 288
 Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95
 gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga 336
 Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110
 gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa 384
 Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu
 115 120 125
 ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc 432
 Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val
 130 135 140
 tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa 480
 Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys
 145 150 155 160
 gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct 528
 Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala
 165 170 175
 gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat 576
 Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp
 180 185 190
 gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat 624
 Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp
 195 200 205

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gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag 672
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu
    210                      215                      220

atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga 720
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly
225                      230                      235                      240

gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag 768
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu
    245                      250                      255

cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc 816
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val
    260                      265                      270

caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg 864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu
    275                      280                      285

cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc 912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg
    290                      295                      300

ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt 960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val
305                      310                      315                      320

gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1008
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys
    325                      330                      335

ggg ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1056
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
    340                      345                      350

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg 1104
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
    355                      360                      365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc 1152
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
    370                      375                      380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa 1200
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
385                      390                      395                      400

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Gly Arg

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<210> 780

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

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Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	35	40	45
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	50	55	60
Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln	65	70	75
Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	85	90	95
Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	100	105	110
Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	115	120	125
Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val	130	135	140
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys	145	150	155
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala	165	170	175
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp	180	185	190
Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp	195	200	205
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu	210	215	220
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly	225	230	235
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu	245	250	255
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val	260	265	270
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu	275	280	285
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg	290	295	300
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val	305	310	315
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys	325	330	335

Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr
 340 345 350

Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

Gly Arg

<210> 781

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXA02629

<400> 781

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 Met Ser Lys Asp Pro
 1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
 10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
 25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
 40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
 55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
 70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
 90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
 105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
 120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
 135 140 145

tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val
 185 190 195

tgagttggtc ggggtgtgagt aga 708

<210> 782

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg
 1 5 10 15

Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr
 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met

165 170 175
 Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr
 180 185 190
 Ser Val Val
 195

<210> 783
 <211> 402
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(379)
 <223> RXA02318

<400> 783
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 Met Asn Ser Leu Phe
 1 5
 gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat 163
 Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His
 10 15 20
 ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att 211
 Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile
 25 30 35
 gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc 259
 Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr
 40 45 50
 tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata 307
 Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile
 55 60 65
 acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag 355
 Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys
 70 75 80 85
 acc ttg gcc att tcg gca gag gct taagggttaaa gattatgagc aac 402
 Thr Leu Ala Ile Ser Ala Glu Ala
 90

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 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 784
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 1 5 10 15
 Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys

	20		25		30
Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro					
35		40		45	
Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His					
50		55		60	
Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile					
65		70		75	80
Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala					
85		90			

<210> 785

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXA01517

<400> 785

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gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg	115
Met His Ala Val Leu	
1 5	

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg	163
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val	
10 15 20	

atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca	211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser	
25 30 35	

acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg	259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val	
40 45 50	

ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc	307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly	
55 60 65	

caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg	355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly	
70 75 80 85	

cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa	403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu	
90 95 100	

gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct	451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala	
105 110 115	

tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat	499
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Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp
 120 125 130

gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat 547
 Ala Val Leu His Gly Thr Ile Ala Glu His Val Asp Asn Leu Asp
 135 140 145

ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggcctttcat 597
 Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
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gca 600

<210> 786

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

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 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 787

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01304

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Met Pro Ala Gln Asn
1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser
10 15 20

gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag 211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln
25 30 35

gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt 259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe
40 45 50

gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc 307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg
55 60 65

gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg 355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr
70 75 80 85

ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg 403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met
90 95 100

acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta 451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu
105 110 115

tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc 499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu
120 125 130

atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg 547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly
135 140 145

gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagatttt 596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu
150 155 160

ttgcttatcg acg 609

<210> 788

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 788

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Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala
20 25 30

<400> 789																
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				Leu	Ile	Val	Ser	Thr								
				1	5											
cag	ccc	att	act	gat	cgc	agc	gca	ctc	tcg	gca	gaa	cac	gca	gag	gtg	163
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val	
				10					15	20						
atc	aaa	gca	acg	ctt	cct	ctc	gtg	ggc	ggc	aag	att	aat	gag	atc	acg	211
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr	
				25					30	35						
ccg	gtt	ttc	tac	aac	aag	atg	ttt	gcg	gct	cac	cca	gaa	ttg	atc	gct	259
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala	
				40					45	50						
aac	acc	ttc	aac	cgt	ggc	aat	cag	aag	caa	ggc	gat	cag	cag	aag	gcg	307
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala	
				55					60	65						

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat	355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp	
70 75 80 85	
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg	403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val	
90 95 100	
tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg	451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	
105 110 115	
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	
120 125 130	
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	
135 140 145	
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc	595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	
150 155 160 165	
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca	643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	
170 175 180	
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	
185 190 195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag	739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	
200 205 210	
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	
215 220 225	
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	
230 235 240 245	
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	
250 255 260	
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	
265 270 275	
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	
280 285 290	
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	
295 300 305	

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa 1075
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
 310 315 320 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
 330 335 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385

cccagaact tcc 1281

<210> 790
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 790
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 Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30
 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335
 Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350
 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365
 Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380
 Ile Ser
 385

<210> 791

<211> 990

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(967)

<223> RXS02560

<400> 791

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 ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115
 Met Gln Gly Asn Ser

1

5

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20

gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35

ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50

cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
 Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
 90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
 Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
 105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
 Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
 120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
 135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
 150 155 160 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
 170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
 185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
 200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
 215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883

Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260
 cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275
 agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
 280 285
 attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 792

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 Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30
 Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45
 Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160
 Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
260 265 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
275 280 285

Arg

<210> 793

<211> 1425

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1402)

<223> RXA00382

<400> 793

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ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat 115
Met Thr Ser Ser Asn
1 5

acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct 163
Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro
10 15 20

ggg ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa 211
Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln
25 30 35

gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac 259
Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp
40 45 50

gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg 307
Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met
55 60 65

ggg cac gct cac cca gca gtg gtc gag gct gtg cag aag gcc gtc gtg 355
Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val
70 75 80 85

gat ggt ctt tct ttc ggc gct ccc acc atc ggt gag gtt gag ttg gcc 403
Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala
90 95 100

caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac 451
Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn
105 110 115

tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac	499
Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg Leu Ala Arg Gly Tyr	
120 125 130	
act cag cgt tcc aag att ttg aag ttt gag ggc tgc tac cac ggc cac	547
Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly Cys Tyr His Gly His	
135 140 145	
gtc gat gcg ctg ctc gca tct gct ggt tct ggt gtc gca act ttc gct	595
Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly Val Ala Thr Phe Ala	
150 155 160 165	
ctg cct gat tcc cca ggc atc acc ggc gct cag act tct gac act att	643
Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln Thr Ser Asp Thr Ile	
170 175 180	
gtt gtt cct tac aac gac att gaa gcc gtg cgc aac gct ttt gcg gag	691
Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg Asn Ala Phe Ala Glu	
185 190 195	
tac cca ggc gag atc gcc tgc atc atc gca gag gca gcc ggt ggc aac	739
Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu Ala Ala Gly Gly Asn	
200 205 210	
atg ggc acc gtc gct cca aag gac aac ttt aac gac aag ctt ctc gcg	787
Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn Asp Lys Leu Leu Ala	
215 220 225	
atc gct cac gct gac ggc gcg ctg ctg atc ctc gat gaa gtc atg acc	835
Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu Asp Glu Val Met Thr	
230 235 240 245	
ggc ttc cgc acc tct tac cgt ggc tgg ttc ggc gta gac aag gtt gcc	883
Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly Val Asp Lys Val Ala	
250 255 260	
gct gac ctg gtc acc ttc ggc aag gtc gtc tcc ggc ggc cta cct gcc	931
Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser Gly Gly Leu Pro Ala	
265 270 275	
gca gcg ttt ggc ggc aag gct gaa atc atg aac atg ctg gcc cca cag	979
Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn Met Leu Ala Pro Gln	
280 285 290	
ggc ccc gtc tac caa gca ggc aca ctg tcc ggc aac ccg gtt gcg gtc	1027
Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly Asn Pro Val Ala Val	
295 300 305	
gca gct ggt cgg gca tcg ctt aag ctt gcc gac gaa tcc ctc tac aca	1075
Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp Glu Ser Leu Tyr Thr	
310 315 320 325	
acc atc aac gcc aac gca gat cgt ctc cac ggt ttg atc tct gat gcc	1123
Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly Leu Ile Ser Asp Ala	
330 335 340	
tta acc cac gaa ggc gta gcc cac cac att cag cgt gcc tca aac atg	1171
Leu Thr His Glu Gly Val Ala His His Ile Gln Arg Ala Ser Asn Met	
345 350 355	

ctg tct atc cgt ttt gca gaa ggt gag ggc cac aac ttc tct gat atg 1219
 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp Met
 360 365 370

aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg 1267
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu
 375 380 385

gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg 1315
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val
 390 395 400 405

tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc 1363
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu
 410 415 420

aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac 1412
 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser
 425 430

cattgtccat cta 1425

<210> 794

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 794

Met Thr Ser Ser Asn Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala
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Gln Lys Leu Thr Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly
 20 25 30

Ser Val Gly Gly Gln Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr
 35 40 45

Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
 50 55 60

Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
 65 70 75 80

Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
 85 90 95

Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
 100 105 110

Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
 130 135 140

Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
 145 150 155 160

Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
 165 170 175

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Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
      180                      185                      190

Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
      195                      200                      205

Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
      210                      215                      220

Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
      225                      230                      235                      240

Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
      245                      250                      255

Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
      260                      265                      270

Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
      275                      280                      285

Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
      290                      295                      300

Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
      305                      310                      315                      320

Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
      325                      330                      335

Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
      340                      345                      350

Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
      355                      360                      365

Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
      370                      375                      380

Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
      385                      390                      395                      400

Glu Thr Trp Phe Val Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys
      405                      410                      415

Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys
      420                      425                      430

Ala Ser

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<210> 795

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<400> 795

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tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa 163
Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu
10 15 20

ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
40 45 50

aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355
Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
70 75 80 85

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atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451
Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala
      105                      110                      115

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atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag 547
Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys
135 140 145

ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag 643
Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu
170 175 180

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
200 205 210

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gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835
Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
280 285 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca 1027
Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc 1075
Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
310 315 320 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca 1123
Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg 1171
Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat 1220
Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
360 365 370

agtcacctgc aaa 1233

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<210> 796

<211> 370

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 796

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Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
1 5 10 15

Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
20 25 30

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
35 40 45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
50 55 60

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Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65 70 75 80
 Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
 85 90 95
 Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
 100 105 110
 Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
 115 120 125
 Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
 130 135 140
 Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
 145 150 155 160
 Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
 165 170 175
 Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
 180 185 190
 Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
 195 200 205
 Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
 210 215 220
 Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
 225 230 235 240
 Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
 245 250 255
 Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
 260 265 270
 Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
 275 280 285
 Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
 290 295 300
 Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
 305 310 315 320
 Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser
 325 330 335
 Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys
 340 345 350
 His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala
 355 360 365
 Ala Asn
 370

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aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa 643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu
170 175 180

aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac 691
 Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn
 185 190 195

cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat 739
 Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp
 200 205 210

ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc 787
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tagttgggga gggtcggggc acc 810

<210> 798

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 798

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 20 25 30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu
 35 40 45

Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg
 50 55 60

Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg
 65 70 75 80

Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu
 85 90 95

Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile
 100 105 110

Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu
 115 120 125

Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn
 130 135 140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
 145 150 155 160

Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
 165 170 175

Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
 180 185 190

Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
 195 200 205

Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala

210 215 220

Ala Ala Gln Leu Ala
225

<210> 799
<211> 956
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(933)
<223> RXA00306

<400> 799

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ggt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
ggt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255

atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 800

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 800

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
290 295 300

Pro Ala Asp Leu Leu Asp Ser
305 310

<210> 801

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXA00884

<400> 801

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Met Ser Val Phe Gly
1 5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163

Val	Tyr	Ile	His	Val	Pro	Phe	Cys	Ser	Thr	Arg	Cys	Gly	Tyr	Cys	Asp	
				10					15					20		
ttc	aac	acc	tat	act	gct	ggg	gaa	tta	ggg	agt	act	gca	ggc	ccg	gac	211
Phe	Asn	Thr	Tyr	Thr	Ala	Gly	Glu	Leu	Gly	Ser	Thr	Ala	Gly	Pro	Asp	
			25					30					35			
acc	tat	ctt	gac	tcg	ttg	gaa	gtt	gag	ttg	gag	atg	gct	gtg	gct	tcg	259
Thr	Tyr	Leu	Asp	Ser	Leu	Glu	Val	Glu	Leu	Glu	Met	Ala	Val	Ala	Ser	
		40				45						50				
ctg	gat	aat	cct	cgg	cag	gcg	gaa	act	atc	ttt	att	ggc	ggg	ggg	acc	307
Leu	Asp	Asn	Pro	Arg	Gln	Ala	Glu	Thr	Ile	Phe	Ile	Gly	Gly	Gly	Thr	
	55					60					65					
ccg	tcg	ttg	att	ggg	gcg	gac	ggg	ttg	gcc	agg	gtt	ttg	ggg	gct	gtg	355
Pro	Ser	Leu	Ile	Gly	Ala	Asp	Gly	Leu	Ala	Arg	Val	Leu	Gly	Ala	Val	
70					75				80						85	
cgc	aat	act	ttt	ggc	att	gcg	gat	ggg	gcg	gaa	gtc	acc	acg	gag	tcc	403
Arg	Asn	Thr	Phe	Gly	Ile	Ala	Asp	Gly	Ala	Glu	Val	Thr	Thr	Glu	Ser	
				90					95					100		
aat	ccg	gag	tct	acc	tcg	cct	gag	ttt	ttt	gat	ggc	ctg	cgt	gag	gcg	451
Asn	Pro	Glu	Ser	Thr	Ser	Pro	Glu	Phe	Phe	Asp	Gly	Leu	Arg	Glu	Ala	
			105					110					115			
ggc	tac	aac	agg	att	tcg	tta	ggg	atg	cag	tcg	gcg	tcg	tca	agc	gtt	499
Gly	Tyr	Asn	Arg	Ile	Ser	Leu	Gly	Met	Gln	Ser	Ala	Ser	Ser	Ser	Val	
		120					125					130				
ttg	aag	gtg	ctg	gac	cgc	acg	cac	acc	cca	ggg	cgc	ccg	gtg	gcg	gcg	547
Leu	Lys	Val	Leu	Asp	Arg	Thr	His	Thr	Pro	Gly	Arg	Pro	Val	Ala	Ala	
	135					140					145					
gcc	aag	gag	gca	cgt	gag	gcg	ggg	ttt	gag	cat	gtc	aat	ttg	gac	atg	595
Ala	Lys	Glu	Ala	Arg	Glu	Ala	Gly	Phe	Glu	His	Val	Asn	Leu	Asp	Met	
150					155					160					165	
att	tat	ggc	acg	ccg	aca	gag	acc	gat	gat	gat	gtc	cgc	aag	acg	ctg	643
Ile	Tyr	Gly	Thr	Pro	Thr	Glu	Thr	Asp	Asp	Asp	Val	Arg	Lys	Thr	Leu	
				170					175					180		
aat	gcg	gtg	ctc	gaa	gcg	aac	gtg	gat	cac	gtg	tct	gcc	tat	tcc	ttg	691
Asn	Ala	Val	Leu	Glu	Ala	Asn	Val	Asp	His	Val	Ser	Ala	Tyr	Ser	Leu	
			185				190						195			
atc	gtg	aaa	gat	ggc	acg	gcg	atg	gcg	cgc	aag	gtg	cac	aag	ggc	gag	739
Ile	Val	Lys	Asp	Gly	Thr	Ala	Met	Ala	Arg	Lys	Val	His	Lys	Gly	Glu	
		200					205					210				
ctg	cca	gcg	ccg	gac	gag	gat	gtc	tac	gct	gat	cgt	ttt	gag	ctt	atc	787
Leu	Pro	Ala	Pro	Asp	Glu	Asp	Val	Tyr	Ala	Asp	Arg	Phe	Glu	Leu	Ile	
	215					220					225					
gac	gct	cgc	ctg	cgc	tca	gct	ggg	ttc	gat	tgg	tac	gag	gtg	tcc	aac	835
Asp	Ala	Arg	Leu	Arg	Ser	Ala	Gly	Phe	Asp	Trp	Tyr	Glu	Val	Ser	Asn	
230					235				240						245	
tgg	gcg	aaa	ccc	ggc	gga	gaa	tgc	aag	cac	aac	atg	ggc	tat	tgg	gtc	883
Trp	Ala	Lys	Pro	Gly	Gly	Glu	Cys	Lys	His	Asn	Met	Gly	Tyr	Trp	Val	

	250	255	260	
gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc				931
Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly				
	265	270	275	
gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag				979
Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln				
	280	285	290	
att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg				1027
Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala				
	295	300	305	
gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa				1075
Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln				
	310	315	320	325
ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac				1123
Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp				
	330	335	340	
cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg				1171
Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu				
	345	350	355	
gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac				1219
Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp				
	360	365	370	
att ttg ctt agt gaa gaa gac taaatattta gtagggttac aga				1263
Ile Leu Leu Ser Glu Glu Asp				
	375	380		

<210> 802

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

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Cys	Gly	Tyr	Cys	Asp	Phe	Asn	Thr	Tyr	Thr	Ala	Gly	Glu	Leu	Gly	Ser
			20					25					30		

Thr	Ala	Gly	Pro	Asp	Thr	Tyr	Leu	Asp	Ser	Leu	Glu	Val	Glu	Leu	Glu
		35					40					45			

Met	Ala	Val	Ala	Ser	Leu	Asp	Asn	Pro	Arg	Gln	Ala	Glu	Thr	Ile	Phe
	50					55					60				

Ile	Gly	Gly	Gly	Thr	Pro	Ser	Leu	Ile	Gly	Ala	Asp	Gly	Leu	Ala	Arg
65					70					75					80

Val	Leu	Gly	Ala	Val	Arg	Asn	Thr	Phe	Gly	Ile	Ala	Asp	Gly	Ala	Glu
				85					90					95	

Val	Thr	Thr	Glu	Ser	Asn	Pro	Glu	Ser	Thr	Ser	Pro	Glu	Phe	Phe	Asp
			100					105					110		


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Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
   115                               120                   125

Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
   130                               135                   140

Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
   145                               150                   155                   160

Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
   165                               170                   175

Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
   180                               185                   190

Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
   195                               200                   205

Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
   210                               215                   220

Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp
   225                               230                   235                   240

Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
   245                               250                   255

Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
   260                               265                   270

His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
   275                               280                   285

Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
   290                               295                   300

Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
   305                               310                   315                   320

Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala
   325                               330                   335

Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn
   340                               345                   350

Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp
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Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp
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<210> 803

<211> 522

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(499)

<223> RXN02503

<400> 803

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ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
Met Thr Leu Lys Ile
1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile
90 95 100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly
105 110 115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro
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tgacctggag attctccac tgc 522

<210> 804

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

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20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Ser
 85 90 95

Arg Glu Ala Leu Ile Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro
 100 105 110

Glu Arg Arg Lys Gly Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala
 115 120 125

Gln Gly Asn Pro Pro
 130

<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02503

<400> 805

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 Met Thr Leu Lys Ile
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145

atgggcaagg tca 558

<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

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Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His

145

<210> 807

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00377

<400> 807

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													Val	Trp	Leu	Leu	Phe	
													1				5	
cta	aat	tgg	gat	aaa	tgg	ggc	aag	att	gag	cgc	atg	tct	gct	ctt	act		163	
Leu	Asn	Trp	Asp	Lys	Trp	Gly	Lys	Ile	Glu	Arg	Met	Ser	Ala	Leu	Thr			
				10					15						20			
att	cca	gct	gcg	cgt	cgc	acg	cta	aat	aac	gcg	ccc	att	att	gat	gcc		211	
Ile	Pro	Ala	Ala	Arg	Arg	Thr	Leu	Asn	Asn	Ala	Pro	Ile	Ile	Asp	Ala			
				25				30						35				
gct	aat	ggc	aag	acc	ccg	act	cgc	act	ccg	gtg	tgg	ttt	atg	cgc	cag		259	
Ala	Asn	Gly	Lys	Thr	Pro	Thr	Arg	Thr	Pro	Val	Trp	Phe	Met	Arg	Gln			
			40				45					50						
gcg	ggt	agg	tcg	ttg	cct	gag	tac	aag	aag	gtc	cgt	gag	gga	atc	agc		307	
Ala	Gly	Arg	Ser	Leu	Pro	Glu	Tyr	Lys	Lys	Val	Arg	Glu	Gly	Ile	Ser			
						60					65							
atg	ttg	gat	tcc	tgt	ttc	atg	ccg	gag	ttg	ttg	gcg	gag	att	act	ttg		355	
Met	Leu	Asp	Ser	Cys	Phe	Met	Pro	Glu	Leu	Leu	Ala	Glu	Ile	Thr	Leu			
					75					80					85			
cag	ccg	gtt	cgt	cgt	cat	gat	gtg	gat	gct	gcg	att	ttg	ttc	tct	gac		403	
Gln	Pro	Val	Arg	Arg	His	Asp	Val	Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp			
				90					95					100				
att	gtg	gtg	ccg	ttg	cgt	gct	gcg	ggt	gtt	ggt	gtg	gaa	atc	gtg	gcg		451	
Ile	Val	Val	Pro	Leu	Arg	Ala	Ala	Gly	Val	Gly	Val	Glu	Ile	Val	Ala			
			105					110					115					
ggt	cgt	gga	cct	gtg	ttg	gat	gcg	ccg	gtg	ccg	agc	cgt	ggg	gat	gtg		499	
Gly	Arg	Gly	Pro	Val	Leu	Asp	Ala	Pro	Val	Arg	Ser	Arg	Gly	Asp	Val			
			120				125					130						
ttg	aat	ctt	cct	att	ttg	gag	ggc	aac	gtt	ccg	gag	gtg	gag	cag	ggt		547	
Leu	Asn	Leu	Pro	Ile	Leu	Glu	Gly	Asn	Val	Pro	Glu	Val	Glu	Gln	Gly			
			135			140					145							
att	ggc	atc	att	ttg	gat	gag	ttg	tct	gat	tct	cag	gcg	ttg	att	ggt		595	
Ile	Gly	Ile	Ile	Leu	Asp	Glu	Leu	Ser	Asp	Ser	Gln	Ala	Leu	Ile	Gly			
				155					160						165			
ttt	gct	ggt	gcg	ccg	ttt	acg	ttg	gcg	agt	tac	ttg	gtt	gag	ggt	ggt		643	
Phe	Ala	Gly	Ala	Pro	Phe	Thr	Leu	Ala	Ser	Tyr	Leu	Val	Glu	Gly	Gly			
				170					175					180				
cct	tcc	aag	aat	cat	gag	aag	acc	aaa	gca	atg	atg	cat	ggt	gat	cct		691	
Pro	Ser	Lys	Asn	His	Glu	Lys	Thr	Lys	Al									

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg 835
Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
230 235 240 245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg 883
Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
250 255 260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg 931
Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
265 270 275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg 979
Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
280 285 290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg 1027
Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
295 300 305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg 1075
Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
310 315 320 325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat 1123
Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
330 335 340

gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt 1171
Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
345 350 355

cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat 1219
Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
360 365 370

tct taaactaaga ggagtttcat gcg 1245
Ser

<210> 808

<211> 374

<212> PRT

<213> Corynebacterium glutamicum

<400> 808

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20 25 30

Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val
35 40 45

Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val
50 55 60

Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu
65 70 75 80

Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
 85 90 95
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
 100 105 110
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
 115 120 125
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
 130 135 140
 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
 145 150 155 160
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
 165 170 175
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
 180 185 190
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
 195 200 205
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
 210 215 220
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
 225 230 235 240
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
 245 250 255
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu
 260 265 270
 Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp
 275 280 285
 Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser
 290 295 300
 Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala
 305 310 315 320
 Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala
 325 330 335
 Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu
 340 345 350
 Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala
 355 360 365
 Val Ser Ile Ile His Ser
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<210> 809

<211> 681

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(658)

<223> RXN02504

<400> 809

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gacggcctga ctctggctga gcttccagaa aggcgcaaag gtg gga act tcc gct 115
 Val Gly Thr Ser Ala
 1 5

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att 163
 Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile
 10 15 20

ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc 211
 Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser
 25 30 35

ggc gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc 259
 Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val
 40 45 50

ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg 307
 Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met
 55 60 65

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac 355
 Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp
 70 75 80 85

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
 170 175 180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
 Leu Gly Asp Arg Ser

185

<210> 810

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
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Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met
 20 25 30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
 145 150 155 160

Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala
 165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
 180 185

<210> 811

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

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attgacaccg gcatgggcaa gggtcacctcc ggtgaactcg atg ctt gtg atg ctc 115
 Met Leu Val Met Leu

	1	5	
gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa			163
Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu			
	10	15	20
gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt			211
Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu			
	25	30	35
gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac			259
Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn			
	40	45	50
atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc			307
Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr			
	55	60	65
gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac			355
Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His			
	70	75	80
gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc			403
Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly			
	90	95	100
gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt			451
Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly			
	105	110	115
gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt			499
Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu			
	120	125	130
atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc			548
Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser			
	135	140	145
ccgaaatttc cat			561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

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Asp	Arg	Ala	Thr	Glu	Val	Phe	Asp	Ala	Asp	Ile	Ile	Met	Pro	Ala	Pro
		20						25					30		

Ala	Gln	Gly	Ala	Leu	Ala	Ile	Glu	Cys	Arg	Ala	Asp	Asp	Thr	Glu	Thr
		35				40						45			

Val	Arg	Ala	Leu	Asn	Met	Leu	Met	His	Ala	Asp	Thr	Phe	Val	Ser	Ala
	50					55					60				

Val	Ala	Glu	Arg	Thr	Val	Leu	Asn	Arg	Leu	Glu	Ala	Gly	Cys	Thr	Ala
65					70					75					80

<400> 813																					
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									Met	Tyr	Ile	Val	Gly	5							
									1												
att	tgt	cta	caa	tta	gtg	gtt	atg	agc	caa	ccg	atg	tca	gca	ccc	gac	163					
Ile	Cys	Leu	Gln	Leu	Val	Val	Met	Ser	Gln	Pro	Met	Ser	Ala	Pro	Asp						
						10							15	20							
tcc						gct	cca	gga	aca	gag	cgc	ggg	cat	gaa	cgc	acc	cat	ttt	gcg	gta	211
Ser						Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val	
								25							30	35					
gtc						ggg	gac	tcc	cag	gat	cca	gca	cag	gca	aca	gct	cct	aga	gcg	cca	259
Val						Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro	
							40							45	50						
gca						gaa	tca	att	act	ttg	att	ggg	att	ggg	acc	gat	ggg	ttt	gag	ggg	307
Ala						Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	Asp	Gly	Phe	Glu	Gly	
						55							60	65							
ctc						gga	ctc	aag	gca	cag	caa	gca	tta	caa	cgt	gcc	tct	gtg	gtg	att	355
Leu						Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile	
						70							75	80							
																				85	
gga						tca	tgg	cgc	cag	ctc	aat	ctc	gta	cct	gat	gcc	att	aag	gca	gag	403
Gly						Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	Ala	Ile	Lys	Ala	Glu	
								90							95	100					
cgt						cgc	cca	tgg	ccg	ggg	aat	acc	aag	cat	cct	gat	tta	gat	gcc	ttg	451
Arg						Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu	
								105							110	115					

ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat	499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp	
120 125 130	
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg	547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met	
135 140 145	
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc	595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys	
150 155 160 165	
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga	643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly	
170 175 180	
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa	691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln	
185 190 195	
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg	739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr	
200 205 210	
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc	787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser	
215 220 225	
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat	835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His	
230 235 240 245	
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc	883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg	
250 255 260	
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac	931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp	
265 270 275	
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg	979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met	
280 285 290	
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta	1027
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu	
295 300 305	
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt	1075
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val	
310 315 320 325	
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt	1123
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser	
330 335 340	
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta	1171
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val	
345 350 355	

caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc 1219
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly
 360 365 370

cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct 1267
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro
 375 380 385

gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag 1315
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys
 390 395 400 405

ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc 1363
 Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg
 410 415 420

atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act 1411
 Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr
 425 430 435

cca gaa gcg gtg aat tagcatcaaaa aaccaacccc atg 1449
 Pro Glu Ala Val Asn
 440

<210> 814

<211> 442

<212> PRT

<213> Corynebacterium glutamicum

<400> 814

Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
 1 5 10 15

Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
 20 25 30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
 325 330 335
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
 340 345 350
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
 355 360 365
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
 370 375 380
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
 385 390 395 400
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile
 405 410 415
 Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val
 420 425 430
 Thr Lys Pro Val Thr Pro Glu Ala Val Asn
 435 440

<210> 815

<211> 1345

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1345)

<223> FRXA01162

<400> 815

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Met Tyr Ile Val Gly
1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp
10 15 20

tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val
25 30 35

gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro
40 45 50

gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly
55 60 65

ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att 355
Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile
70 75 80 85

gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag 403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu
90 95 100

cgt cgc cca tgg ccg ggt aat acc aag cat cct gat gcc att aag gca gag 451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu
105 110 115

ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat 499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp
120 125 130

cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg 547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met
135 140 145

gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc 595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys
150 155 160 165

gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga 643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly
170 175 180

caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa 691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln
185 190 195

ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg 739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr

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200	205	210	
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc			787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser			
215	220	225	
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat			835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His			
230	235	240	245
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc			883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg			
	250	255	260
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
	265	270	275
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
	280	285	290
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			1027
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			
	295	300	305
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt			1075
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val			
310	315	320	325
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt			1123
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser			
	330	335	340
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta			1171
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val			
	345	350	355
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc			1219
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly			
	360	365	370
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct			1267
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro			
	375	380	385
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag			1315
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys			
390	395	400	405
ctt cac aca ctc caa gaa caa cac ggc gga			1345
Leu His Thr Leu Gln Glu Gln His Gly Gly			
	410	415	

<210> 816

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 816

Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
 1 5 10 15
 Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
 20 25 30
 Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95
 Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly

	325		330		335
Val Ser Thr	Leu Ser Val Lys Glu Thr	Leu Ser Pro Lys Thr	Leu Lys		
	340		345		350
Asp Ile Arg Tyr Val Gln Gly	Pro Glu Ser Ala Ser	Pro His Ala Ile			
	355		360		365
Phe Met Asn Lys Gly Leu Gly	Ile Asp Leu Val	Pro Glu Thr Ala Trp			
	370		375		380
Met Met Leu Arg Pro Gly Gly Lys Leu Ile	Ala Gln Ala Ser Thr Glu				
	385		390		395
Asp Asn Ile Ala Lys Leu His Thr	Leu Gln Glu Gln His Gly Gly				
	405		410		415

<210> 817

<211> 873

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(850)

<223> RXA01692

<400> 817

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gttcgggttc tggcaattgt tgggactagg attaatgccc	atg acg att tcc caa	115
	Met Thr Ile Ser Gln	
	1 5	

gaa aac cag cca ata atc cag cca gtc tcc tta att ggt gga ggt cct	163
Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu Ile Gly Gly Gly Pro	
10 15 20	

ggt gca tgg gac tta att acg gtg cgt ggg atg aat cgc ctt cag gag	211
Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met Asn Arg Leu Gln Glu	
25 30 35	

gct gat gtc att ttg gct gat cac ttg ggg ccc act gat gag ttg gaa	259
Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro Thr Asp Glu Leu Glu	
40 45 50	

aaa ttg tgc gac atc agc tcg aag act gtt gtt gat gtg tcc aag ctt	307
Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val Asp Val Ser Lys Leu	
55 60 65	

ccg tat ggg cgg cag gtc act cag gag cgt act aat gag atg ctt gtt	355
Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr Asn Glu Met Leu Val	
70 75 80 85	

gaa tac gca cag cag gga cta aag gtg gtt cgc ctt aaa ggt ggt gac	403
Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg Leu Lys Gly Gly Asp	
90 95 100	

cct tat gtc ttc ggt cgg ggt ttt gaa gag ttg gag ttt ttg ggc gag	451
Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu Glu Phe Leu Gly Glu	

105	110	115	
cat gga att gaa tgc gag gtc att ccg ggt gtg acc agt gcg gtg tcc			499
His Gly Ile Glu Cys Glu Val Ile Pro Gly Val Thr Ser Ala Val Ser			
120	125	130	
ggt cca gcg gcg gca ggt att cct att act aat cgg gga gtg gtg cat			547
Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn Arg Gly Val Val His			
135	140	145	
tcc ttt acc gtg gtg tct gga cat ttg cct cca ggc cat ccg aag tca			595
Ser Phe Thr Val Val Ser Gly His Leu Pro Pro Gly His Pro Lys Ser			
150	155	160	165
ctg gtt gat tgg gct gcg ttg gcc aaa tcg ggt ggc acc ttg tcc atc			643
Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly Gly Thr Leu Ser Ile			
170	175	180	
atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac			691
Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp			
185	190	195	
ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act			739
Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr			
200	205	210	
act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca			787
Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala			
215	220	225	
gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga			835
Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly			
230	235	240	245
caa gtt gct ggc ctc taagcagatc gcctaagaat ggg			873
Gln Val Ala Gly Leu			
250			

<210> 818

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 818

Met Thr Ile Ser Gln Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu
1 5 10 15

Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met
20 25 30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro
35 40 45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val
50 55 60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
65 70 75 80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg

<210> 819
<211> 1917
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1894)
<223> RXN00371
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<400> 819
gtcgtggaca atcccggatc gaaaatttga ttcggctttt ttcattggctg ttgatggagt 60

acgttgggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
Met Thr Ile Ala His
1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
40 45 50

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ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt	307
Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu	
55 60 65	
aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act	355
Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr	
70 75 80 85	
gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att	403
Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile	
90 95 100	
cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc	451
Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg	
105 110 115	
atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt	499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg	
120 125 130	
cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act	547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr	
135 140 145	
cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga	595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly	
150 155 160 165	
gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca	643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr	
170 175 180	
ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg	691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val	
185 190 195	
gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att	739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile	
200 205 210	
gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg	787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu	
215 220 225	
gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc	835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala	
230 235 240 245	
cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat	883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn	
250 255 260	
atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt	931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg	
265 270 275	
ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat	979
Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp	
280 285 290	

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat	1027
Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp	
295 300 305	
gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg	1075
Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp	
310 315 320 325	
cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca	1123
Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala	
330 335 340	
cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct	1171
Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser	
345 350 355	
gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc	1219
Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly	
360 365 370	
atc gtc gaa gga cgc tac cag tgg gtt gtc ctc acc agc gtc aac gca	1267
Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala	
375 380 385	
gtg aag gca gtc tgg gag aaa atc acc gaa ttc ggc ctc gat tca cgt	1315
Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg	
390 395 400 405	
tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa acc gcc gct	1363
Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala	
410 415 420	
gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct gca cgt acc	1411
Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr	
425 430 435	
agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa tat ttc gaa	1459
Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu	
440 445 450	
gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca gat atc gca	1507
Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala	
455 460 465	
acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa	1555
Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu	
470 475 480 485	
gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca agc gct gat	1603
Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp	
490 495 500	
atc cga gat atg atc aag acc ggc gga ttt gat gca gtt gcc ttc acc	1651
Ile Arg Asp Met Ile Lys Thr Gly Glu Phe Asp Ala Val Ala Phe Thr	
505 510 515	
tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac	1699
Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His	
520 525 530	
cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct	1747

Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala
 535 540 545

gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc gcc gaa gta 1795
 Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val
 550 555 560 565

cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct 1843
 Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala
 570 575 580

aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg 1891
 Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg Arg Lys Ala
 585 590 595

tct taaaagggttt ttcactaggg tgt 1917
 Ser

<210> 820

<211> 598

<212> PRT

<213> Corynebacterium glutamicum

<400> 820

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
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Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30

Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45

Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60

Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80

Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95

Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110

Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125

Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140

Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160

Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190

Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg
 305 310 315 320
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala
 325 330 335
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu
 340 345 350
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu
 355 360 365
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu
 370 375 380
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe
 385 390 395 400
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly
 405 410 415
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu
 420 425 430
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe
 435 440 445
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro
 450 455 460
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu
 465 470 475 480
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala
 485 490 495
 Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp
 500 505 510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile
515 520 525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met
530 535 540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro
545 550 555 560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val
565 570 575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg
580 585 590

Arg Arg Arg Lys Ala Ser
595

<210> 821

<211> 1024

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1024)

<223> FRXA00371

<400> 821

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acgttggctcg ttttcgagac aagtactaga aaagatatgg atg act atc gcc cat 115
Met Thr Ile Ala His
1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451

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Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg
      105                      110                      115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg
      120                      125                      130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr
      135                      140                      145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly
      150                      155                      160                      165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr
      170                      175                      180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val
      185                      190                      195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile
      200                      205                      210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu
      215                      220                      225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala
      230                      235                      240                      245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn
      250                      255                      260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg
      265                      270                      275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979
Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp
      280                      285                      290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg 1024
Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val
      295                      300                      305

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<210> 822

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

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Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
  1                      5                      10                      15

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Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val
 305

<210> 823

<211> 755

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(732)

<223> FRXA00374

<400> 823

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Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala	
1 5 10 15	
atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc	96
Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser	
20 25 30	
gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc	144
Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu	
35 40 45	
gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa	192
Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys	
50 55 60	
acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct	240
Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro	
65 70 75 80	
gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa	288
Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu	
85 90 95	
tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca	336
Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala	
100 105 110	
gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg	384
Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp	
115 120 125	
gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca	432
Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro	
130 135 140	
agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt	480
Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val	
145 150 155 160	
gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt	528
Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly	
165 170 175	
aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca	576
Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala	
180 185 190	
gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc	624
Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile	
195 200 205	
gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat	672

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggtt ttactagggt tgt 755
 Arg Lys Ala Ser

<210> 824
 <211> 244
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 824
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Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg

225 230 235 240

Arg Lys Ala Ser

<210> 825
 <211> 1467
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1444)
 <223> RXN00383

<400> 825
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 agccgtctcc atcattcatt cttaaactaa gaggagtttc atg cgt ttt gcc atc 115
 Met Arg Phe Ala Ile
 1 5
 atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20
 gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35
 ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50
 gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65
 act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85
 tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
 90 95 100
 gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
 105 110 115
 ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
 120 125 130
 cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu
 135 140 145
 ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc 595
 Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser

150	155	160	165	
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag				643
Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu	170	175	180	
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa				691
Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu	185	190	195	
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag				739
Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys	200	205	210	
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca				787
Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala	215	220	225	
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa				835
Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu	230	235	240	245
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att				883
Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile	250	255	260	
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca				931
Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala	265	270	275	
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca				979
Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala	280	285	290	
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc				1027
Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser	295	300	305	
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc				1075
Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe	310	315	320	325
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg				1123
Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala	330	335	340	
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc				1171
Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg	345	350	355	
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc				1219
Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr	360	365	370	
ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg				1267
Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val	375	380	385	
cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct				1315
Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala	390	395	400	405

acc gtt tgc gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420

gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435

gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat 1464
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445

tga 1467

<210> 826

<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 826

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Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
 20 25 30

Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45

Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60

Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80

Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95

Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110

Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140

Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160

Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu
 165 170 175

Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190

Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205


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Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210                               215                   220

Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
225                               230                   235                   240

Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
                245                               250                   255

Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
                260                               265                   270

Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
                275                               280                   285

Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
                290                               295                   300

Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
305                               310                   315                   320

Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
                325                               330                   335

Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
                340                               345                   350

Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
                355                               360                   365

Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
                370                               375                   380

Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
385                               390                   395                   400

Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
                405                               410                   415

Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
                420                               425                   430

Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
                435                               440                   445

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<210> 827

<211> 382

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(382)

<223> FRXA00376

<400> 827

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                               Met Arg Phe Ala Ile
                               1           5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
          10           15           20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
          25           30           35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
          40           45           50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
          55           60           65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
          70           75           80           85

tct cag tat ttc gcg ggc ggt gcg ctg 382
Ser Gln Tyr Phe Ala Gly Gly Ala Leu
          90

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<210> 828

<211> 94

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 828

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Met Arg Phe Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala
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Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
          20           25           30

Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
          35           40           45

Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
          50           55           60

Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
          65           70           75           80

Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
          85           90

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<210> 829

<211> 1037

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1014)

<223> FRXA00383

<400> 829

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1 5 10 15	
tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat	96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp	
20 25 30	
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat	144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp	
35 40 45	
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat	192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp	
50 55 60	
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag	240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys	
65 70 75 80	
gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc	288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg	
85 90 95	
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg	336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala	
100 105 110	
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc	384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser	
115 120 125	
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa	432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Glu	
130 135 140	
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct	480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala	
145 150 155 160	
gtg ctg ctg cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca	528
Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala	
165 170 175	
att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc	576
Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser	
180 185 190	
gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg	624
Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro	
195 200 205	
ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac	672
Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His	
210 215 220	

ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg 1008
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 ctg gga taagcaccca aaaacactat tga 1037
 Leu Gly

<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

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 20 25 30
 Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser

115					120					125					
Ala	Ile	Thr	Lys	Asp	Gly	Glu	Gly	Phe	Ala	Ile	Lys	Gly	Gly	Gly	Glu
130						135					140				
Gly	Thr	Tyr	Asp	Lys	Val	Ile	Leu	Ala	Val	Pro	Ala	Pro	Thr	Ala	Ala
145					150					155					160
Val	Leu	Leu	Arg	Asp	Leu	Ala	Pro	Ala	Ala	Ala	Pro	His	Leu	Arg	Ala
				165					170					175	
Ile	Lys	Leu	Ala	Ser	Ser	Ala	Val	Val	Gly	Met	Arg	Phe	Asp	Ser	Ser
			180					185					190		
Glu	Gly	Leu	Pro	Asp	Asn	Ser	Gly	Val	Leu	Val	Ala	Val	Asn	Glu	Pro
		195					200					205			
Gly	Ile	Thr	Ala	Lys	Ala	Phe	Thr	Phe	Ser	Ser	Lys	Lys	Trp	Pro	His
	210					215					220				
Leu	Glu	Ala	Arg	Gly	Gly	Ala	Leu	Val	Arg	Ala	Ser	Phe	Gly	Arg	Leu
225					230					235					240
Gly	Asp	Glu	Ala	Ser	Ala	Arg	Met	Asp	Glu	Asp	Leu	Leu	Val	Asp	Ala
				245					250					255	
Ala	Leu	Asp	Asp	Leu	Leu	Thr	Ile	Thr	Gly	Phe	Asp	Gly	Arg	Ala	Ala
			260					265					270		
Gly	Leu	Gly	Glu	Ile	Phe	Val	Gln	Arg	Trp	Phe	Gly	Gly	Leu	Pro	Ala
		275					280					285			
Tyr	Gly	Val	Asp	His	Ile	Ala	Thr	Val	Ser	Ala	Ala	Arg	Ala	Glu	Ile
	290					295					300				
Ala	Ala	Val	Pro	Gly	Val	Glu	Ala	Ile	Gly	Ala	Trp	Ala	Gly	Gly	Val
305					310					315					320
Gly	Val	Pro	Ala	Val	Ile	Ala	Asp	Ala	Gln	Ala	Ala	Val	His	Arg	Leu
				325					330					335	

Leu Gly

<210> 831
 <211> 873
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(850)
 <223> RXA01253

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 Met Thr Thr Leu Asn
 1 5

atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc	163
Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly	
10 15 20	
aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct	211
Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala	
25 30 35	
gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat	259
Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp	
40 45 50	
ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc	307
Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr	
55 60 65	
gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc	355
Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly	
70 75 80 85	
cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc	403
Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser	
90 95 100	
ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc	451
Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala	
105 110 115	
acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca	499
Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr	
120 125 130	
cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc	547
Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly	
135 140 145	
ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca	595
Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro	
150 155 160 165	
ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc	643
Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala	
170 175 180	
tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc	691
Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val	
185 190 195	
caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga	739
Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg	
200 205 210	
aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg	787
Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala	
215 220 225	
ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc	835
Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg	
230 235 240 245	

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 Ala Glu Arg Leu Ala
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873

<210> 832

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 832

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Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met
 20 25 30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe
 180 185 190

Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly
 195 200 205

Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys
 210 215 220

Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val
 225 230 235 240

Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala
 245 250

<210> 833

<211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1021)
 <223> RXA02134

<400> 833

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ccgaagcgcc cgagcaaac acggagtaac tttctaagcg atg tcc ggc aaa gca 115
                                   Met Ser Gly Lys Ala
                                   1 5

ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163
Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn
                                   10 15 20

ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211
Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu
                                   25 30 35

ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259
Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val
                                   40 45 50

atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307
Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala
                                   55 60 65

atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355
Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp
                                   70 75 80 85

gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403
Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn
                                   90 95 100

cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451
Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly
                                   105 110 115

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
                                   120 125 130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
                                   135 140 145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
                                   150 155 160 165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
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aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691

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Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
 185 190 195
 gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
 200 205 210
 gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
 215 220 225
 acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
 230 235 240 245
 aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
 250 255 260
 tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
 265 270 275
 gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
 280 285 290
 att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg 1021
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
 295 300 305
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<210> 834

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 834

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 20 25 30

Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45

Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60

Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80

Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95

Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110

Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
115 120 125

Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
130 135 140

Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
145 150 155 160

Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
165 170 175

Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
180 185 190

Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
195 200 205

Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
210 215 220

Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
225 230 235 240

Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
245 250 255

Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
260 265 270

Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
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His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
290 295 300

Ala Met Val
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<210> 835

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

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aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
Met Val Pro Ala Glu
1 5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
10 15 20

aag Lys	gat Asp	ttc Phe	cat His	gac Asp	tcc Ser	ctc Leu	acc Thr	aag Lys	cca Pro	ccc Pro	gga Gly	tct Ser	ttg Leu	ggc Gly	aag Lys	211
			25				30				35					
ttg Leu	gag Glu	cag Gln	atc Ile	ggc Gly	tgt Cys	ttc Phe	att Ile	tcc Ser	gca Ala	tgc Cys	cag Gln	ggc Gly	cag Gln	att Ile	ccg Pro	259
			40				45				50					
cca Pro	cgt Arg	cca Pro	ctc Leu	aac Asn	aac Asn	tca Ser	aag Lys	atc Ile	gtt Val	gtt Val	ttc Phe	gct Ala	ggc Gly	gat Asp	cac His	307
			55				60				65					
ggc Gly	gtt Val	gca Ala	act Thr	aaa Lys	ggc Gly	gtg Val	tcc Ser	gcg Ala	tac Tyr	cca Pro	tcc Ser	tca Ser	gta Val	agc Ser	ttg Leu	355
			70				75				80				85	
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			90				95				100					
gca Ala	cgc Arg	acc Thr	acc Thr	ggc Gly	acg Thr	tcc Ser	gtc Val	cga Arg	ctt Leu	att Ile	gat Asp	acc Thr	tcc Ser	ctc Leu	gac Asp	451
			105				110				115					
cac His	gaa Glu	gca Ala	tgg Trp	ggc Gly	gac Asp	gag Glu	cgc Arg	gta Val	tct Ser	agg Arg	tcc Ser	tgc Cys	gga Gly	tcc Ser	atc Ile	499
			120				125				130					
gat Asp	gtt Val	gaa Glu	gac Asp	gcc Ala	atg Met	acc Thr	caa Gln	gaa Glu	cag Gln	gtc Val	gaa Glu	cgc Arg	gca Ala	ctg Leu	aag Lys	547
			135				140				145					
atc Ile	ggc Gly	aag Lys	cgc Arg	att Ile	gcg Ala	gat Asp	caa Gln	gaa Glu	gtg Val	gac Asp	gca Ala	ggc Gly	gcc Ala	gac Asp	att Ile	595
			150				155				160				165	
tta Leu	atc Ile	ccc Pro	ggc Gly	gat Asp	tta Leu	gga Gly	att Ile	ggc Gly	aac Asn	acc Thr	acc Thr	acc Thr	gcc Ala	gct Ala	gcc Ala	643
			170				175				180					
ctc Leu	gtt Val	gga Gly	acg Thr	ttc Phe	acc Thr	ctc Leu	gca Ala	gag Glu	cct Pro	gtt Val	gtt Val	gtc Val	gta Val	ggc Gly	cgc Arg	691
			185				190				195					
ggc Gly	acc Thr	gga Gly	atc Ile	gac Asp	gat Asp	gaa Glu	gcc Ala	tgg Trp	aaa Lys	ctc Leu	aaa Lys	gtc Val	tcc Ser	gcg Ala	atc Ile	739
			200				205				210					
cgc Arg	gac Asp	gcc Ala	atg Met	ttc Phe	cgc Arg	gcc Ala	cgc Arg	gac Asp	ctg Leu	cgc Arg	caa Gln	gac Asp	ccc Pro	atc Ile	gcc Ala	787
			215				220				225					
atc Ile	gcc Ala	cgg Arg	aaa Lys	atc Ile	tct Ser	tcc Ser	cca Pro	gac Asp	ctt Leu	gca Ala	gcc Ala	atg Met	gca Ala	gca Ala	ttc Phe	835
			230				235				240				245	
att Ile	gcc Ala	caa Gln	gca Ala	gca Ala	gtt Val	cga Arg	cgc Arg	acc Thr	ccc Pro	gtg Val	ctt Leu	ctc Leu	gac Asp	ggc Gly	gtt Val	883
			250				255				260					
gta Gly	gtc Glu	acc Glu	gcc Glu	gca Glu	gcc Glu	ctc Glu	cta Glu	gcc Glu	aac Glu	aaa Glu	ctg Glu	gcc Glu	cca Glu	ggc Glu	gcc Glu	931

Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala
 265 270 275

agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc 979
 Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
 280 285 290

gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg 1027
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
 295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag 1075
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
 310 315 320 325

att gcc gtt gac ctg atg aac gac atg tgc aca ttt tct tcc gcc ggc 1123
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
 330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg 1171
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
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gag taactttcta agcgatgtcc ggc 1197
 Glu

<210> 836

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

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 20 25 30

Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
 340 345 350
 Pro Glu Gln Asn Thr Glu
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<210> 837

<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA02136

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 Met Arg Thr Leu Val
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ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163

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      20             25             30
Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His
      35             40             45

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Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val
 50 55 60

Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp
 65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu
 85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala
 100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val
 115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp
 130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val
 145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe
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<210> 839

<211> 575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(552)

<223> RXN03114

<400> 839

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 Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15

cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta 96
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30

agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac 144
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
 35 40 45

att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat 192
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60

gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg 240
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80

gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct 288
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95

gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc 336

Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575
 Pro Leu Leu Glu Ser Pro Ala Leu
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<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
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 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
 35 40 45
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser

165

170

175

Pro Leu Leu Glu Ser Pro Ala Leu
180

<210> 841

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXN01810

<400> 841

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                                     Met Asn Asn Ala Phe
                                     1 5

cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
                10                15                20

gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
                25                30                35

att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
                40                45                50

aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr
                55                60                65

gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc 355
Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly
                70                75                80                85

aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc 403
Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu
                90                95                100

tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat 451
Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn
                105                110                115

att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att 499
Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile
                120                125                130

gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt 547
Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu
                135                140                145

aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc 595
Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg

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150	155	160	165	
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg				643
Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met				
	170	175	180	
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc				691
Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile				
	185	190	195	
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt				739
Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg				
	200	205	210	
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc				787
Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr				
	215	220	225	
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt				835
Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly				
	230	235	240	245
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att				883
Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile				
	250	255	260	
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat				931
Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp				
	265	270	275	
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc				979
Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val				
	280	285	290	
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt				1027
Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly				
	295	300	305	
ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa				1075
Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln				
	310	315	320	325
cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa				1123
Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln				
	330	335	340	
act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc				1171
Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly				
	345	350	355	
ggc gag tagatggttg tgaaggaggt tga				1200
Gly Glu				

<210> 842

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 842

Met Asn Asn Ala Phe Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala
 1 5 10 15
 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser
 20 25 30
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr
 35 40 45
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp
 50 55 60
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu
 65 70 75 80
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile
 85 90 95
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu
 100 105 110
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro
 115 120 125
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn
 130 135 140
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His
 145 150 155 160
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val
 165 170 175
 Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp
 180 185 190
 Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu
 195 200 205
 Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val
 210 215 220
 Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr
 225 230 235 240
 Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly
 245 250 255
 Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu
 260 265 270
 Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu
 275 280 285
 Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr
 290 295 300
 Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr
 305 310 315 320
 Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu

325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Arg Ala Ser Arg Glu
340 345 350

Leu Tyr Val Gln Gly Gly Glu
355

<210> 843
<211> 963
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(933)
<223> RXS03205

<400> 843

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg	48
Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro	
1 5 10 15	
gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccggtttt 963
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 844

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 845

<211> 956

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> FRXA00306

<400> 845

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 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

48

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 846

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 847
 <211> 819
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(796)
 <223> RXC01715

<400> 847
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 ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115
 Val Ser Glu Leu Asp
 1 5
 att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
 Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
 10 15 20
 cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
 Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
 25 30 35
 caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
 Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
 40 45 50
 gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
 Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
 55 60 65
 atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
 Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
 70 75 80 85
 gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
 Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe

	90	95	100	
tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac				451
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His				
	105	110	115	
ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt				499
Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val				
	120	125	130	
tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag				547
Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys				
	135	140	145	
cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca				595
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro				
	150	155	160	165
gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa				643
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu				
	170	175	180	
tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg				691
Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu				
	185	190	195	
atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag				739
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu				
	200	205	210	
ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag				787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys				
	215	220	225	
ggt ctt cct taaaagctgc ttttctaaac gat				819
Val Leu Pro				
230				
<210> 848				
<211> 232				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 848				
Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser				
1 5 10 15				
Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg				
20 25 30				
Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala				
35 40 45				
Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg				
50 55 60				
Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp				
65 70 75 80				
Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln				

85										90					95				
Val	Ser	Glu	Val	Phe	Trp	Ile	Gly	Asn	Ala	Leu	His	Arg	Pro	Ser	Glu				
			100					105					110						
Phe	Asn	Lys	Ala	His	Leu	Pro	Ser	Phe	Ile	Met	Gly	Glu	Glu	Ala	Lys				
		115					120					125							
Asp	Trp	Ile	Thr	Val	Tyr	Pro	Phe	Val	Arg	Ser	Tyr	Asp	Trp	Tyr	Ile				
		130					135				140								
Met	Glu	Pro	Leu	Lys	Arg	Ser	Arg	Ile	Leu	Arg	Glu	His	Gly	Gln	Ala				
145					150					155					160				
Ala	Val	Glu	Phe	Pro	Asp	Val	Arg	Ala	Asn	Thr	Val	Pro	Ala	Phe	Ala				
				165					170					175					
Leu	Gly	Asp	Tyr	Glu	Trp	Val	Leu	Ala	Phe	Glu	Ala	Asp	Glu	Leu	His				
			180					185					190						
Arg	Ile	Val	Asp	Leu	Met	His	Lys	Met	Arg	Tyr	Thr	Glu	Ala	Arg	Leu				
		195					200					205							
His	Val	Arg	Glu	Glu	Leu	Pro	Phe	Ile	Ser	Gly	Gln	Arg	Val	Asp	Ile				
		210				215					220								
Ala	Asp	Leu	Ile	Lys	Val	Leu	Pro												
225						230													

<210> 849

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00420

<400> 849

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ttcaccacct	gaaaattttc	gggggtaacc	tttaaaggcg	atg	aac	agt	tct	cac	115
				Met	Asn	Ser	Ser	His	
				1				5	

ggc	acg	tcc	agc	tcc	ggc	gct	tcg	gcc	ggt	gcc	cac	gga	gcc	ctt	ccc	163
Gly	Thr	Ser	Ser	Ser	Gly	Ala	Ser	Ala	Gly	Ala	His	Gly	Ala	Leu	Pro	
				10					15					20		

cta	gaa	gct	cag	aaa	ctg	aac	ggt	tgg	ggc	cgc	aca	gcc	ccc	acc	acc	211
Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	Thr	Ala	Pro	Thr	Thr	
			25					30					35			

gct	gag	gta	ctt	acc	acc	cca	gac	cta	gac	atc	att	gtg	gat	gca	gtc	259
Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	Ile	Val	Asp	Ala	Val	
		40					45					50				

cgc	caa	gtc	gct	gaa	caa	aac	gac	tcc	aag	ccg	gac	tac	ctc	aag	cgc	307
Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	Asp	Tyr	Leu	Lys	Arg	

55	60	65	
ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa			355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln			
70	75	80	85
aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac			403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His			
	90	95	100
tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc			451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr			
	105	110	115
ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct			499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro			
	120	125	130
gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca			547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro			
	135	140	145
gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac			595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His			
150	155	160	165
gtg gtc tcc atg gaa ctc ctc gtt gca gac gga cgc atc ctg cac ctc			643
Val Val Ser Met Glu Leu Leu Val Ala Asp Gly Arg Ile Leu His Leu			
	170	175	180
gag cca gaa ggc acc gcc gaa gac cca cag ggc gac ctg ttc tgg gca			691
Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly Asp Leu Phe Trp Ala			
	185	190	195
acc gtt ggt ggc atg ggc ctg acc ggc atc atc gtc cgt gca cgc atc			739
Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile Val Arg Ala Arg Ile			
	200	205	210
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc			787
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg			
	215	220	225
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag			835
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu			
	230	235	240
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag			883
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu			
	250	255	260
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt			931
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu			
	265	270	275
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag			979
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys			
	280	285	290
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg			1027
Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp			
	295	300	305

act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc 1075
 Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala
 310 315 320 325

atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac 1123
 Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr
 330 335 340

caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag 1171
 Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys
 345 350 355

ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct 1219
 Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro
 360 365 370

ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca 1267
 Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala
 375 380 385

ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc 1315
 Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser
 390 395 400 405

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca 1363
 Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
 410 415 420

ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc 1411
 Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
 425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac 1459
 Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
 440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat 1507
 Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
 455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt 1555
 Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
 470 475 480 485

gag ctt tct taagaaaggg cttgaactaa aca 1587
 Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
 1 5 10 15

His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
 20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
 35 40 45
 Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
 50 55 60
 Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
 65 70 75 80
 Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
 85 90 95
 Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
 100 105 110
 Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
 115 120 125
 Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350

Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp
 450 455 460
 Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp
 465 470 475 480
 Met Ser Arg Arg Leu Glu Leu Ser
 485

<210> 851

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> FRXA00420

<400> 851

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Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr	
1 5 10 15	
gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc	96
Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe	
20 25 30	
tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc	144
Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser	
35 40 45	
aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag	192
Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu	
50 55 60	
cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc	240
Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser	
65 70 75 80	
gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg	288
Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu	

	85	90	95	
tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc				336
Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg				
	100	105	110	
cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa				384
Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu				
	115	120	125	
ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag				432
Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu				
	130	135	140	
aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga				480
Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg				
	145	150	155	160
aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga				528
Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg				
	165	170	175	
ctt gag ctt tct taagaaaggg cttgaactaa aca				563
Leu Glu Leu Ser				
	180			
<210> 852				
<211> 180				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 852				
Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr				
1 5 10 15				
Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe				
20 25 30				
Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser				
35 40 45				
Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu				
50 55 60				
Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser				
65 70 75 80				
Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu				
85 90 95				
Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg				
100 105 110				
Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu				
115 120 125				
Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu				
130 135 140				
Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg				

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
 Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
 150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622
 Val Val Ser Met Glu Leu Leu Val Ala
 170

<210> 854

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 854

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
 1 5 10 15

His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
 20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
 35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
 50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
 65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
 85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
 100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
 115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140

Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160

Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala
 165 170

<210> 855

<211> 930

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(907)

<223> RXN00708

<400> 855

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taccgatccc	cttccctgaa	gtttcgctaa	cctggcgtac	atg	act	ctt	tcc	ctt	115							
				Met	Thr	Leu	Ser	Leu								
				1				5								
cct	cca	att	ggt	ttc	ggc	acc	gtt	cat	ctt	gat	ggc	gca	cct	ggc	gtt	163
Pro	Pro	Ile	Gly	Phe	Gly	Thr	Val	His	Leu	Asp	Gly	Ala	Pro	Gly	Val	
			10					15						20		
gaa	gcc	atc	gct	act	gcc	att	gat	gct	ggt	tac	cgc	ctc	atc	gac	acc	211
Glu	Ala	Ile	Ala	Thr	Ala	Ile	Asp	Ala	Gly	Tyr	Arg	Leu	Ile	Asp	Thr	
			25					30					35			
gcg	tac	aac	tat	gaa	aat	gaa	ggt	acc	gtg	ggc	aag	gct	gtc	cgc	gag	259
Ala	Tyr	Asn	Tyr	Glu	Asn	Glu	Gly	Thr	Val	Gly	Lys	Ala	Val	Arg	Glu	
		40					45					50				
tcg	ggt	gtc	ccc	cgc	gag	gaa	ttg	att	gtt	acc	agt	aag	ctc	cct	ggc	307
Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly	
	55					60					65					
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	
	70				75				80						85	
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	
				90				95						100		
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	
			105				110						115			
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu	
		120					125					130				
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	547
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	
		135				140					145					
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	
	150				155					160					165	
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	
			170					175						180		
agc	aac	ggt	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	
			185				190						195			
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739
Glu	Arg	T														

cgc agc aac ttg gag gcg gta aag att tcg ctt atc gac gaa gac gtc 835
 Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu Ile Asp Glu Asp Val
 230 235 240 245
 cag gcg att acc gct ttg gcg cgc aaa aac ggc cgg atc aaa gat caa 883
 Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly Arg Ile Lys Asp Gln
 250 255 260
 gat cca gcc gtc tat gaa gaa ttc tagatagtta catcaagggtt ccg 930
 Asp Pro Ala Val Tyr Glu Glu Phe
 265

<210> 856

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp
 1 5 10 15
 Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
 20 25 30
 Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
 35 40 45
 Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
 50 55 60
 Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
 65 70 75 80
 Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
 85 90 95
 Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
 100 105 110
 Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
 115 120 125
 Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
 130 135 140
 Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
 145 150 155 160
 Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
 165 170 175
 Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
 180 185 190
 Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
 195 200 205
 Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
 210 215 220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
225 230 235 240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
245 250 255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
260 265

<210> 857

<211> 695

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(672)

<223> FRXA00708

<400> 857

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Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
1 5 10 15

att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga 96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
20 25 30

cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc 144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
35 40 45

gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc 192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
50 55 60

gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag 240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
65 70 75 80

cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc 288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
85 90 95

cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc 336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
100 105 110

tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc 384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
115 120 125

att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa 432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
130 135 140

gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc 480
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 ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg
 280 285 290
 aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag 1025
 Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu Asn
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 gtaaggccct gca 1038

<210> 860

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 860

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Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser
 20 25 30

Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile
 35 40 45


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Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
  50                      55                      60

Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
  65                      70                      75                      80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
                      85                      90                      95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
                100                      105                      110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
                115                      120                      125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro
  130                      135                      140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly
  145                      150                      155                      160

Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
                165                      170                      175

Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
                180                      185                      190

Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
                195                      200                      205

Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
  210                      215                      220

Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Ala Lys Asn His
  225                      230                      235                      240

Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly
                245                      250                      255

Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn
                260                      265                      270

Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile
                275                      280                      285

Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu
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Asn
305

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<210> 861

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1660)

<223> RXS00389

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Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro	
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aat	atc	acg	gca	atc	ggc	ttt	acc	ggc	tca	cgc	cag	ggc	ggc	ttg	gca	835
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala	
230					235					240					245	
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala	
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gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala	
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gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val	
		280					285					290				
acc	ggc	agt	tcc	ggg	caa	ttg	tgc	acc	aag	cct	ggc	ctc	gtt	ttc	atc	1027
Thr	Gly	Ser	Ser	Gly	Gln	Leu	Cys	Thr	Lys	Pro	Gly	Leu	Val	Phe	Ile	
	295					300					305					
ccg	cgc	ggc	gtt	gtt	ggc	gat	gct	ttt	gtg	gcg	ctc	gta	gca	gcc	aaa	1075
Pro	Arg	Gly	Val	Val	Gly	Asp	Ala	Phe	Val	Ala	Leu	Val	Ala	Ala	Lys	
310					315					320					325	
ttt	aaa	gaa	acc	acg	ggc	caa	acg	atg	ctc	acg	caa	ggc	atc	gct	cag	1123
Phe	Lys	Glu	Thr	Thr	Gly	Gln	Thr	Met	Leu	Thr	Gln	Gly	Ile	Ala	Gln	
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gca	tgg	cag	cgc	gga	gtc	gac	aac	ctt	gca	gca	cag	cca	agt	gta	aaa	1171
Ala	Trp	Gln	Arg	Gly	Val	Asp	Asn	Leu	Ala	Ala	Gln	Pro	Ser	Val	Lys	
			345					350					355			
atc	ctc	gcc	caa	ggc	acc	ccc	gga	gat	gga	gag	aac	gcg	ccg	ggc	ccg	1219
Ile	Leu	Ala	Gln	Gly	Thr	Pro	Gly	Asp	Gly	Glu	Asn	Ala	Pro	Gly	Pro	
		360					365					370				
gtg	gtg	ttt	gaa	agt	gat	gtg	cag	gcg	ttg	cta	aat	aat	gtg	gtg	ttg	1267
Val	Val	Phe	Glu	Ser	Asp	Val	Gln	Ala	Leu	Leu	Asn	Asn	Val	Val	Leu	
	375					380					385					
cag	gaa	gaa	atc	ttc	ggc	gcg	gca	tcg	ctg	gtg	gtg	cgt	tat	gat	tcc	1315
Gln	Glu	Glu	Ile	Phe	Gly	Ala	Ala	Ser	Leu	Val	Val	Arg	Tyr	Asp	Ser	
390					395					400					405	
ccg	gat	caa	ctc	cac	caa	gta	gcc	aat	tca	ctc	gag	gga	caa	tta	aca	1363
Pro	Asp	Gln	Leu	His	Gln	Val	Ala	Asn	Ser	Leu	Glu	Gly	Gln	Leu	Thr	
				410					415					420		
gcc	acg	atc	cac	gca	tcc	cag	gat	gat	ttc	cag	gaa	gtc	tcg	aaa	ctt	1411
Ala	Thr	Ile	His	Ala	Ser</											

455 460 465
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 Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile
 470 475 480 485

 gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg 1603
 Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
 490 495 500

 ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa 1651
 Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
 505 510 515

 ata gac cgt taatagctgg tctttacatt tgc 1683
 Ile Asp Arg
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 <211> 520
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 862
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 Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr
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 Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
 35 40 45

 Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
 50 55 60

 Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
 65 70 75 80

 Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
 85 90 95

 Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
 100 105 110

 Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
 115 120 125

 Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
 130 135 140

 Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
 145 150 155 160

 Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
 165 170 175

 Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
 180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
 195 200 205
 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
 485 490 495
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp
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 Ala Val Pro Arg Glu Ile Asp Arg

520

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<222> (101)..(859)  
<223> RXS00419
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Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly
 170 175 180

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
 185 190 195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
 200 205 210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
 230 235 240 245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882
 Ala Ile Phe Arg Lys Leu Pro Phe
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<210> 864
 <211> 253
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 864
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Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly
 20 25 30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
 50 55 60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala

165								170				175			
Leu	Arg	Gly	Ser	Gly	Ala	Asn	Val	Leu	Val	Val	Arg	Pro	Gly	Gln	Val
			180										190		
Arg	Thr	Lys	Met	Ser	Ala	Asp	Gly	Gly	Glu	Ala	Pro	Leu	Thr	Val	Asn
			195				200						205		
Arg	Glu	Asp	Val	Ala	Asp	Ala	Val	Tyr	Asp	Ala	Val	Val	Asn	Lys	Lys
			210				215						220		
Asp	Ile	Ile	Phe	Val	His	Pro	Leu	Phe	Gln	Tyr	Val	Ser	Phe	Ala	Phe
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Gln	Phe	Ile	Pro	Arg	Ala	Ile	Phe	Arg	Lys	Leu	Pro	Phe			
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<211> 1673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1650)

<223> RXC00416

<400> 865

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Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala

1

5

10

15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp

20

25

30

cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly

35

40

45

ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga 192

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly

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55

60

tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt 240

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly

65

70

75

80

tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala

85

90

95

tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg 336

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val

100

105

110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat 384

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn

115

120

125

tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg	432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	
130 135 140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc	480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala	
145 150 155 160	
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc	528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe	
165 170 175	
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg	576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala	
180 185 190	
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg	624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu	
195 200 205	
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt	672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu	
210 215 220	
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac	720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His	
225 230 235 240	
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca	768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser	
245 250 255	
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg	816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val	
260 265 270	
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg	864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val	
275 280 285	
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac	912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn	
290 295 300	
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc	960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala	
305 310 315 320	
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat	1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr	
325 330 335	
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc	1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr	
340 345 350	
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa	1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln	
355 360 365	
gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat	1152

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Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370                               375                               380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca 1200
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385                               390                               395                               400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag 1248
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
405                               410                               415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac 1296
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
420                               425                               430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg 1344
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
435                               440                               445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc 1392
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
450                               455                               460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg 1440
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465                               470                               475                               480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc 1488
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
485                               490                               495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg 1536
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
500                               505                               510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg 1584
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
515                               520                               525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg 1632
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
530                               535                               540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa 1673
Val Val Thr His Asn Glu
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<210> 866

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 866

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Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
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Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20                               25                               30

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Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly

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35					40					45					
Leu	Ser	Asp	Met	Asn	Tyr	Ile	Asp	Met	Pro	Thr	Phe	Tyr	Pro	Ala	Gly
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Trp	Phe	Trp	Leu	Gly	Gly	Arg	Leu	Ala	Asn	Leu	Leu	Gly	Leu	Pro	Gly
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Trp	Glu	Ala	Phe	Gln	Pro	Trp	Ala	Ile	Val	Ser	Met	Ala	Val	Ala	Ala
				85					90					95	
Ser	Val	Leu	Val	Pro	Val	Trp	Gln	Arg	Ile	Thr	Gly	Ser	Leu	Pro	Val
			100					105					110		
Ala	Thr	Gly	Ile	Ala	Leu	Val	Thr	Thr	Cys	Ile	Ile	Leu	Ala	Met	Asn
		115					120					125			
Ser	Glu	Glu	Pro	Tyr	Ala	Ala	Ile	Val	Ala	Met	Gly	Ile	Pro	Ala	Met
	130					135					140				
Leu	Val	Leu	Ala	Ser	Arg	Ile	Ala	Lys	Gly	Asp	Lys	Phe	Ala	Leu	Ala
145					150					155					160
Gly	Gly	Ile	Ile	Tyr	Leu	Gly	Val	Ser	Ala	Thr	Phe	Tyr	Thr	Leu	Phe
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Thr	Gly	Ala	Ile	Ala	Leu	Ser	Ala	Val	Ala	Val	Cys	Ile	Val	Val	Ala
			180					185					190		
Ala	Ile	Val	Gln	Arg	Ser	Ile	Lys	Pro	Leu	Leu	Trp	Leu	Ala	Val	Leu
		195					200					205			
Gly	Gly	Gly	Ser	Ile	Val	Ile	Ala	Leu	Ile	Ser	Trp	Gly	Pro	Tyr	Leu
	210					215					220				
Leu	Ala	Ser	Ile	Asn	Gly	Ala	Glu	Arg	Ser	Gly	Asp	Ser	Ala	Thr	His
225				230						235					240
Tyr	Leu	Pro	Leu	Glu	Gly	Thr	Gln	Phe	Pro	Val	Pro	Phe	Leu	Ala	Ser
			245					250					255		
Ser	Val	Val	Gly	Leu	Leu	Cys	Leu	Val	Gly	Leu	Ile	Tyr	Leu	Val	Val
			260				265					270			
Arg	Phe	His	Asn	Asn	Glu	Val	Arg	Ala	Met	Trp	Val	Gly	Ile	Ala	Val
		275					280					285			
Phe	Tyr	Ala	Trp	Met	Gly	Met	Ser	Met	Ala	Ile	Thr	Leu	Leu	Gly	Asn
	290					295					300				
Thr	Leu	Leu	Gly	Phe	Arg	Leu	Asp	Thr	Val	Leu	Val	Leu	Ile	Phe	Ala
305					310					315					320
Thr	Ala	Gly	Val	Leu	Gly	Ile	Ala	Asp	Phe	Arg	Leu	Ala	Ser	Val	Tyr
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Gln	Leu	Tyr	Pro	Thr	Gln	Ile	Thr	Glu	Arg	Thr	Ala	Thr	His	Leu	Thr
			340					345					350		
Asn	Leu	Ile	Val	Val	Leu	Val	Leu	Leu	Gly	Gly	Leu	Tyr	Tyr	Ala	Gln
		355					360					365			

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Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370                               375                               380

Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385                               390                               395                               400

Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
                               405                               410                               415

Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
                               420                               425                               430

Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
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Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
                               450                               455                               460

Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465                               470                               475                               480

Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
                               485                               490                               495

Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
                               500                               505                               510

Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
                               515                               520                               525

Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
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Val Val Thr His Asn Glu
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<210> 867

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXC02206

<400> 867

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accttatgac ctcaagtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt      115
                               Met Val Gly Ser Ser
                               1                               5

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ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg      163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                               10                               15                               20

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ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat      211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn

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25										30					35					
tct	ggt	ggc	acg	ctt	atc	gac	gtc	tcc	ccc	aac	tac	acc	acc	ggc	gtc	259				
Ser	Gly	Gly	Thr	Leu	Ile	Asp	Val	Ser	Pro	Asn	Tyr	Thr	Thr	Gly	Val					
40						45			50											
gcg	gaa	gaa	atg	ctc	ggc	acg	atg	ttg	gat	gcg	gaa	gtc	tct	cgt	tcg	307				
Ala	Glu	Glu	Met	Leu	Gly	Thr	Met	Leu	Asp	Ala	Glu	Val	Ser	Arg	Ser					
55						60			65											
gct	gtc	gtc	att	tcc	tcc	agc	gca	ggg	gtc	aac	ccc	gct	ctg	ccg	ctc	355				
Ala	Val	Val	Ile	Ser	Ser	Ser	Ala	Gly	Val	Asn	Pro	Ala	Leu	Pro	Leu					
70						75			80			85								
ggc	cga	cgt	gtg	gat	tgc	tcc	cgc	cgc	aat	ttg	att	gcc	caa	tta	gat	403				
Gly	Arg	Arg	Val	Asp	Cys	Ser	Arg	Arg	Asn	Leu	Ile	Ala	Gln	Leu	Asp					
			90						95			100								
gtc	acc	ctg	cgg	gca	tta	aac	act	gac	tat	ttg	gat	ttg	tgg	tct	gtg	451				
Val	Thr	Leu	Arg	Ala	Leu	Asn	Thr	Asp	Tyr	Leu	Asp	Leu	Trp	Ser	Val					
			105						110			115								
ggc	tat	tgg	gat	gag	ggc	acc	cca	ccg	cat	gag	gtg	gcc	gat	act	ttg	499				
Gly	Tyr	Trp	Asp	Glu	Gly	Thr	Pro	Pro	His	Glu	Val	Ala	Asp	Thr	Leu					
120						125						130								
gat	tac	gcc	gtg	cgc	acc	ggc	cga	gtc	cga	tat	gcc	ggg	gtc	cga	gga	547				
Asp	Tyr	Ala	Val	Arg	Thr	Gly	Arg	Val	Arg	Tyr	Ala	Gly	Val	Arg	Gly					
135						140			145											
tat	tcc	ggt	tgg	cag	tta	gcg	gtc	acc	cac	gct	gca	tcc	aat	cat	gca	595				
Tyr	Ser	Gly	Trp	Gln	Leu	Ala	Val	Thr	His	Ala	Ala	Ser	Asn	His	Ala					
150			155						160			165								
gcg	gcc	tcc	gcc	cgc	ccc	gtg	gtc	gtt	gca	caa	aat	gaa	tac	agc	ctg	643				
Ala	Ala	Ser	Ala	Arg	Pro	Val	Val	Val	Ala	Gln	Asn	Glu	Tyr	Ser	Leu					
			170						175			180								
ctg	gaa	cgc	cgc	gca	gaa	caa	gaa	ctc	ctc	cct	gcc	acc	caa	cac	cta	691				
Leu	Glu	Arg	Arg	Ala	Glu	Gln	Glu	Leu	Leu	Pro	Ala	Thr	Gln	His	Leu					
			185			190						195								
ggg	gtc	gga	ttc	ttt	gct	ggc	gct	ccg	ctg	ggg	caa	ggc	gtg	ctg	act	739				
Gly	Val	Gly	Phe	Phe	Ala	Gly	Ala	Pro	Leu	Gly	Gln	Gly	Val	Leu	Thr					
200						205						210								
gct	aaa	tac	cgc	tcc	gaa	att	ccc	cat	gat	tcc	aga	gct	gca	tcc	aca	787				
Ala	Lys	Tyr	Arg	Ser	Glu	Ile	Pro	His	Asp	Ser	Arg	Ala	Ala	Ser	Thr					
215						220			225											
gga	cgc	gac	gca	gaa	gtc	caa	agc	tac	cta	gat	aat	cga	ggc	cgc	atc	835				
Gly	Arg	Asp	Ala	Glu	Val	Gln	Ser	Tyr	Leu	Asp	Asn	Arg	Gly	Arg	Ile					
230			235						240			245								
att	gtc	gat	gct	ctt	gat	act	gca	gcc	aaa	gga	tta	ggc	att	agc	ccc	883				
Ile	Val	Asp	Ala	Leu	Asp	Thr	Ala	Ala	Lys	Gly	Leu	Gly	Ile	Ser	Pro					
			250						255			260								
gct	gtc	aca	gcc	acc	acc	tgg	gtg	cgt	gat	cgt	ccc	gga	gtg	aca	gct	931				
Ala	Val	Thr	Ala	Thr	Thr	Trp	Val	Arg	Asp	Arg	Pro	Gly	Val	Thr	Ala					
			265			270						275								

gct gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act
 Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr

<210> 868
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 868																
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Ser	Thr	Trp	Gly	Ser	Gly	Thr	Glu	Leu	Ala	Glu	Ala	Gly	Asp	Ile	Phe	
			20					25					30			
Lys	Ala	Phe	Ile	Asn	Ser	Gly	Gly	Thr	Leu	Ile	Asp	Val	Ser	Pro	Asn	
		35					40					45				
Tyr	Thr	Thr	Gly	Val	Ala	Glu	Glu	Met	Leu	Gly	Thr	Met	Leu	Asp	Ala	
	50					55					60					
Glu	Val	Ser	Arg	Ser	Ala	Val	Val	Ile	Ser	Ser	Ser	Ala	Gly	Val	Asn	
65					70					75					80	
Pro	Ala	Leu	Pro	Leu	Gly	Arg	Arg	Val	Asp	Cys	Ser	Arg	Arg	Asn	Leu	
				85					90					95		
Ile	Ala	Gln	Leu	Asp	Val	Thr	Leu	Arg	Ala	Leu	Asn	Thr	Asp	Tyr	Leu	
			100					105					110			
Asp	Leu	Trp	Ser	Val	Gly	Tyr	Trp	Asp	Glu	Gly	Thr	Pro	Pro	His	Glu	
		115					120					125				
Val	Ala	Asp	Thr	Leu	Asp	Tyr	Ala	Val	Arg	Thr	Gly	Arg	Val	Arg	Tyr	
	130					135					140					
Ala	Gly	Val	Arg	Gly	Tyr	Ser	Gly	Trp	Gln	Leu	Ala	Val	Thr	His	Ala	
145					150					155					160	
Ala	Ser	Asn	His	Ala	Ala	Ala	Ser	Ala	Arg	Pro	Val	Val	Val	Ala	Gln	
				165					170					175		
Asn	Glu	Tyr	Ser	Leu	Leu	Glu	Arg	Arg	Ala	Glu	Gln	Glu	Leu	Leu	Pro	
			180					185					190			
Ala	Thr	Gln	His	Leu	Gly	Val	Gly	Phe	Phe	Ala	Gly	Ala	Pro	Leu	Gly	
		195					200					205				
Gln	Gly	Val	Leu	Thr	Ala	Lys	Tyr	Arg	Ser	Glu	Ile	Pro	His	Asp	Ser	
	210					215					220					

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 869
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXS03074

<400> 869
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 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

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att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
      105                      110                      115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
      120                      125                      130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
      135                      140                      145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
      150                      155                      160                      165

cag taatttgttt tgacgacgca gta 621
Gln

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<210> 870
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

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<400> 870
Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
  1                      5                      10                      15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
      20                      25                      30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35                      40                      45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50                      55                      60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
      65                      70                      75                      80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
      85                      90                      95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
      100                      105                      110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
      115                      120                      125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
      130                      135                      140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
      145                      150                      155                      160

Glu Ala Pro Ile Lys Gln
      165

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<400> 871
tttgtgggca atctggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60

cag taatttgttt tgacgacgca gta 621
Gln

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<400> 872
Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
  1              5              10              15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
          20              25              30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35              40              45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50              55              60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
  65              70              75              80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
          85              90              95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
      100              105              110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
      115              120              125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
      130              135              140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
  145              150              155              160

Glu Ala Pro Ile Lys Gln
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<220>  
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<222> (101)..(1729)  
<223> RXA02315
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gaatcgatc cgtacctgga gacgatctag actgttgtgc atg tcc agc acg cca 115
                                         Met Ser Ser Thr Pro
                                         1                               5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
          10                      15                      20

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act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt	211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu	
25 30 35	
gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag	259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu	
40 45 50	
cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg	307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg	
55 60 65	
ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg	355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu	
70 75 80 85	
cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc	403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu	
90 95 100	
tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg	451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr	
105 110 115	
att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc	499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile	
120 125 130	
act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg	547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly	
135 140 145	
gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg	595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu	
150 155 160 165	
gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca	643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser	
170 175 180	
tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg	691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly	
185 190 195	
gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg	739
Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly	
200 205 210	
ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat	787
Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr	
215 220 225	
aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc	835
Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val	
230 235 240 245	
tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg	883
Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val	
250 255 260	

gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat	931
Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp	
265 270 275	
cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat	979
Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp	
280 285 290	
ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc	1027
Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly	
295 300 305	
acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt	1075
Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu	
310 315 320 325	
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc	1123
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe	
330 335 340	
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc	1171
Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly	
345 350 355	
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg	1219
Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu	
360 365 370	
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc	1267
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val	
375 380 385	
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct	1315
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala	
390 395 400 405	
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc	1363
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala	
410 415 420	
ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc	1411
Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile	
425 430 435	
ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac	1459
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn	
440 445 450	
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt	1507
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly	
455 460 465	
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc	1555
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser	
470 475 480 485	
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac	1603
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp	
490 495 500	
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc	1651

Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515

gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530

caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540

gcg 1752

<210> 874

<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 874

Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
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Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
 370 375 380
 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
 385 390 395 400
 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
 405 410 415
 Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
 420 425 430
 Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
 435 440 445
 Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450 455 460
 Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
 465 470 475 480
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
 485 490 495
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
 500 505 510
 Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
 515 520 525
 Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
 530 535 540

<210> 875
 <211> 1080
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1057)
 <223> RXA02319

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 agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
 Met Ser Asn Tyr Ser
 1 5
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
 10 15 20
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
 25 30 35
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
 40 45 50
 gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307
 Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His
 55 60 65
 gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355
 Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly
 70 75 80 85
 ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403
 Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln
 90 95 100
 cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc 451
 Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg
 105 110 115
 gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa 499
 Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys
 120 125 130
 gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc 547
 Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg
 135 140 145
 acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc 595
 Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly
 150 155 160 165
 ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc 643
 Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg
 170 175 180

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caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac 691
Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp
      185                      190                      195

gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac 739
Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn
      200                      205                      210

gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg 787
Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met
      215                      220                      225

caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa 835
Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu
      230                      235                      240                      245

aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc 883
Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr
      250                      255                      260

ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc 931
Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu
      265                      270                      275

atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg 979
Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met
      280                      285                      290

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa 1027
Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
      295                      300                      305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct 1077
Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
      310                      315

aaa 1080

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<210> 876

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 876

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Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
 1                      5                      10                      15

Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
      20                      25                      30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
      35                      40                      45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
      50                      55                      60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
      65                      70                      75                      80

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aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
Met Ser His Thr Glu

	1	5	
ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc			163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg	10	20	
ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt			211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly	25	35	
gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg			259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala	40	50	
ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat			307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	55	65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg			355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	70	85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg			403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	90	100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc			451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	105	115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg			499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	120	130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg			547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	135	145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg			595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	150	165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc			643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	170	180	
gcc gca gtt ggc gtg ggg tgc atg tct gct ggc gtg aac ttg gcc aac			691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	185	195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc			739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	200	210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg			787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	215	225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg			835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	230	245	

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cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca      883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
                250                255                260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc      931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
                265                270                275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg      979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
                280                285                290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc                      1017
Ala Leu Ala Phe Ser
                295

```

<210> 878

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 878

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Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
  1                5                10                15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
                20                25                30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
                35                40                45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
                50                55                60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
                65                70                75                80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
                85                90                95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
                100                105                110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
                115                120                125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
                130                135                140

Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
                145                150                155                160

Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
                165                170                175

Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
                180                185                190

Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr

```

195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys		
210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu		
225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu		
	245	250
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp		
	260	265
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala		
	275	280
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser		
290	295	

<210> 879
 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(982)
 <223> FRXA00393

<400> 879
 tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60
 aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115
 ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130
 ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145
 ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165
 gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180
 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195
 aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290
 cat tagcggttag ctaaaacgct ttt 1005
 His

<210> 880

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 880

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro	275	280	285
Cys Ser Arg Ala Trp His	290		

<210> 881

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<223> RXA00391

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
185 190 195

<400> 882																
Leu	Leu	Arg	Asp	Ser	Gln	Arg	Val	Gly	Leu	Ala	Ile	Asp	Pro	Ser	Ile	
1				5					10					15		
Ala	Leu	Val	Met	Ala	Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	
			20					25					30			
Gln	Leu	Thr	Pro	Leu	Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	
		35					40					45				
Phe	Leu	Gly	Gly	Glu	Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	
	50					55					60					
Ile	Ala	Gly	Met	Gln	Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	
65					70					75					80	
Pro	Leu	Ala	Ile	Asp	Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	
				85					90					95		
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser	
			100					105					110			
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile	
		115					120					125				
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu	
	130					135					140					
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val	
145					150					155					160	
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly	
				165					170					175		
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu	
			180					185					190			
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His	
		195					200					205				
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu	

210	215	220
Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His		
225	230	235 240

<210> 883
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> RXS02908

<400> 883
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 gtgactggtc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro
 1 5
 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
 10 15 20
 tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
 25 30 35
 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
 40 45 50
 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
 55 60 65
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
 70 75 80 85
 ctg ttt tagtcttcat tcttgctggc tgc 384
 Leu Phe

<210> 884
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 884
 Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1 5 10 15
 Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly

20	25	30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val		
35	40	45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu		
50	55	60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg		
65	70	75
80		
Arg Ala Ile Ala Lys Leu Phe		
85		

<210> 885
 <211> 705
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(682)
 <223> RXA00997

<400> 885
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 gcaccatggt gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
 Met Thr Thr Trp Lys
 1 5
 gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
 Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
 10 15 20
 tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
 Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
 25 30 35
 ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
 Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
 40 45 50
 tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
 Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
 55 60 65
 gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
 Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
 70 75 80 85
 gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
 Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
 90 95 100
 atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
 Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
 105 110 115
 ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499

Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
 120 125 130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
 Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
 135 140 145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
 Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
 150 155 160 165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
 Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
 170 175 180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
 Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
 185 190

atcttgacc tga 705

<210> 886

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
 1 5 10 15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
 20 25 30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
 35 40 45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
 50 55 60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
 65 70 75 80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
 85 90 95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
 100 105 110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
 115 120 125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
 130 135 140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
 145 150 155 160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
 165 170 175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
 180 185 190

Lys Lys

<210> 887

<211> 861

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02189

<400> 887

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attgagccag ttctctcaag caaaccgata ctggtgggat gtg gac gcg gcc gac 115
 Val Asp Ala Ala Asp
 1 5

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc 163
 Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly
 10 15 20

gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt 211
 Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu
 25 30 35

ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt 259
 Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly
 40 45 50

tgc ggc tcg gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat 307
 Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn
 55 60 65

gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca 355
 Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala
 70 75 80 85

ggc cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc 403
 Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu
 90 95 100

ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc 451
 Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala
 105 110 115

atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc 499
 Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg
 120 125 130

gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg 547
 Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met
 135 140 145

cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc 595

Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile
 150 155 160 165
 acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc 643
 Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr
 170 175 180
 ggt gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc 691
 Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile
 185 190 195
 aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca 739
 Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro
 200 205 210
 gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt 787
 Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu
 215 220 225
 cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc 835
 Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg
 230 235 240 245
 ccc taaaaaacca acggcgctca ttt 861
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<210> 888

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 888

Val Asp Ala Ala Asp Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr
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Asp Ser Ala His Gly Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu
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Lys Asp Val Arg Leu Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys
 35 40 45

Ile Leu Glu Ile Gly Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala
 50 55 60

Asn Asp Val Pro Asn Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln
 65 70 75 80

Met Leu Lys Tyr Ala Gly His Asp His Asn Val His Leu Val Gln Ala
 85 90 95

Asp Ala Met Ser Leu Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe
 100 105 110

Ser Val Phe Gly Ala Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met
 115 120 125

Lys Glu Ile Ala Arg Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser
 130 135 140

Ile Thr His Pro Met Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala
 145 150 155 160

Gly Leu Thr Ala Ile Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu
 165 170 175

Glu Asp Glu Glu Thr Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr
 180 185 190

Met Gly Ala Arg Ile Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp
 195 200 205

His Leu Ile Glu Pro Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly
 210 215 220

Gln Trp Ser Pro Leu Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe
 225 230 235 240

Leu Ala Thr Tyr Arg Pro
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 Val Ala Lys Ala Asp
 1 5

tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
 Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
 10 15 20

aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
 Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
 25 30 35

gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
 Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
 40 45 50

aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
 Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
 55 60 65

gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
 Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
 70 75 80 85

ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
 Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly

	90	95	100	
atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct				451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser				
	105	110	115	
tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg				499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met				
	120	125	130	
gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc				547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser				
	135	140	145	
acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg				595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met				
	150	155	160	165
cgc ctg ctg ccc cag gcg gcg cgc gca gta tcg tcc aac ccg gag gcc				643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala				
	170	175	180	
tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa				691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu				
	185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag				739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln				
	200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag				787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu				
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Asn				
230				

<210> 890

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 890

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Phe	Asp	Asp	Val	Gly	Lys	Asn	Tyr	Asp	Leu	Thr	Asn	Thr	Val	Leu	Ser
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Phe	Gly	Gln	Asp	Arg	Val	Trp	Arg	Lys	Arg	Thr	Arg	Gln	Arg	Leu	Asp
		35					40					45			

Leu	Lys	Pro	Gly	Glu	Lys	Val	Leu	Asp	Leu	Ala	Ala	Gly	Thr	Ala	Val
	50					55					60				

Ser	Thr	Val	Glu	Leu	Ala	Lys	Ser	Gly	Ala	Phe	Cys	Val	Ala	Cys	Asp
65						70				75				80	

Phe	Ser	Gln	Gly	Met	Leu	Ala	Ala	Gly	Lys	Asp	Arg	Asp	Val	Ser	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85								90				95			
Val	Val	Gly	Asp	Gly	Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp
			100					105					110		
Ala	Val	Thr	Ile	Ser	Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala
		115					120					125			
Gly	Leu	Lys	Glu	Met	Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr
	130					135					140				
Val	Ala	Glu	Phe	Ser	Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr
145					150				155						160
Lys	Glu	Tyr	Leu	Met	Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser
				165				170						175	
Ser	Asn	Pro	Glu	Ala	Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp
			180					185					190		
Pro	Ser	Gln	Ala	Glu	Leu	Ala	Arg	Glu	Ile	Asn	Gln	Asn	Gly	Trp	Ser
		195					200					205			
Asp	Cys	Gly	Trp	Gln	Asn	Leu	Thr	Phe	Gly	Ile	Val	Ala	Leu	His	Ser
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<223> RXN02912
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													Val	Thr	Ser	Pro	Glu	
													1				5	
tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac																	163	
Leu	Gln	Asn	Ile	Leu	Asn	Asn	Tyr	Trp	Ser	Gly	Arg	Ala	Glu	Ala	Tyr			
				10						15		20						
cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc																	211	
His	Leu	Asn	Gln	Thr	Gln	Ser	Glu	Arg	Ala	Gln	Phe	Glu	Arg	Pro	Ile			
				25		30				35								
tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg																	259	
Trp	Glu	Lys	Val	Trp	Ser	Lys	Ala	Leu	Pro	Ile	Val	Ser	Glu	Glu	Ala			
40				45				50										
gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt																	307	
Val	Lys	Val	Leu	Asp	Leu	Gly	Cys	Gly	Ala	Gly	Tyr	Val	Thr	His	Leu			

55	60	65	
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa			355
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu			
70	75	80	85
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt			403
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly			
	90	95	100
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc			451
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe			
	105	110	115
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act			499
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr			
	120	125	130
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa			547
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys			
	135	140	145
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc			595
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly			
	150	155	160
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc			643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe			
	170	175	180
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg			691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr			
	185	190	195
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc			739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu			
	200	205	210
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag			787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln			
	215	220	225
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc			835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe			
	230	235	240
agg gga att aaa tcc agt tagtgctgtt ttaagcggtc gag			876
Arg Gly Ile Lys Ser Ser			
	250		

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<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly
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Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln

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Phe	Glu	Arg	Pro	Ile	Trp	Glu	Lys	Val	Trp	Ser	Lys	Ala	Leu	Pro	Ile	
35					40					45						
Val	Ser	Glu	Glu	Ala	Val	Lys	Val	Leu	Asp	Leu	Gly	Cys	Gly	Ala	Gly	
50					55					60						
Tyr	Val	Thr	His	Leu	Leu	Ser	Asp	Cys	Gly	Tyr	Glu	Thr	Ile	Gly	Val	
65					70					75					80	
Asp	Gly	Ser	Glu	Glu	Met	Ile	Asn	Gln	Ala	Thr	Gln	Glu	Asn	Gly	Leu	
85					90					95						
Arg	Arg	Ser	Thr	Gly	Arg	Ala	Thr	Ala	Ile	Phe	Gln	Val	Gly	Asp	Ala	
100					105					110						
His	Asp	Pro	Glu	Phe	Arg	Glu	Gly	Ser	Phe	Asp	Ala	Ile	Thr	Ser	Arg	
115					120					125						
Tyr	Val	Leu	Trp	Thr	Leu	Leu	Asp	Pro	Gln	Ala	Ala	Ile	Asn	Arg	Trp	
130					135					140						
Val	Ser	Leu	Leu	Lys	Pro	Gly	Gly	Val	Ile	Ala	Cys	Val	Asp	Ala	Ala	
145					150					155					160	
Trp	Tyr	Pro	Lys	Gly	Ile	Asp	Ala	Gly	Thr	Glu	Val	Asp	Ser	Val	Asp	
165					170					175						
Gly	Pro	Ser	Ala	Phe	Val	Glu	Thr	Tyr	Thr	Pro	Glu	Leu	Leu	Arg	Asn	
180					185					190						
Leu	Pro	Met	Ser	Thr	Thr	Ser	Thr	Gly	His	Asn	Phe	Ala	Glu	Leu	Phe	
195					200					205						
His	Asn	Ala	Gly	Leu	Lys	Glu	Val	Thr	Leu	Thr	Pro	Ile	Glu	Gly	Leu	
210					215					220						
Ala	Glu	Leu	Asp	Gln	Arg	Phe	Gly	Leu	Ser	Pro	Gly	His	Glu	Ser	Thr	
225					230					235					240	
Pro	Gln	Phe	Leu	Phe	Arg	Gly	Ile	Lys	Ser	Ser						
245					250											

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<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXS00998

<400> 893

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				Met	Thr	Ser	Arg	Asp	

1

5

gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163
Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg
10 15 20
gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
25 30 35
ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259
Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg
40 45 50
gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307
Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly
55 60 65
ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355
Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser
70 75 80 85
gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403
Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn
90 95 100
aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451
Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala
105 110 115
gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499
Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
120 125 130
gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr
135 140 145
atg gtg ctg aac aag tagccctata ctcgggcacc atg 585
Met Val Leu Asn Lys
150

<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

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20 25 30
Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr
35 40 45
Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
50 55 60
Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala

65		70		75		80
Glu Ser Thr Gly	Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met					
	85		90		95	
Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser						
	100		105		110	
Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr						
	115		120		125	
His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg						
	130		135		140	
Thr Thr Leu Arg Thr Met Val Leu Asn Lys						
145		150				

<210> 895

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1075)

<223> RXA01215

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ccccaaacgt ccacaaccag gaaggctaag caggatcctc	atg act gct cac tgg	115
	Met Thr Ala His Trp	
	1 5	

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca	163
Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro	
	10 15 20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca	211
Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro	
	25 30 35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag	259
Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu	
	40 45 50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag	307
Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln	
	55 60 65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg	355
Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu	
	70 75 80 85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca	403
Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro	
	90 95 100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct	451
Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala	

105	110	115	
cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg			499
Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val			
120	125	130	
tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca			547
Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro			
135	140	145	
gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa			595
Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu			
150	155	160	165
aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc			643
Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg			
170	175	180	
gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg			691
Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met			
185	190	195	
gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc			739
Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val			
200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
250	255	260	
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
265	270	275	
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
280	285	290	
aac ctg acc gtt ttg tgc atc gca ccg ctg ctg gct cgc acc atc aac			1027
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
295	300	305	
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			1075
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
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<210> 896

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 896

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			20					25					30		
Val	Asn	Val	Thr	Pro	Met	Thr	Ala	Arg	Asp	Phe	Ala	Asn	Gly	Glu	Ile
		35					40					45			
Tyr	Val	Arg	Phe	Glu	Glu	Ser	Val	Arg	Gly	Ser	Asp	Cys	Phe	Val	Leu
	50					55					60				
Gln	Ser	His	Thr	Gln	Pro	Leu	Asn	Lys	Trp	Leu	Met	Glu	Gln	Leu	Leu
	65				70						75				80
Met	Ile	Asp	Ala	Leu	Lys	Arg	Gly	Ser	Ala	Lys	Arg	Ile	Thr	Ala	Ile
				85					90					95	
Leu	Pro	Phe	Tyr	Pro	Tyr	Ala	Arg	Gln	Asp	Lys	Lys	His	Arg	Gly	Arg
			100					105					110		
Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly
		115					120					125			
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly
	130						135				140				
Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr
145					150					155					160
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser
			165						170					175	
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu
		180						185					190		
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val
	195						200					205			
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys
	210					215					220				
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala
225					230					235					240
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile
			245						250					255	
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser
			260					265					270		
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser
		275					280					285			
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu
	290					295					300				
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu
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Phe Glu Gly Glu Ala
325

<210> 897

<211> 1470

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1447)

<223> RXN00558

<400> 897

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tcgaaactta cctactttgg cctcttcgca cttcagcacc gtg gtc aag aag ccc 115
Val Val Lys Lys Pro
1 5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat 163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp
10 15 20

ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc 211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu
25 30 35

cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga 259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly
40 45 50

aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc 307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly
55 60 65

acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag 355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu
70 75 80 85

ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag 403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys
90 95 100

cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat 451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His
105 110 115

gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc 499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val
120 125 130

aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca 547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala
135 140 145

gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag 595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu
150 155 160 165

cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tgc cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	
gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca	883
Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser	
250 255 260	
ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc	931
Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe	
265 270 275	
ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag	979
Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln	
280 285 290	
cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca	1027
Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro	
295 300 305	
ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc	1075
Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser	
310 315 320 325	
atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa	1123
Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu	
330 335 340	
gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa	1171
Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys	
345 350 355	
tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att	1219
Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile	
360 365 370	
gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc	1267
Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val	
375 380 385	
cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc	1315
Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser	
390 395 400 405	

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc 1363
Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys
410 415 420

ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca 1411
Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala
425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt 1457
Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser Ser
440 445

aggcgatagg ggt 1470

<210> 898

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 898

Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
20 25 30

Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
35 40 45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
50 55 60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
65 70 75 80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
85 90 95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
100 105 110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
115 120 125

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
130 135 140

His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
145 150 155 160

Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
165 170 175

Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
180 185 190

Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
195 200 205

Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro

210					215					220					
Asp	Ser	Val	Ile	Lys	Gly	Arg	Asn	Val	Asn	Glu	Ala	Arg	Leu	Glu	Ile
225					230					235				240	
Gly	Arg	Lys	Leu	Ala	Ala	Glu	Ala	Pro	Ala	Val	Gly	Asp	Leu	Val	Ile
			245						250					255	
Pro	Thr	Pro	Glu	Ser	Gly	Thr	Pro	Ala	Ala	Val	Gly	Phe	Ala	Gln	Ala
			260					265					270		
Ser	Gly	Ile	Pro	Phe	Gly	Gln	Gly	Met	Val	Lys	Asn	Ala	Tyr	Val	Gly
		275					280					285			
Arg	Thr	Phe	Ile	Gln	Pro	Ser	Asp	Thr	Leu	Arg	Gln	Leu	Gly	Ile	Arg
		290				295					300				
Leu	Lys	Leu	Asn	Pro	Leu	Arg	Glu	Val	Ile	Ala	Gly	Lys	Arg	Leu	Val
305					310					315					320
Val	Val	Asp	Asp	Ser	Ile	Val	Arg	Gly	Asn	Thr	Gln	Arg	Ala	Val	Ile
				325					330					335	
Arg	Met	Leu	Arg	Glu	Ala	Gly	Ala	Ala	Glu	Val	His	Val	Arg	Ile	Ala
			340					345					350		
Ser	Pro	Pro	Val	Lys	Trp	Pro	Cys	Phe	Tyr	Gly	Ile	Asp	Phe	Ala	Thr
			355				360					365			
Pro	Gly	Glu	Leu	Ile	Ala	Asn	Ala	Val	Thr	Ser	Asp	Asn	Glu	Ala	Glu
			370			375					380				
Met	Val	Glu	Ala	Val	Arg	Ser	Ala	Ile	Gly	Ala	Asp	Thr	Leu	Gly	Tyr
385					390					395					400
Val	Ser	Ile	Asp	Ser	Met	Val	Ala	Ala	Thr	Glu	Gln	Pro	Ala	Asn	Glu
				405					410					415	
Leu	Cys	Ile	Ala	Cys	Phe	Asp	Gly	Lys	Tyr	Pro	Met	Gly	Leu	Pro	Gln
			420				425						430		
Gly	Asn	Ser	Asn	Ala	Asp	Leu	Val	Arg	Lys	Met	Gln	Ala	Thr	Ala	Ser
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Ser

<210> 899

<211> 524

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (61)..(501)

<223> FRXA00558

<400> 899

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Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
  1          5          10          15

ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156
Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
      20          25          30

att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
      35          40          45

acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc 252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
      50          55          60

atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg 300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
      65          70          75          80

att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc 348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
      85          90          95

gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc 396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
      100          105          110

gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa 444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
      115          120          125

ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga 492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
      130          135          140

cac acc ctg taagcagcgc gtgatccatt cgg 524
His Thr Leu
145

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<210> 900

<211> 147

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 900

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Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
      20          25          30

Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
      35          40          45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
      50          55          60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
      65          70          75          80

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<400> 901																	
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aatagcttgg				atcaagtttt	gcaggataaa	ctgtgcaacc	atg	cgc	att	ctg	gta	115					
							Met	Arg	Ile	Leu	Val						
							1						5				
atc	ggc	tcg	ggc	gcc	cgt	gag	cac	gcc	ctc	ctc	cgt	gga	ctg	tca	act	163	
Ile	Gly	Ser	Gly	Ala	Arg	Glu	His	Ala	Leu	Leu	Arg	Gly	Leu	Ser	Thr		
				10					15					20			
gac	cct	gca	acc	act	gaa	ctc	cac	gtt	gcc	cca	ggt	aac	gct	ggt	ctt	211	
Asp	Pro	Ala	Thr	Thr	Glu	Leu	His	Val	Ala	Pro	Gly	Asn	Ala	Gly	Leu		
				25					30					35			
gga	tcg	atc	gca	act	gtc	cac	cct	ggc	atc	aag	gct	gat	gat	cca	gag	259	
Gly	Ser	Ile	Ala	Thr	Val	His	Pro	Gly	Ile	Lys	Ala	Asp	Asp	Pro	Glu		
		40					45					50					
gct	gtc	act	gcg	ttg	gct	aaa	gaa	ctg	aac	tct	gat	ctg	ggt	ggt	atc	307	
Ala	Val	Thr	Ala	Leu	Ala	Lys	Glu	Leu	Asn	Ser	Asp	Leu	Val	Val	Ile		
		55					60					65					
ggc	cca	gag	atc	cct	ttg	gtt	gcg	ggt	gtt	gct	gat	gca	ctt	cgc	gcg	355	
Gly	Pro	Glu	Ile	Pro	Leu	Val	Ala	Gly	Val	Ala	Asp	Ala	Leu	Arg	Ala		
70					75					80					85		
gcg	ggt	atc	gct	gtg	ttt	ggt	cct	aac	aag	gac	gct	gct	cgt	atc	gag	403	
Ala	Gly	Ile	Ala	Val	Phe	Gly	Pro	Asn	Lys	Asp	Ala	Ala	Arg	Ile	Glu		
				90					95					100			
ggc	tcc	aag	gct	ttc	gct	aag	gat	gtc	atg	gct	gcg	cag	ggt	gtt	cgt	451	
Gly	Ser	Lys	Ala	Phe	Ala	Lys	Asp	Val	Met	Ala	Ala	Gln	Gly	Val	Arg		
			105					110					115				

act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att	499
Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile	
120 125 130	
gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat	547
Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp	
135 140 145	
ggg ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca	595
Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr Pro Asp Arg Ala Ala	
150 155 160 165	
gca cgt gct cac gta gat gca gtg ctt gag ggc gga aat cca gtt ttg	643
Ala Arg Ala His Val Asp Ala Val Leu Gly Gly Asn Pro Val Leu	
170 175 180	
ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg ttc tgc ctg gtt	691
Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu Phe Cys Leu Val	
185 190 195	
gat ggc gag acg gta gtt cct ctg ctg cca gcg cag gat cac aag cgt	739
Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln Asp His Lys Arg	
200 205 210	
gcg tac gac aac gat gag ggc cca aac act ggt ggc atg ggt gct tat	787
Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly Met Gly Ala Tyr	
215 220 225	
gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag cgc att gtc gat	835
Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln Arg Ile Val Asp	
230 235 240 245	
gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca cgt ggt tgc gcg	883
Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala Arg Gly Cys Ala	
250 255 260	
tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt gca gaa ggc cct	931
Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly Ala Glu Gly Pro	
265 270 275	
gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca gaa acc cag gct	979
Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro Glu Thr Gln Ala	
280 285 290	
gta ctg gca cta ctg aag act cct cta gca gta ctg ctc aac gca gtt	1027
Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu Leu Asn Ala Val	
295 300 305	
gct act gga acc ttg gca gag cag cca gca ctg gag tgg gag gat gct	1075
Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu Trp Glu Asp Ala	
310 315 320 325	
tac gcc ctg act gtg gtg ttg gct tct tac aac tac cca gag gca cct	1123
Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr Pro Glu Ala Pro	
330 335 340	
cgt act ggt gat gtc atc cgc aac gct gat gca gat aac gtt ctt cac	1171
Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp Asn Val Leu His	
345 350 355	

gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc tct gcg ggc ggt 1219
Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val Ser Ala Gly Gly
360 365 370

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc 1267
Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg
375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac 1315
Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His
390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc 1363
Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile
410 415 420

taaaagcagt acgcagatag gct 1386

<210> 902

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 902

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu
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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp
85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala
100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala
115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp
130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr
145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly
165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser
180 185 190

BGI-121CP

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala
 195 200 205
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly
 210 215 220
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val
 225 230 235 240
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val
 245 250 255
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp
 260 265 270
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp
 275 280 285
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val
 290 295 300
 Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu
 305 310 315 320
 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn
 325 330 335
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala
 340 345 350
 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu
 355 360 365
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr
 370 375 380
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu
 385 390 395 400
 Leu Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu
 405 410 415
 Gly Arg Ile Ser Ile
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<210> 903

<211> 364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(364)

<223> FRXA00629

<400> 903

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 Met Arg Ile Leu Val

	1	5	
atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act			163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr			
	10	20	
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu			
	25	35	
gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu			
	40	50	
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile			
	55	65	
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala			
	70	85	
gcg ggt atc			364
Ala Gly Ile			

<210> 904

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 904

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu
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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
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Asp Ala Leu Arg Ala Ala Gly Ile
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<211> 803

<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA00626

<400> 905

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Asp	Arg	Ala	Ala	Ala	Arg	Ala	His	Val	Asp	Ala	Val	Leu	Glu	Gly	Gly	
1				5					10					15		
aat	cca	ggt	ttg	ctg	gag	tcc	ttc	ctt	gat	ggc	cct	gag	ggt	tcc	ctg	96
Asn	Pro	Val	Leu	Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	
			20					25					30			
ttc	ttc	ctg	ggt	gat	ggc	gag	acg	gta	ggt	cct	ctg	ctg	cca	gcg	cag	144
Phe	Phe	Leu	Val	Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	
		35					40					45				
gat	cac	aag	cgt	gcg	tac	gac	aac	gat	gag	ggc	cca	aac	act	ggt	ggc	192
Asp	His	Lys	Arg	Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	
	50					55					60					
atg	ggt	gct	tat	gcg	ccg	ctt	cct	tgg	ctg	cct	gaa	gat	ggc	gtc	cag	240
Met	Gly	Ala	Tyr	Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	
65					70				75					80		
cgc	att	gtc	gat	gag	gtc	tgc	gtt	cct	ggt	gct	cgt	gag	atg	gtg	gca	288
Arg	Ile	Val	Asp	Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	
			85					90						95		
cgt	ggt	tgc	gcg	tac	tcc	ggt	ctg	ctt	tac	gca	ggt	atc	gca	tgg	ggt	336
Arg	Gly	Cys	Ala	Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	
			100				105						110			
gca	gaa	ggc	cct	gca	gta	gtg	gag	ttc	aac	tgc	cgc	ttc	ggc	gat	cca	384
Ala	Glu	Gly	Pro	Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	
		115					120					125				
gaa	acc	cag	gct	gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	432
Glu	Thr	Gln	Ala	Val	Leu	Ala	Leu	Leu	Lys	Thr	Pro	Leu	Ala	Val	Leu	
	130					135					140					
ctc	aac	gca	ggt	gct	act	gga	acc	ttg	gca	gag	cag	cca	gca	ctg	gag	480
Leu	Asn	Ala	Val	Ala	Thr	Gly	Thr	Leu	Ala	Glu	Gln	Pro	Ala	Leu	Glu	
145					150				155					160		
tgg	gag	gat	gct	tac	gcc	ctg	act	gtg	gtg	ttg	gct	tct	tac	aac	tac	528
Trp	Glu	Asp	Ala	Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	
			165					170						175		
cca	gag	gca	cct	cgt	act	ggt	gat	gtc	atc	cgc	aac	gct	gat	gca	gat	576
Pro	Glu	Ala	Pro	Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	
			180					185					190			
aac	ggt	ctt	cac	gct	ggt	acc	gca	ctc	aat	gct	gaa	ggc	gag	ctg	gtc	624
Asn	Val	Leu	His	Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	
		195					200					205				
tct	gcg	ggc	ggt	cgt	gtt	ctt	aac	gtg	atc	ggt	gtg	ggt	gag	acc	ctg	672
Ser	Ala	Gly	Gly	Arg	Val	Leu	Asn	Val	Ile	Gly	Val	Gly	Glu	Thr	Leu	
	210					215					220					
gag	gct	gca	cgc	gat	aac	gcg	tac	acc	acc	atc	aag	gac	att	gaa	ctt	720
Glu	Ala	Ala	Arg	Asp	Asn	Ala	Tyr	Thr	Thr	Ile	Lys	Asp	Ile	Glu	Leu	
225					230					235					240	

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 Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
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cgt atc tcg atc taaaagcagt acgcagatag gct 803
 Arg Ile Ser Ile
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<210> 906

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<212> PRT

<213> Corynebacterium glutamicum

<400> 906

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Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln
 35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly
 50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln
 65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala
 85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly
 100 105 110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro
 115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu
 130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu
 145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr
 165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp
 180 185 190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val
 195 200 205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu
 210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu
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Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
 245 250 255

Arg Ile Ser Ile
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<223> RXA02623

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 Val Asn Ser Asp Ser
 1 5

acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln
 10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser
 25 30 35

gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp
 40 45 50

act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu
 55 60 65

ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser
 120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691
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<400> 908

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 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile
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Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln
 180 185 190

Leu Asn Trp Arg Gly
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<210> 909

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	Met	Tyr	Ile	Pro	Glu	
	1				5	

tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg	163
Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu	
10 15 20	

gga tca gga gaa tta ggc aaa gaa gta gcc atc gct ttc cag cgt ctc	211
Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu	
25 30 35	

ggc ctg gaa gtc cat gca gtt gat cgc tac gaa cat gcc cca gcc cac	259
Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His	
40 45 50	

cag gtc gct cac ttc tcc tat gtc atc gac atg aca gat gca gcc cag	307
Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln	
55 60 65	

gtg cgg gaa ttg gtg gag cgt gtg cgc cca gat ttt gtc att cct gaa	355
Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu	
70 75 80 85	

atc gaa gca ctg gca acc gat gaa ctg gtg aag atc gaa gaa gag ggg	403
Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly	
90 95 100	

cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac	451
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn	
105 110 115	

cgc gaa ggc atc cgc aag ctg gcg gca gag gaa ctg ggt ctt cca acc	499
Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu Leu Gly Leu Pro Thr	
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tcc aac tat gag ttc tgc tcc act ttc gag gaa ttc tcc gca gct gct	547
Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala	
135 140 145	

gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc	595
Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser	
150 155 160 165	

ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca	643
Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala	
170 175 180	

tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc	691
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Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	Asn	Ser	Arg	Val	Ile		
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gtg	gaa	gct	ttc	gtg	gaa	ttc	gat	tac	gag	atc	acc	ctg	ttg	aca	gta	739	
Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val		
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agg	tcc	atc	gat	ccc	acc	acc	tct	aag	cct	gcg	acc	tgg	ttc	tgt	gag	787	
Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu		
	215					220					225						
ccc	att	ggg	cac	cgc	caa	gaa	gac	ggc	gac	tac	gtg	gaa	tcc	tgg	cag	835	
Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	Val	Glu	Ser	Trp	Gln		
230					235					240					245		
cca	atg	gag	atg	act	cct	cgc	gcg	ctg	gaa	aac	gca	cgc	tca	gta	gcc	883	
Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Ser	Val	Ala		
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gca	cgc	atc	acc	aac	gca	ttg	ggc	gga	cgc	ggc	gta	ttt	ggg	gtg	gag	931	
Ala	Arg	Ile	Thr	Asn	Ala	Leu	Gly	Gly	Arg	Gly	Val	Phe	Gly	Val	Glu		
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ctc	ttt	gtc	tcc	ggc	gat	gac	gtg	tac	ttc	tct	gaa	gtc	tcc	cca	cgc	979	
Leu	Phe	Val	Ser	Gly	Asp	Asp	Val	Tyr	Phe	Ser	Glu	Val	Ser	Pro	Arg		
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cca	cac	gac	acc	ggc	ctt	gtc	acc	ctt	gcc	acc	cag	cgt	ttc	tct	gaa	1027	
Pro	His	Asp	Thr	Gly	Leu	Val	Thr	Leu	Ala	Thr	Gln	Arg	Phe	Ser	Glu		
	295					300					305						
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Phe	Glu	Leu	His	Ala	Lys	Ala	Ile	Leu	Gly	Leu	Pro	Val	Asp	Val	Thr		
310					315					320					325		
ctg	att	tct	cca	ggg	gcc	tcc	gct	gtc	atc	tac	ggg	ggc	atc	gaa	tct	1123	
Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser		
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gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa	1171	
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu		
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act	gat	ctt	cgt	atc	ttt	gcc	aag	cca	gag	gcc	ttc	acc	aag	cgt	cgc	1219	
Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg		
		360					365					370					
atg	ggg	gtt	gca	gtg	tcc	acc	gct	gag	gat	gtg	gct	gca	gcc	agg	gac	1267	
Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp		
		375				380					385						
cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	gtt	cat	cca	gga	aat	tcc	1315	
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser		
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Ala	Glu	Ala															

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<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 910

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Lys Val Met Leu Leu Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile
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Ala Phe Gln Arg Leu Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu
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His Ala Pro Ala His Gln Val Ala His Phe Ser Tyr Val Ile Asp Met
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Thr Asp Ala Ala Gln Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp
 65           70           75           80

Phe Val Ile Pro Glu Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys
          85           90           95

Ile Glu Glu Glu Gly Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala
          100          105          110

Lys Leu Thr Met Asn Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu
          115          120          125

Leu Gly Leu Pro Thr Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu
          130          135          140

Phe Ser Ala Ala Ala Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro
          145          150          155          160

Val Met Ser Ser Ser Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp
          165          170          175

Asp Leu Gln Ala Ala Trp Asp Tyr Ala Met Ser Gly Ala Arg Val Ala
          180          185          190

Asn Ser Arg Val Ile Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile
          195          200          205

Thr Leu Leu Thr Val Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala
          210          215          220

Thr Trp Phe Cys Glu Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr
          225          230          235          240

Val Glu Ser Trp Gln Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn
          245          250          255

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly
          260          265          270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser
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Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr
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Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu
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Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala
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Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val
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His Pro Gly Asn Ser Ala Glu Ala
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 <223> RXN00537

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 Met Ser Thr Phe Val
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aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro
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ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307
 Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser Lys Val His Leu Arg
 55 60 65

tac ttc ggt gaa acc acc act gag gaa atg gct tcc aag att ctt gcc 355
 Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala Ser Lys Ile Leu Ala
 70 75 80 85

ggc atc ggc gag aac gct ggt gtg gtc gac atc gga gac ggc aac gcc 403

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				90					95					100			
gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451	
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro		
			105					110					115				
cac	cag	ggc	gct	gcg	acc	ggc	gtc	ggc	ggc	atc	gtc	cgc	gac	att	atg	499	
His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met		
		120					125					130					
gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547	
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly		
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Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp		
	150				155					160					165		
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Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly		
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gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691	
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala		
			185					190					195				
ctg	tgc	gtg	ggt	acc	ctc	aag	gtg	gaa	gac	ctc	aag	ctt	gca	ttc	gca	739	
Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala		
		200					205					210					
tcc	ggc	acc	ggc	aac	aag	gtg	atc	ctg	ttc	ggt	tcc	cgc	acc	ggc	ctt	787	
Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu		
	215					220					225						
gat	ggc	atc	ggt	ggc	gtg	tcc	gtc	ctg	ggt	tcc	gca	tcc	ttc	gaa	gaa	835	
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu		
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Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala		
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gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931	
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val		
			265					270						275			
gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979	
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr		
		280					285					290					
tct	gag	ctg	gca	gcc	gca	ggc	gac	ggc	ggc	atg	cgc	gtc	aac	cta	gac	1027	
Ser	Glu	Leu	Ala	Ala	Ala	Gly	Asp	Gly	Gly	Met	Arg	Val	Asn	Leu	Asp		
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aac	gtc	cca	ctg	cgc	gca	gag	aac	atg	tct	gca	gct	gaa	atc	ctg	gct	1075	
Asn	Val	Pro	Leu	Arg	Ala	Glu	Asn	Met	Ser	Ala	Ala	Glu	Ile	Leu	Ala		
	310				315					320					325		
tcc	gag	tcc	cag	gag	cgc	atg	tgt	gct	gtt	gtc	acc	cct	gaa	aac	gtt	1123	
Ser	Glu	Ser	Gln	Glu	Arg	Met	Cys	Ala	Val	Val	Thr	Pro	Glu	Asn	Val		

330										335										340									
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Glu	Arg	Phe	Leu	Glu	Ile	Cys	Ala	Lys	Trp	Asp	Val	Thr	Cys	Ala	Glu														
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atc	ggc	gaa	gtt	acc	gac	gag	aag	gac	cgc	tac	gtt	gtg	gtc	cac	aac					1219									
Ile	Gly	Glu	Val	Thr	Asp	Glu	Lys	Asp	Arg	Tyr	Val	Val	Val	His	Asn														
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ggt	gaa	gtt	gtt	atc	gac	gca	cct	cca	tca	acc	atc	gat	gaa	ggc	cct					1267									
Gly	Glu	Val	Val	Ile	Asp	Ala	Pro	Pro	Ser	Thr	Ile	Asp	Glu	Gly	Pro														
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gtc	tac	aac	cgc	cca	gtt	gct	cgc	cct	gag	aac	cag	gac	gaa	ctg	cag					1315									
Val	Tyr	Asn	Arg	Pro	Val	Ala	Arg	Pro	Glu	Asn	Gln	Asp	Glu	Leu	Gln														
390					395				400					405															
ctc	gaa	ggc	gag	atc	gct	cgc	cca	gtc	gac	gtt	gaa	gag	atc	aag	gct					1363									
Leu	Glu	Gly	Glu	Ile	Ala	Arg	Pro	Val	Asp	Val	Glu	Glu	Ile	Lys	Ala														
			410					415						420															
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Ala	Trp	Leu	Lys	Leu	Val	Ala	Ser	Pro	Ala	Leu	Ala	Ser	Arg	Ala	Phe														
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atc	acc	gag	cag	tac	gac	cgc	tac	gtc	cgc	ggc	aac	acc	gtt	cag	gca					1459									
Ile	Thr	Glu	Gln	Tyr	Asp	Arg	Tyr	Val	Arg	Gly	Asn	Thr	Val	Gln	Ala														
		440				445						450																	
aag	aac	gcc	aat	gct	ggc	gtc	ttg	cgt	atc	gac	gaa	gag	acc	aac	cgt					1507									
Lys	Asn	Ala	Asn	Ala	Gly	Val	Leu	Arg	Ile	Asp	Glu	Glu	Thr	Asn	Arg														
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ggc	gtt	gcg	atc	tcc	gcc	gac	gca	tcc	ggc	cgt	tac	acc	aag	ctc	gag					1555									
Gly	Val	Ala	Ile	Ser	Ala	Asp	Ala	Ser	Gly	Arg	Tyr	Thr	Lys	Leu	Glu														
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Pro	Asn	Thr	Gly	Ala	Gln	Leu	Ala	Leu	Ala	Glu	Ala	Tyr	Arg	Asn	Val														
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gtc	tcc	acc	ggt	gca	cgc	cca	gtg	gct	gtc	acc	aac	tgc	ctg	aac	ttc					1651									
Val	Ser	Thr	Gly	Ala	Arg	Pro	Val	Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe														
			505				510						515																
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His	Gly	Leu	Ala	Asp	Gly	Ser	Lys	Leu	Leu	Gly	Ile	Pro	Val	Ser	Gly														
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Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln	Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro														
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acc	cca	gtc	gtg	ggt	gtt	ttg	gga	gtc	ttg	gac	aac	gtc	gag	cag	agc					1843									
Thr	Pro	Val	Val	Gly	Val	Leu	Gly	Val	Leu	Asp	Asn	Val	Glu	Gln	Ser														
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atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt 1891
 Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu Leu Gly
 585 590 595

gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc 1939
 Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val Ser Gly
 600 605 610

gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag 1987
 Ala Gly Leu Asn Gly Leu Pro Val Val Asp Leu Leu Asn Glu Gln
 615 620 625

cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac 2035
 Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala Ser His
 630 635 640 645

gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc 2083
 Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu Ala Ile
 650 655 660

cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc 2131
 His Gln Lys Lys Gly Met Asp Val Asp Leu Ser Gln Ile His Pro Ser
 665 670 675

ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca 2179
 Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser Arg Ile Val Val Ala
 680 685 690

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt 2227
 Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val
 695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc 2275
 Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val
 710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa 2323
 Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu
 730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct 2371
 Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala
 745 750 755

aac gca gta gtt gca taattttctg ctgtgaagcc ggg 2409
 Asn Ala Val Val Ala
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<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

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 20 25 30

Ala Arg Ile Lys Glu Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu
 35 40 45
 Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser
 50 55 60
 Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala
 65 70 75 80
 Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile
 85 90 95
 Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro
 100 105 110
 Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile
 115 120 125
 Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp
 130 135 140
 Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe
 145 150 155 160
 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
 165 170 175
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
 180 185 190
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
 195 200 205
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
 210 215 220
 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
 225 230 235 240
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
 245 250 255
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
 260 265 270
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
 275 280 285
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
 290 295 300
 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
 305 310 315 320
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
 325 330 335
 Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp
 340 345 350

Val	Thr	Cys	Ala	Glu	Ile	Gly	Glu	Val	Thr	Asp	Glu	Lys	Asp	Arg	Tyr	355	360	365	
Val	Val	Val	His	Asn	Gly	Glu	Val	Val	Ile	Asp	Ala	Pro	Pro	Ser	Thr	370	375	380	
Ile	Asp	Glu	Gly	Pro	Val	Tyr	Asn	Arg	Pro	Val	Ala	Arg	Pro	Glu	Asn	385	390	395	400
Gln	Asp	Glu	Leu	Gln	Leu	Glu	Gly	Glu	Ile	Ala	Arg	Pro	Val	Asp	Val	405	410	415	
Glu	Glu	Ile	Lys	Ala	Ala	Trp	Leu	Lys	Leu	Val	Ala	Ser	Pro	Ala	Leu	420	425	430	
Ala	Ser	Arg	Ala	Phe	Ile	Thr	Glu	Gln	Tyr	Asp	Arg	Tyr	Val	Arg	Gly	435	440	445	
Asn	Thr	Val	Gln	Ala	Lys	Asn	Ala	Asn	Ala	Gly	Val	Leu	Arg	Ile	Asp	450	455	460	
Glu	Glu	Thr	Asn	Arg	Gly	Val	Ala	Ile	Ser	Ala	Asp	Ala	Ser	Gly	Arg	465	470	475	480
Tyr	Thr	Lys	Leu	Glu	Pro	Asn	Thr	Gly	Ala	Gln	Leu	Ala	Leu	Ala	Glu	485	490	495	
Ala	Tyr	Arg	Asn	Val	Val	Ser	Thr	Gly	Ala	Arg	Pro	Val	Ala	Val	Thr	500	505	510	
Asn	Cys	Leu	Asn	Phe	Gly	Ser	Pro	Glu	Asn	Ala	Gly	Val	Met	Trp	Gln	515	520	525	
Phe	Lys	Glu	Ala	Val	His	Gly	Leu	Ala	Asp	Gly	Ser	Lys	Leu	Leu	Gly	530	535	540	
Ile	Pro	Val	Ser	Gly	Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln	Thr	Gly	Asp	545	550	555	560
Glu	Pro	Ile	Leu	Pro	Thr	Pro	Val	Val	Gly	Val	Leu	Gly	Val	Leu	Asp	565	570	575	
Asn	Val	Glu	Gln	Ser	Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu	Asp	Asn	Asp	580	585	590	
Leu	Tyr	Leu	Leu	Gly	Glu	Thr	Phe	Asp	Glu	Phe	Gly	Gly	Ser	Ile	Trp	595	600	605	
Gln	Gln	Val	Ser	Gly	Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro	Val	Val	Asp	610	615	620	
Leu	Leu	Asn	Glu	Gln	Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly	Ser	Asp	Leu	625	630	635	640
Phe	Ala	Ala	Ser	His	Asp	Leu	Ser	Glu	Gly	Gly	Leu	Gly	Gln	Thr	Leu	645	650	655	
Ala	Glu	Leu	Ala	Ile	His	Gln	Lys	Lys	Gly	Met	Asp	Val	Asp	Leu	Ser	660	665	670	
Gln	Ile	His	Pro	Ser	Leu	Phe	Thr	Ser	Leu	Phe	Ala	Glu	Ser	Ala	Ser				

675	680	685
Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala		
690	695	700
Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser		
705	710	715
Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val		
	725	730
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Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly		
	740	745
		750
His Ala Val Gly Ala Asn Ala Val Val Ala		
755	760	

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<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (54)..(638)

<223> FRXA02805

<400> 913

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 Val Phe
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cct ggc gtt gtt gac ggc att tcc cat tac ggc aac tgc ctc ggc ctg 107
 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
 5 10 15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
 20 25 30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
 35 40 45 50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
 55 60 65

tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299
 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
 70 75 80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
 85 90 95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
 100 105 110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
 115 120 125 130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
 135 140 145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
 150 155 160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
 165 170 175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
 Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp
 180 185 190

gtc 638
 Val
 195

<210> 914

<211> 195

<212> PRT

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<400> 914

Val Phe Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu
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Gly Leu Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala
 20 25 30

Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu
 35 40 45

Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu
 50 55 60

Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu
 65 70 75 80

Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val
 85 90 95

Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu
 100 105 110

Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly
 115 120 125

Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly
 130 135 140

Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met
 145 150 155 160

Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala
 165 170 175

Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys
 180 185 190

Trp Asp Val
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tcc gcg gca aca ccg ttc aag caa aag aac gcc aat gct ggc gtc ttg      100
Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu
                    15                      20                      25

cgt atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca      148
Arg Ile Asp Glu Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala
                    30                      35                      40

tcc ggc cgt tac acc aag ctc gag cca aac act ggc gcg cag ctt gca      196
Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala
                    45                      50                      55

ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg      244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val
                    60                      65                      70

gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt      292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val
                    75                      80                      85                      90

atg tgg cag ttc aag gaa gca gtc cac ggt ctg gca gac gga tcc aag      340
Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys
                    95                      100                      105

ctt ttg ggc att cca gtg tcc ggc ggt aac gtc tcc ttc tac aac cag      388
Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln
                    110                      115                      120

act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga      436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly
                    125                      130                      135

gtc ttg gac aac gtc gag cag agc atc ggc aac gtc ctc cca tcc gag      484
Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu
                    140                      145                      150

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gac aac gat ctc tac ctc ctg ggt gag acc ttc gat gag ttc ggt ggc 532
 Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly
 155 160 165 170

tcc atc tgg cag cag gtt tct ggc gct ggc ctc aac ggt ctg cca cca 580
 Ser Ile Trp Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro
 175 180 185

gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt 628
 Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly
 190 195 200

tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc 676
 Ser Asp Leu Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly
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cag acc ctc gca gag ctt gcg 697
 Gln Thr Leu Ala Glu Leu Ala
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<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 916

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Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
 50 55 60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
 65 70 75 80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn

180 185 190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala
195 200 205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu
210 215 220

Ala
225

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ccc	gct	tcc	cgc	atc	gtg	gtt	gca	acc	aac	cgc	ggc	gaa	gag	ttg	gaa	96
Pro	Ala	Ser	Arg	Ile	Val	Val	Ala	Thr	Asn	Arg	Gly	Glu	Glu	Leu	Glu	
			20				25						30			
aag	cgc	gca	gca	gag	ctg	ggt	gtt	cca	gtg	ttc	aag	ctg	ggc	tgc	acc	144
Lys	Arg	Ala	Ala	Glu	Leu	Gly	Val	Pro	Val	Phe	Lys	Leu	Gly	Cys	Thr	
		35				40					45					
aac	gat	tca	gcc	gtc	atc	gct	gtc	aag	ggc	gca	gac	gtt	gag	ttc	act	192
Asn	Asp	Ser	Ala	Val	Ile	Ala	Val	Lys	Gly	Ala	Asp	Val	Glu	Phe	Thr	
	50				55				60							
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Val	Ser	Val	Glu	Glu	Leu	Arg	Glu	Ala	Trp	Thr	Asn	Thr	Leu	Pro	Glu	
65				70				75					80			
gcc	ttc	ggt	cac	gca	gtt	gga	gct	aac	gca	gta	gtt	gca	taatttttctg			289
Ala	Phe	Gly	His	Ala	Val	Gly	Ala	Asn	Ala	Val	Val	Ala				
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								Val		Ser		Ala		Lys		Ile		5															
ggt		gtc		att		acc		ttc		cca		ggc		acc		ctt		gac		gat		gta		gat		gca		gca		cgc		163	
Gly		Val		Ile		Thr		Phe		Pro		Gly		Thr		Leu		Asp		Asp		Val		Asp		Ala		Ala		Arg		20	
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gct		gct		cgc		atc		gca		ggc		gca		gaa		gta		atc		agc		ctg		tgg		cac		gct		gac		211	
Ala		Ala		Arg		Ile		Ala		Gly		Ala		Glu		Val		Ile		Ser		Leu		Trp		His		Ala		Asp		35	
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gag		gat		ctc		aag		ggc		gtc		gac		gca		ggt		gtc		ggt		ccc		ggt		gga		ttc		tcc		259	
Glu		Asp		Leu		Lys		Gly		Val		Asp		Ala		Val		Val		Val		Pro		Gly		Gly		Phe		Ser		50	
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tac		ggc		gat		tac		ctg		cgc		acc		ggc		gca		atc		tct		gca		ctg		gcg		cca		gta		307	
Tyr		Gly		Asp		Tyr		Leu		Arg		Thr		Gly		Ala		Ile		Ser		Ala		Leu		Ala		Pro		Val		65	
		55										60										65											
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Met		Gln		Ser		Val		Ile		Glu		Gln		Ala		Gly		Lys		Gly		Met		Pro		Val		Leu		Gly		85	
		70								75								80															
att		tgc		aac		ggc		ttc		cag		atc		ctc		acc		gaa		gca		cgc		ctg		ctt		cca		ggc		403	
Ile		Cys		Asn		Gly		Phe		Gln		Ile		Leu		Thr		Glu		Ala		Arg		Leu		Leu		Pro		Gly		100	
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Ala		Leu		Thr		Arg		Asn		Lys		Gly		Leu		His		Phe		His		Cys		Val		Asp		Ala		His		115	
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ctc		gtt		gta		gag		aac		aac		acc		act		gca		tgg		acc		aac		act		ttg		gaa		aag		499	
Leu		Val		Val		Glu		Asn		Asn		Thr		Thr		Ala		Trp		Thr		Asn		Thr		Leu		Glu		Lys			

120	125	130	
ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag			547
Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln			
135	140	145	
gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg			595
Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val			
150	155	160	165
ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt			643
Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly			
	170	175	180
atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa			691
Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu			
	185	190	195
cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg			739
His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu			
	200	205	210
ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc			789
Phe Leu Ser Ala Val Gly Thr Ile Ala Ala			
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<211> 223			
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Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser			
	20	25	30
Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val			
	35	40	45
Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser			
	50	55	60
Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly			
	65	70	75
Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala			
	85	90	95
Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His			
	100	105	110
Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr			
	115	120	125
Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly			
	130	135	140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly
 145 150 155 160
 Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val
 165 170 175
 Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu
 180 185 190
 Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile
 195 200 205
 Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
 210 215 220

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<211> 1014

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(991)

<223> RXA00620

<400> 921

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aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115
 Met Arg Pro Glu Leu
 1 5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
 Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
 10 15 20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
 Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
 25 30 35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
 Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
 40 45 50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
 Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
 55 60 65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
 Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
 70 75 80 85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
 Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
 90 95 100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
 Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
 105 110 115

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agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
      120                      125                      130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
      135                      140                      145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
150                      155                      160                      165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
      170                      175                      180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
      185                      190                      195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp
      200                      205                      210

gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat 787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr
      215                      220                      225

gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac 835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn
230                      235                      240                      245

tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag 883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu
      250                      255                      260

cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac 931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr
      265                      270                      275

atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att 979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile
      280                      285                      290

ggt tct tgc gtc taagctgctt gattttccct aaa 1014
Gly Ser Cys Val
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<210> 922

<211> 297

<212> PRT

<213> Corynebacterium glutamicum

<400> 922

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Met Arg Pro Glu Leu Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val
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Arg Glu Ile Tyr Glu Ile Asp Asp Lys His Ile Leu Met Val Ala Ser
      20              25              30

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Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp
    35                      40                      45

Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile
    50                      55                      60

Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro
    65                      70                      75                      80

Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu
    85                      90                      95

Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val
    100                     105                     110

Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly
    115                     120                     125

Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr
    130                     135                     140

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val
    145                     150                     155                     160

Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser
    165                     170                     175

Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val
    180                     185                     190

Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr
    195                     200                     205

Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp
    210                     215                     220

Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys
    225                     230                     235                     240

Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys
    245                     250                     255

Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala
    260                     265                     270

Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys
    275                     280                     285

Phe Cys Gln Trp Ile Gly Ser Cys Val
    290                     295

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<212> DNA

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<220>

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<222> (101)..(1270)

<223> RXN00770

<400> 923

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                                   Leu Leu Ser Pro Tyr
                                   1 5

gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163
Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys
                                   10 15 20

ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211
Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln
                                   25 30 35

gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259
Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile
                                   40 45 50

gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307
Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala Pro Met Ala Lys Arg
                                   55 60 65

gcc acc cgc cca gag gtt ctt ggc aac ctc gga ggc ttc gca gga ctc 355
Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly Gly Phe Ala Gly Leu
                                   70 75 80 85

ttt gag ctc gga aaa tac aag aag cca atc ctc gca gca gga tct gac 403
Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu Ala Ala Gly Ser Asp
                                   90 95 100

gga gtc ggc acc aag ctt gtc atc gcc cag atg atg gac aag cac gac 451
Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met Met Asp Lys His Asp
                                   105 110 115

acc atc ggc atc gac ctt gtt gca atg tgt gtg gat gac ctc gtt gtc 499
Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val Asp Asp Leu Val Val
                                   120 125 130

acc ggc gca gag cca ctg ttc ctc cag gac tac atc gcc atc ggc aag 547
Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr Ile Ala Ile Gly Lys
                                   135 140 145

gtt gtc cca gag cac gtt gct gag atc gtc tcc ggt atc gca gaa ggc 595
Val Val Pro Glu His Val Ala Glu Ile Val Ser Gly Ile Ala Glu Gly
                                   150 155 160 165

tgt gtc cag gca ggc tgt gct ctg ctc ggt ggc gaa acc gca gaa cac 643
Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly Glu Thr Ala Glu His
                                   170 175 180

cca ggt gtt atg gaa cca gac cac tac gat gtc tcc gca act gca gtc 691
Pro Gly Val Met Glu Pro Asp His Tyr Asp Val Ser Ala Thr Ala Val
                                   185 190 195

ggc gtt gtc gaa gca gat gaa ctg cta gga cca gac cgc gtc cgc gca 739
Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro Asp Arg Val Arg Ala
                                   200 205 210

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ggc gac gtc ctc atc ggc atg gct tcc tcc ggt ctg cac tcc aac ggt 787
Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly Leu His Ser Asn Gly
215 220 225

tac tcc ctg gct cgc cac gtc ctc ctg gaa aag gca ggc ctg gcg ctt 835
Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys Ala Gly Leu Ala Leu
230 235 240 245

gac gga cac atc gaa gaa ctc gga cgc acc ctc ggt gaa gaa ctt ctc 883
Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu Gly Glu Glu Leu Leu
250 255 260

gag cca acc cgc atc tac gcc aag gac tgc ctg gca ctg atc gca gag 931
Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu Ala Leu Ile Ala Glu
265 270 275

tgc gaa gtt cac acc ttc tgc cac gtc acc ggc ggc ggc ctc gca ggc 979
Cys Glu Val His Thr Phe Cys His Val Thr Gly Gly Gly Leu Ala Gly
280 285 290

aac ctc gag cgg gtt gtc cca gaa ggg ctc gtc gca gaa atg tcc cga 1027
Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg
295 300 305

gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc 1075
Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly
310 315 320 325

aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc 1123
Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly
330 335 340

atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg 1171
Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met
345 350 355

ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac 1219
Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn
360 365 370

ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc 1267
Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly
375 380 385

tac taagcccaac tgtctgctct aag 1293
Tyr
390

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<210> 924

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 924

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20 25 30

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Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45
 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60
 Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95
 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110
 Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu
 245 250 255
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu
 260 265 270
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly
 275 280 285
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val
 290 295 300
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr
 305 310 315 320
 Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe
 325 330 335
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp
 340 345 350
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile

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Gly Glu His Pro Gly Tyr			
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ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa		98	
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu			
15 20 25			
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt		146	
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val			
30 35 40			
tca tac gca gca gca gga gtc gac atc gaa gcc gcc gat cgt gcc gtc		194	
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val			
45 50 55 60			
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt		242	
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu			
65 70 75			
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag		290	
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys			
80 85 90			
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc		338	
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val			
95 100 105			
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt		386	
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val			
110 115 120			
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc		434	
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe			
125 130 135 140			
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct		482	
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala			
145 150 155			
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct		530	

Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala
 160 165 170
 ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac 578
 Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp
 175 180 185
 cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa 626
 His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu
 190 195 200
 ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg 674
 Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met
 205 210 215 220
 gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val
 225 230 235
 ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu
 240 245 250
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<210> 926

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 926

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Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
145 150 155 160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
165 170 175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro
245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
260 265

<210> 927

<211> 338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

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Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu
1 5 10 15

ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96
Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144
Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192
Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240
Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288
Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgtctt 335

Ile Leu Asn Gly Glu His Pro Gly Tyr
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aag

338

<210> 928

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu
1 5 10 15

Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
20 25 30

Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
35 40 45

Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
50 55 60

Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
65 70 75 80

Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
85 90 95

Ile Leu Asn Gly Glu His Pro Gly Tyr
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<210> 929

<211> 1320

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1297)

<223> RXN02345

<400> 929

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Val Thr Ser Thr Gly
1 5

aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac 163
Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp
10 15 20

ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa 211
Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln
25 30 35

tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta 259
Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val

40	45	50	
gct gct gat gtt gtt ctc ggc gat tac acc aac att gat gat ctg cgc Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn Ile Asp Asp Leu Arg 55 60 65			307
gtc gcc atc gaa ggc gcc gat gtg atg acc ttc gac cac gag cac gtc Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe Asp His Glu His Val 70 75 80 85			355
ccc aac gaa cac ctg cac caa ctc atc gca gaa ggc gtc aac gtt cag Pro Asn Glu His Leu His Gln Leu Ile Ala Glu Gly Val Asn Val Gln 90 95 100			403
cca cgc cca gaa gcg ctg gtc aac gca caa gac aaa ctt gtc atg cgc Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp Lys Leu Val Met Arg 105 110 115			451
aag cgt cta cgt gaa ctc ggc gca cca gtc cca cca ttt gct gcc att Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro Pro Phe Ala Ala Ile 120 125 130			499
gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca gtt gat ggc caa Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala Val Asp Gly Gln 135 140 145			547
gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc aag ggc gta tgg Val Cys Leu Lys Ala Arg Gly Gly Tyr Asp Gly Lys Gly Val Trp 150 155 160 165			595
ttc cca gcc gat gta gca gag ctt cag tgc ctt gtg gca gag ctt ctc Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val Ala Glu Leu Leu 170 175 180			643
gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt gcc ctc aac agg Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val Ala Leu Asn Arg 185 190 195			691
gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga gaa acc aaa gcg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly Glu Thr Lys Ala 200 205 210			739
tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg tgt gca gaa gca Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val Cys Ala Glu Ala 215 220 225			787
atc gct ccc gca cct gaa cta tcc gca gaa ctg cag gaa tcc acc aga Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln Glu Ser Thr Arg 230 235 240 245			835
gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc act ggt gtc ttg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val Thr Gly Val Leu 250 255 260			883
gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg cag cca gag atc Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly Gln Pro Glu Ile 265 270 275			931
ttt gtc aac gag ctc gcc atg cgt tca cac aac acc ggc cac tgg act Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr Gly His Trp Thr 280 285 290			979

caa gat ggc tgc gtg acc agc caa ttc gag cag cac ctc cgc gca gtc 1027
 Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His Leu Arg Ala Val
 295 300 305

ctc gac tac cca ctg ggt gct acc gac act ttg gct gat tac acc gtg 1075
 Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala Asp Tyr Thr Val
 310 315 320 325

atg gcc aac gtg ctc ggt gcc gac acc gac cca gag atg ccc atg gca 1123
 Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu Met Pro Met Ala
 330 335 340

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac 1171
 Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His
 345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac 1219
 Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn
 360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc 1267
 Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys
 375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta 1317
 Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
 390 395

gca 1320

<210> 930
 <211> 399
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 930
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 20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser
 35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn
 50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe
 65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu
 85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp
 100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro
 115 120 125


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Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu
 130                      135                      140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp
145                      150                      155                      160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu
                      165                      170                      175

Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys
                      180                      185                      190

Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser
                      195                      200                      205

Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly
210                      215                      220

Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu
225                      230                      235                      240

Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly
                      245                      250                      255

Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn
260                      265                      270

Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn
275                      280                      285

Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln
290                      295                      300

His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu
305                      310                      315                      320

Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro
                      325                      330                      335

Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro
340                      345                      350

Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys
355                      360                      365

Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala
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Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(810)

<223> FRXA02345

<400> 931

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Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
20 25 30	
aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tcg ctt gtg	144
Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt	192
Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga	240
Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
65 70 75 80	
gaa acc aaa gcg tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg	288
Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc	384
Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg	432
Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	

225	230	235	240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa				768
Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu				
	245	250	255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat				810
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<210> 932

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 932

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Val	Asp	Gly	Gln	Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly
		20						25					30		
Lys	Gly	Val	Trp	Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val
		35					40					45			
Ala	Glu	Leu	Leu	Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val
	50					55					60				
Ala	Leu	Asn	Arg	Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly
	65				70					75					80
Glu	Thr	Lys	Ala	Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val
			85						90					95	
Cys	Ala	Glu	Ala	Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln
		100						105					110		
Glu	Ser	Thr	Arg	Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val
		115					120					125			
Thr	Gly	Val	Leu	Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly
	130						135				140				
Gln	Pro	Glu	Ile	Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr
	145				150					155					160
Gly	His	Trp	Thr	Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His
			165						170					175	
Leu	Arg	Ala	Val	Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala
		180						185					190		
Asp	Tyr	Thr	Val	Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu
		195					200					205			
Met	Pro	Met	Ala	Thr	Arg	Met	Val	Glu	Val	Gly	Arg	Lys	Tyr	Pro	Asp
	210					215					220				

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile
225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu
245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
260 265 270

<210> 933

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(595)

<223> RXN02350

<400> 933

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ataaacccgat acgtactttt cgcgccttaag gagaatttca gtg ggt cct cta gtt 115
Val Gly Pro Leu Val 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val 35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259
Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala 50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307
His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala 65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355
His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly 85

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403
Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451
Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499
Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547
Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala

135 140 145
aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595
Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
150 155 160 165

taatgaatcc gatcgtggtg ctg 618

<210> 934

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 934

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Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
20 25 30

Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn
35 40 45

Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
50 55 60

Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
65 70 75 80

Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
85 90 95

Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
100 105 110

Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
115 120 125

Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr
130 135 140

Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys
145 150 155 160

Lys Arg Leu Leu Gly
165

<210> 935

<211> 223

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(223)

<223> FRXA02346

<400> 935

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 Val Gly Pro Leu Val
 1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala
 10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val
 25 30 35

tct gca cac cgc 223
 Ser Ala His Arg
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<210> 936

<211> 41

<212> PRT

<213> Corynebacterium glutamicum

<400> 936

Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
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 20 25 30

Glu Val Gly Val Val Ser Ala His Arg
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<210> 937

<211> 252

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (20)..(229)

<223> FRXA02350

<400> 937

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 1 5 10

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 Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala
 15 20 25

ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc 148
 Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val
 30 35 40

acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc 196
 Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala
 45 50 55

aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg 249
 Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly
 60 65 70

ctg 252

<210> 938

<211> 70

<212> PRT

<213> Corynebacterium glutamicum

<400> 938

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 20 25 30

Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp
 35 40 45

Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu
 50 55 60

Lys Lys Arg Leu Leu Gly
 65 70

<210> 939

<211> 999

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(976)

<223> RXA01087

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 Met Gln Thr Leu Ala
 1 5

gct att gtt cgt gcc acg aag caa cct ttt gag atc acc acc att gat 163
 Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp
 10 15 20

ctg gat gca cca cga cca gat gaa gtt caa atc cgt gtt att gct gcc 211
 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala
 25 30 35

gga gtg cgc cac act gac gca att gtt cgt gat cag att tac cca act 259
 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr
 40 45 50

ttt ctt ccc gca gtt ttc ggc cac gaa ggc gcc gga gta gtt gtc gcc 307
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 55 60 65

gtg ggt tct gca gtc acc tcg gtg aaa cca gat gac aag gta gtg ctg	355
Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu	
70 75 80 85	
gga ttc aac tct tgt ggc cag tgc ttg aag tgt ttg ggc ggt aag cct	403
Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro	
90 95 100	
gcg tac tgt gag aaa ttc tat gac cgc aac ttc gca tgc acc cgc gat	451
Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe Ala Cys Thr Arg Asp	
105 110 115	
gcc ggg cac act act ttg ttt acc cgt gca aca aaa gag cag gca gag	499
Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr Lys Glu Gln Ala Glu	
120 125 130	
gcc atc atc gac acc ctt gat gat gtt ttc tac gat gcg gat gcg ggt	547
Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr Asp Ala Asp Ala Gly	
135 140 145	
ttc ctg gca tac cca gca act ccc cca gag gct tcg gga gta agc gtg	595
Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala Ser Gly Val Ser Val	
150 155 160 165	
ttg gtt gtc gcg gct ggt acc tct gat ctc ccc caa gca aag gaa gca	643
Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro Gln Ala Lys Glu Ala	
170 175 180	
cta cac act gcc tcc tac ttg ggg cgc tcc acc tca ctg att gtt gat	691
Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr Ser Leu Ile Val Asp	
185 190 195	
ttt gga gtg gct ggc atc cac cgc ctg ctt tca tac gaa gaa gaa ctc	739
Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser Tyr Glu Glu Glu Leu	
200 205 210	
cgc gct gcg ggc gtg ctc atc gtt gcc gct gga atg gat ggt gcg cta	787
Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly Met Asp Gly Ala Leu	
215 220 225	
ccc gga gtt gtc gca ggc tta gtg tcc gca cct gtc gtc gca ctg cca	835
Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro Val Val Ala Leu Pro	
230 235 240 245	
acc tcc gtg gga tac ggc gca ggt gct gga gga atc gca cca ctt ctg	883
Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly Ile Ala Pro Leu Leu	
250 255 260	
acc atg ctt aac gcc tgc gcg ccg gga gtt gga gtg gtc aac att gat	931
Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly Val Val Asn Ile Asp	
265 270 275	
aac ggc tat gga gca gga cac ctg gct gcg cag att gcg gcg agg	976
Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln Ile Ala Ala Arg	
280 285 290	
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<211> 292

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 940

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Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp
      35             40             45

Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala
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Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp
      65             70             75             80

Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys
      85             90             95

Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe
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Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr
      115            120            125

Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr
      130            135            140

Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala
      145            150            155            160

Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro
      165            170            175

Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr
      180            185            190

Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser
      195            200            205

Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly
      210            215            220

Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro
      225            230            235            240

Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly
      245            250            255

Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly
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Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln
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Ile Ala Ala Arg
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 <223> RXA00619

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 Val Ala Asp Lys Lys
 1 5
 aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
 10 15 20
 aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
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 atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
 40 45 50
 gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
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 agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
 70 75 80 85
 atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
 90 95 100
 atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
 105 110 115
 cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
 120 125 130
 atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
 135 140 145
 tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
 150 155 160 165
 acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu

170								175					180					
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Leu	Asn	Arg	Tyr	Pro	Leu	Arg	Gly	Ile	Lys	Gly	Pro	Met	Gly	Thr	Ala			
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Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu	Ala	Arg	Leu	Ser	Asp			
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Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp			
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Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser			
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Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile			
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Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly			
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Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys			
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Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met			
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Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys			
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Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp			
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gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggc	gca	ttc	1171		
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe			
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Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala			
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act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa	1267		
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu			
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Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn			
			390															
atg	cgc	gaa	aat	ggc	ggc	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct	1363		
Met	Arg	Glu	Asn	G														

gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435

gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450

ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
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tac cga cca ggt gag att ctt taaaggtttt taacggcggtt cac 1551
 Tyr Arg Pro Gly Glu Ile Leu
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<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 942

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Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
 35 40 45

Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60

Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80

Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95

His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110

Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125

Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140

Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160

Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190

Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu

195	200	205
Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala	Ala His Leu Gly Phe	
210	215	220
Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp		
225	230	235 240
Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser		
	245	250 255
Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu		
	260	265 270
Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met		
	275	280 285
Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg		
	290	295 300
Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu		
	305	310 315 320
Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala		
	325	330 335
Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp		
	340	345 350
Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr		
	355	360 365
Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala		
	370	375 380
Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val		
	385	390 395 400
Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile		
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Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu		
	420	425 430
Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser		
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Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His		
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Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu		
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<211> 1683

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<223> RXA02622

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Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr
200 205 210

acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln	
215 220 225	
tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag	835
Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys	
230 235 240 245	
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat	883
Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp	
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Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile	
265 270 275	
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc	979
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile	
280 285 290	
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc	1027
Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe	
295 300 305	
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac	1075
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn	
310 315 320 325	
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa	1123
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu	
330 335 340	
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt	1171
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu	
345 350 355	
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc	1219
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser	
360 365 370	
ggc ggt ctg ctt gtt cag gaa gcg gac ttg atc cac gct gag ggc gac	1267
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp	
375 380 385	
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag	1315
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu	
390 395 400 405	
gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag	1363
Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys	
410 415 420	
tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc	1411
Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly	
425 430 435	
atg gga cag gtc aac gcg gtt gac tct gct cgc ttg gct gtc gac cgt	1459
Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg	
440 445 450	

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc 1507
 Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe
 455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act 1555
 Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr
 470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag 1603
 Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu
 490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac 1651
 Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His
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ttc gct cac taaagttttt aaagatttcg ctt 1683
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<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 944

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Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu
 35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys
 50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile
 65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu
 85 90 95

Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala
 100 105 110

Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile
 115 120 125

Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro
 130 135 140

Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu
 145 150 155 160

Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala
 165 170 175

Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr

180					185					190					
Trp	Met	Ser	Glu	Gln	Leu	Ala	Ala	Glu	Asp	Ser	Glu	Thr	Glu	Phe	Pro
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Gly	Trp	Ile	Gly	Thr	Thr	Asn	Thr	Leu	Ser	Arg	Ser	Leu	Arg	Tyr	Gly
	210					215					220				
Glu	Asn	Pro	His	Gln	Ser	Ala	Ala	Leu	Tyr	Val	Gly	Asn	Thr	Arg	Gly
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Leu	Ala	Gln	Ala	Lys	Gln	Phe	His	Gly	Lys	Glu	Met	Ser	Tyr	Asn	Asn
				245					250					255	
Tyr	Thr	Asp	Ser	Asp	Ala	Ala	Trp	Arg	Ala	Ala	Trp	Asp	His	Glu	Arg
			260					265					270		
Pro	Cys	Val	Ala	Ile	Ile	Lys	His	Ala	Asn	Pro	Cys	Gly	Ile	Ala	Val
		275					280					285			
Ser	Asp	Glu	Ser	Ile	Ala	Ala	Ala	His	Arg	Glu	Ala	His	Ala	Cys	Asp
	290					295					300				
Ser	Val	Ser	Ala	Phe	Gly	Gly	Val	Ile	Ala	Ser	Asn	Arg	Glu	Val	Ser
305					310					315					320
Val	Glu	Met	Ala	Asn	Gln	Val	Ala	Glu	Ile	Phe	Thr	Glu	Val	Ile	Ile
				325					330					335	
Ala	Pro	Ser	Tyr	Glu	Glu	Gly	Ala	Val	Glu	Ile	Leu	Ser	Gln	Lys	Lys
			340					345					350		
Asn	Ile	Arg	Ile	Leu	Gln	Ala	Glu	Ala	Pro	Val	Arg	Lys	Gly	Phe	Glu
		355					360					365			
Ser	Arg	Glu	Ile	Ser	Gly	Gly	Leu	Leu	Val	Gln	Glu	Arg	Asp	Leu	Ile
	370				375						380				
His	Ala	Glu	Gly	Asp	Asn	Ser	Ala	Asn	Trp	Thr	Leu	Ala	Ala	Gly	Ser
385					390					395					400
Ala	Val	Ser	Pro	Glu	Val	Leu	Lys	Asp	Leu	Glu	Phe	Ala	Trp	Thr	Ala
				405					410					415	
Val	Arg	Ser	Val	Lys	Ser	Asn	Ala	Ile	Leu	Leu	Ala	Lys	Asn	Gly	Ala
			420					425					430		
Thr	Val	Gly	Val	Gly	Met	Gly	Gln	Val	Asn	Arg	Val	Asp	Ser	Ala	Arg
		435					440					445			
Leu	Ala	Val	Asp	Arg	Ala	Gly	Ala	Glu	Arg	Ala	Thr	Gly	Ser	Val	Ala
	450					455					460				
Ala	Ser	Asp	Ala	Phe	Phe	Pro	Phe	Ala	Asp	Gly	Phe	Glu	Val	Leu	Ala
465					470					475					480
Glu	Ala	Gly	Ile	Thr	Ala	Val	Val	Gln	Pro	Gly	Gly	Ser	Ile	Arg	Asp
				485					490					495	
Asn	Glu	Val	Ile	Glu	Ala	Ala	Asn	Lys	Ala	Gly	Val	Thr	Met	Tyr	Leu
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Thr Gly Ala Arg His Phe Ala His
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1618)
<223> RXN00488

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Met Thr Thr Gln Ser
1 5
cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
10 15 20
tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
25 30 35
cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
40 45 50
aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
55 60 65
atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
70 75 80 85
aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg
90 95 100
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met
105 110 115
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly
120 125 130
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn
135 140 145
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt 595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val
150 155 160 165

atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	1027
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggg att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	1075
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	
310 315 320 325	
ggg gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac	1123
Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His	
330 335 340	
aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt	1171
Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly	
345 350 355	
gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc	1219
Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly	
360 365 370	
tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc	1267
Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile	
375 380 385	
aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct	1315
Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala	
390 395 400 405	

atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac 1363
 Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp
 410 415 420

 cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa 1411
 Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu
 425 430 435

 ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att 1459
 Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile
 440 445 450

 cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc 1507
 His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
 455 460 465

 tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc 1555
 Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser
 470 475 480 485

 gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa 1603
 Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu
 490 495 500

 gct cct aac tac cac tagattttgc tcacttaaagc agc 1641
 Ala Pro Asn Tyr His
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<210> 946

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 946

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
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 Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
 20 25 30

 Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45

 Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60

 Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

 Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

 Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110

 Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125

 Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
 145 150 155 160
 Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
 165 170 175
 Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
 180 185 190
 Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
 195 200 205
 Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
 210 215 220
 Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
 225 230 235 240
 Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
 245 250 255
 Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
 260 265 270
 Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
 275 280 285
 Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala
 290 295 300
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg
 305 310 315 320
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala
 325 330 335
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly
 340 345 350
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn
 355 360 365
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly
 370 375 380
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met
 385 390 395 400
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg
 405 410 415
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp
 420 425 430
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro
 435 440 445
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met
 450 455 460

Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe
465 470 475 480

Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile
485 490 495

Gln Gln Thr Val Glu Ala Pro Asn Tyr His
500 505

<210> 947

<211> 574

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA00492

<400> 947

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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115
Met Thr Thr Gln Ser
1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg
90 95 100

tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met
105 110 115

agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly
120 125 130

ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn

135 140 145 574
 cgc gat atg cgt ttt gaa agc gac atg
 Arg Asp Met Arg Phe Glu Ser Asp Met
 150 155

<210> 948
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 948
 Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
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 Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
 20 25 30
 Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45
 Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60
 Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80
 Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95
 Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110
 Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125
 Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140
 Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met
 145 150 155

<210> 949
 <211> 557
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(534)
 <223> FRXA00488

<400> 949 48
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 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
 1 5 10 15
 gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct 96
 Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala

20	25	30	
aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg			144
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu			
35	40	45	
gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag			192
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys			
50	55	60	
cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc			240
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly			
65	70	75	80
cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc			288
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe			
85	90		95
cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa			336
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu			
100	105		110
ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag			384
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln			
115	120		125
gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att			432
Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile			
130	135		140
gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg			480
Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu			
145	150	155	160
aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac			528
Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn			
165	170		175
tac cac tagattttgc tcacttaaagc agc			557
Tyr His			

<210> 950

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 950

Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
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Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

Tyr His

<210> 951
 <211> 1554
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1531)
 <223> RXA02469

<400> 951
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gccgtgttca gggataactg attaatacaac taggagaccc atg cgt ttt ctt aac 115
 Met Arg Phe Leu Asn
 1 5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
 Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
 10 15 20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
 Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
 25 30 35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
 Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
 40 45 50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
 Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
 55 60 65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
 Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
 70 75 80 85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc	403
Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr	
90 95 100	
gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag	451
Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys	
105 110 115	
cggt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc	499
Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly	
120 125 130	
atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg	547
Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val	
135 140 145	
ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc	595
Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser	
150 155 160 165	
ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc	643
Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala	
170 175 180	
ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc	691
Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr	
185 190 195	
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc	739
Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly	
200 205 210	
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga	787
Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly	
215 220 225	
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac	835
Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp	
230 235 240 245	
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc	883
Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile	
250 255 260	
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc	931
Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr	
265 270 275	
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag	979
Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys	
280 285 290	
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc	1027
Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly	
295 300 305	
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc	1075
Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala	
310 315 320 325	

cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc 1123
 Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro
 330 335 340

cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc 1171
 Arg Asp Val Ala Leu Ala Leu Ala Gly Ala Ser Asn Val Met Val
 345 350 355

gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc 1219
 Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe
 360 365 370

gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg 1267
 Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg
 375 380 385

cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca 1315
 Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala
 390 395 400 405

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att 1363
 Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile
 410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc 1411
 Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser
 425 430 435

ggt gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc 1459
 Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr
 440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca 1507
 Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala
 455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttgt tgtgcctttg aga 1554
 Glu Gly Lys Pro Arg Ala Ser Arg
 470 475

<210> 952

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

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Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser
 20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val
 35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile
 50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp
 65 70 75 80

Ile	Ala	Ala	Glu	Thr	Ile	Ala	Asn	Val	Lys	Lys	Ala	Asp	Leu	Val	Phe	85	90	95
Asp	Thr	Pro	Ile	Thr	Val	Lys	Pro	His	His	Thr	Val	Gly	Tyr	Ala	Arg	100	105	110
Asn	Leu	Ile	His	Lys	Arg	Ala	His	Gly	Ala	Ala	Ile	Val	Leu	Glu	Gly	115	120	125
Asp	Gln	Pro	Val	Gly	Ile	Val	Thr	Asp	Lys	Asp	Leu	Glu	Gly	Ala	Asp	130	135	140
Asn	Phe	Thr	Gln	Val	Gly	Thr	Leu	Met	Ser	Thr	Ser	Leu	Leu	Thr	Leu	145	150	155
Pro	Glu	Asp	Ile	Ser	Pro	Glu	Asp	Ala	Phe	Gly	Ile	Leu	His	Glu	His	165	170	175
Ser	Arg	Lys	Leu	Ala	Pro	Val	Val	Ala	Ala	Asp	Gly	Ser	Leu	Arg	Gly	180	185	190
Ile	Leu	Thr	Arg	Thr	Gly	Ala	Leu	Arg	Ala	Thr	Met	Tyr	Lys	Pro	Ala	195	200	205
Ile	Asp	Ala	Asn	Gly	Arg	Leu	Arg	Val	Gly	Ala	Ala	Ile	Gly	Ile	Asn	210	215	220
Gly	Asp	Ile	Glu	Gly	Arg	Thr	Lys	Thr	Leu	Leu	Asp	Ala	Gly	Ala	Asp	225	230	235
Val	Leu	Val	Val	Asp	Thr	Ala	His	Gly	His	Gln	Ser	Thr	Met	Ile	Ser	245	250	255
Ala	Leu	Lys	Arg	Ile	Arg	Ala	Leu	Asp	Val	Asn	Val	Pro	Ile	Val	Ala	260	265	270
Gly	Asn	Val	Val	Thr	Ala	Asp	Gly	Val	Arg	Asp	Leu	Val	Glu	Ala	Gly	275	280	285
Ala	Asn	Ile	Ile	Lys	Val	Gly	Val	Gly	Pro	Gly	Ala	Met	Cys	Thr	Thr	290	295	300
Arg	Met	Gln	Thr	Gly	Val	Gly	Arg	Pro	Gln	Phe	Ser	Ala	Val	Leu	Glu	305	310	315
Cys	Ala	Ala	Glu	Ala	Arg	Lys	Leu	Gly	Ala	His	Val	Trp	Ala	Asp	Gly	325	330	335
Gly	Val	Arg	Asp	Pro	Arg	Asp	Val	Ala	Leu	Ala	Leu	Ala	Ala	Gly	Ala	340	345	350
Ser	Asn	Val	Met	Val	Gly	Ser	Trp	Phe	Ser	Gly	Thr	Tyr	Glu	Ser	Pro	355	360	365
Gly	Asp	Leu	Arg	Phe	Glu	Ser	Asp	Gly	Arg	Met	Tyr	Lys	Glu	Ser	Phe	370	375	380
Gly	Met	Ala	Ser	Arg	Arg	Ala	Val	Glu	Ser	Arg	Asn	Gln	Lys	Val	Glu	385	390	395

Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr
 405 410 415

Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val
 420 425 430

Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala
 435 440 445

Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser
 450 455 460

Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg
 465 470 475

<210> 953

<211> 1692

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1669)

<223> RXN00487

<400> 953

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 Val Ser Leu Gln Thr
 1 5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
 10 15 20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
 25 30 35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
 40 45 50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
 Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
 55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att 355
 Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile
 70 75 80 85

tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc 403
 Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala
 90 95 100

aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt 451
 Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly
 105 110 115

ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	1027
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	
tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt	1075
Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly	
310 315 320 325	
tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg	1123
Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val	
330 335 340	
gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac	1171
Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn	
345 350 355	
gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg	1219

Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc 1267
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt 1315
 Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc 1363
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt 1411
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc 1459
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg 1507
 Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val
 455 460 465

ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc 1555
 Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg
 470 475 480 485

ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa 1603
 Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu
 490 495 500

gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca 1651
 Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro
 505 510 515

gga acc atc gaa tgg gag taggccttaa atgagccttc gtt 1692
 Gly Thr Ile Glu Trp Glu
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<210> 954

<211> 523

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly
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 20 25 30

Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala
 35 40 45

Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu
 65 70 75 80
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu
 85 90 95
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp
 100 105 110
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
 115 120 125
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
 130 135 140
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
 145 150 155 160
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
 165 170 175
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
 245 250 255
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
 260 265 270
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
 275 280 285
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
 290 295 300
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
 305 310 315 320
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
 325 330 335
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
 340 345 350
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr
450 455 460

Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr
465 470 475 480

Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr
485 490 495

Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val
500 505 510

Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu
515 520

<210> 955

<211> 1486

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> FRXA00487

<400> 955

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agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115
Val Ser Leu Gln Thr
1 5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
10 15 20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
25 30 35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
40 45 50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	1027
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	
tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt	1075

Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
 310 315 320 325
 tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg 1123
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
 330 335 340
 gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac 1171
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
 345 350 355
 gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg 1219
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
 360 365 370
 cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc 1267
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
 375 380 385
 ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt 1315
 Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405
 ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc 1363
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420
 cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt 1411
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435
 gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc 1459
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
 440 445 450
 tct gtt ggt gtt caa ggc gat ggc cgc 1486
 Ser Val Gly Val Gln Gly Asp Gly Arg
 455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

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 20 25 30
 Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala
 35 40 45
 Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
 50 55 60
 Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu
 65 70 75 80

Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu
 85 90 95
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp
 100 105 110
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
 115 120 125
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
 130 135 140
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
 145 150 155 160
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
 165 170 175
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
 245 250 255
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
 260 265 270
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
 275 280 285
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
 290 295 300
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
 305 310 315 320
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
 325 330 335
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
 340 345 350
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp

	405		410		415
Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu					
	420		425		430
Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu					
	435		440		445
Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg					
	450		455		460

<210> 957

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02237

<400> 957

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gcacttctcg agcgttttcgg cttcgaggat taattcttca	gtg tcg ggc gat aac	115
	Val Ser Gly Asp Asn	
	1 5	

caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa	163
Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys	
10 15 20	

tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc	211
Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe	
25 30 35	

agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga	259
Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly	
40 45 50	

cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac	307
Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp	
55 60 65	

tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt	355
Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg	
70 75 80 85	

tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg	403
Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg	
90 95 100	

cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc	451
Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser	
105 110 115	

tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa	499
Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu	
120 125 130	

gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643
Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys
170 175 180

693 aqg

<213> Corynebacterium glutamicum

Val Ser Gly Asp Asn Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro
1 5 10 15

Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val
20 25 30

Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro
35 40 45

Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe
50 55 60

Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His
65 70 75 80

Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala
85 90 95

Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala
100 105 110

Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala
115 120 125

Pro	Pro	Ser	Trp	Glu	Val	Leu	Val	Glu	Arg	Leu	Thr	Gly	Arg	Gly	Thr
130						135					140				

Glu Ser Glu Asp Val Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu
145 150 155 160

Leu Ala Ala Gln Ser Glu Phe Lys His Val Ile Ile Asn Asp Asp Val
165 170 175

Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala
180 185 190

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<220>
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<222> (101)..(1390)
<223> RXA01446
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tgcatactcc aacttcacatg atcggatgtg acgtaaacca atg gct gca atc gtt																	115
Met Ala Ala Ile Val																	5
att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat																	163
Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp																	20
10 15																	
att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac																	211
Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn																	35
25 30																	
aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag																	259
Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys																	50
40 45																	
ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc																	307
Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly																	65
55 60																	
aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc																	355
Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly																	85
70 75 80																	
ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac																	403
Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn																	100
90 95																	
gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa																	451
Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu																	115
105 110																	
cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc																	499
Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly																	130
120 125 130																	
cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac																	547
Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp																	145
135 140 145																	
att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat																	595
Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp																	165
150 155 160																	
tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc																	643
Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val																	180
170 175 180																	

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc	691
Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg	
185 190 195	
ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag	739
Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln	
200 205 210	
ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg	787
Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val	
215 220 225	
gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt	835
Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly	
230 235 240 245	
ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc	883
Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser	
250 255 260	
ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc	931
Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe	
265 270 275	
cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt	979
Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly	
280 285 290	
ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac	1027
Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr	
295 300 305	
gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac	1075
Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp	
310 315 320 325	
tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca	1123
Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro	
330 335 340	
atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca	1171
Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro	
345 350 355	
ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg	1219
Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met	
360 365 370	
cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt	1267
Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu	
375 380 385	
cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt	1315
Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly	
390 395 400 405	
gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc	1363
Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile	
410 415 420	

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 425 430

gag 1413

<210> 960

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

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Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys
 20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu
 35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala
 50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe
 65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu
 85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met
 100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr
 115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly
 130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val
 145 150 155 160

Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn
 165 170 175

Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr
 180 185 190

Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn
 195 200 205

Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala
 210 215 220

Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser
 225 230 235 240

Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr
 245 250 255

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<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1528)
<223> RXA00619
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<400> 961
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cgactaggtt agtttcggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115
Val Ala Asp Lys Lys
1 5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala

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40	45	50	
gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca			307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala			
55	60	65	
agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc			355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg			
70	75	80	85
atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc			403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly			
90	95	100	
atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac			451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His			
105	110	115	
cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct			499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala			
120	125	130	
atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt			547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg			
135	140	145	
tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca			595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala			
150	155	160	165
acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg			643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu			
170	175	180	
ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc			691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala			
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caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat			739
Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp			
200	205	210	
ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac			787
Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp			
215	220	225	
tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct			835
Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser			
230	235	240	245
gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att			883
Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile			
250	255	260	
cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc			931
Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly			
265	270	275	
cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt			979
Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys			
280	285	290	

gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg 1027
 Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met
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gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc 1075
 Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys
 310 315 320 325

tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac 1123
 Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp
 330 335 340

gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc 1171
 Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe
 345 350 355

cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca 1219
 Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala
 360 365 370

act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa 1267
 Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu
 375 380 385

acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac 1315
 Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn
 390 395 400 405

atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct 1363
 Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala
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gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435

gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450

ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
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<210> 962

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 962

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Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
 35 40 45
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175
 Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350

Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365

Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380

Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400

Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415

Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430

Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445

Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
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Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
 465 470 475

<210> 963

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(643)

<223> RXA00688

<400> 963

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 Met Arg Leu Val Leu
 1 5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
 Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
 10 15 20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
 Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
 25 30 35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
 Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
 40 45 50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
 Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
 55 60 65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
 Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
 70 75 80 85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
 Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
 90 95 100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
 Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
 105 110 115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
 Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
 120 125 130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
 Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
 135 140 145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
 Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
 150 155 160 165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
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 170 175 180

taagatttct tctctagtgc tgc 666

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<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 964

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 35 40 45

Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
 50 55 60

Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
 65 70 75 80

Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
 85 90 95

Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
 100 105 110

Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
 115 120 125

Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
 130 135 140

127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
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Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
165 170 175

Lys Ala Leu Gly Lys
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<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(508)

<223> RXA00266

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agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
Met Thr Glu Arg Thr
1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
10 15 20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
25 30 35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
40 45 50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
55 60 65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
70 75 80 85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
90 95 100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
105 110 115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
120 125 130

cct aac ctg taatittttac ggtagaaaa aaa 531
Pro Asn Leu

135

<210> 966
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 966
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 Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys
 20 25 30
 Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys
 35 40 45
 His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
 50 55 60
 Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
 65 70 75 80
 Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
 85 90 95
 Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly
 100 105 110
 Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
 115 120 125
 Ile Ser Ile Trp Phe Pro Asn Leu
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA00489

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 Met Arg Asp His Val
 1 5
 gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp
 10 15 20
 att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat	259
Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn	
40 45 50	
cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc	307
His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly	
55 60 65	
aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc	355
Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg	
70 75 80 85	
cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag	403
His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu	
90 95 100	
gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca	451
Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala	
105 110 115	
gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt	499
Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg	
120 125 130	
gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt	547
Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg	
135 140 145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc	595
Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile	
150 155 160 165	
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc	643
Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala	
170 175 180	
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct	691
Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala	
185 190 195	
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt	739
Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly	
200 205 210	
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca	787
Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala	
215 220 225	
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg	835
Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala	
230 235 240 245	
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc	883
Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile	
250 255 260	
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att	931
Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile	
265 270 275	

gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct 979
 Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala
 280 285 290

gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac 1027
 Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His
 295 300 305

cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag 1075
 Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu
 310 315 320 325

gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg 1123
 Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro
 330 335 340

tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag 1171
 Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys
 345 350 355

tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219
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 360 365 370

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 Asn

<210> 968

<211> 374

<212> PRT

<213> Corynebacterium glutamicum

<400> 968

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 20 25 30

Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp
 35 40 45

Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe
 50 55 60

Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu
 65 70 75 80

Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val
 85 90 95

Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu
 100 105 110

Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg
 115 120 125

Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser
 130 135 140

Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala
145 150 155 160

Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn
165 170 175

Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp
180 185 190

Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His
195 200 205

Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn
210 215 220

Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile
225 230 235 240

Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly
245 250 255

Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp
260 265 270

Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser
275 280 285

Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro
290 295 300

Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser
305 310 315 320

Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly
325 330 335

Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys
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Val Ser Leu His Val Asn
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<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1531)

<223> RXN02281

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	Val	Gln	Lys	Asp	Ser	
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gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc	163					
Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu						
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att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac	211					
Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn						
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aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc	259					
Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr						
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gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc gcc	307					
Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly						
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Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg						
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gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403					
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Arg Leu Thr Ser Asn						
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tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451					
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro						
	105			110		115
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499					
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly						
	120			125		130
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547					
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp						
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gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595					
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro						
	150			155		160
ctt ttc cac ttc ggc ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643					
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile						
	170			175		180
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691					
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu						
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ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739					
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met						
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tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787					
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro						
	215			220		225
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835					
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu						

230	235	240	245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile				
	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro				
	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu				
	280	285	290	
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Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg				
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	310	315	320	325
ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa				1123
Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu				
	330	335	340	
atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac				1171
Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp				
	345	350	355	
aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac				1219
Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn				
	360	365	370	
tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc				1267
Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser				
	375	380	385	
acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga				1315
Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly				
	390	395	400	405
tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg				1363
Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu				
	410	415	420	
cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac				1411
Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr				
	425	430	435	
ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa				1459
Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu				
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tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg				1507
Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg				
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Thr Leu Gly Glu Val Pro Phe Arg				
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 <213> Corynebacterium glutamicum

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 35 40 45
 Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365
 Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380
 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400
 Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
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 Val Gln Lys Asp Ser
 1 5
 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20
 att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn

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Asn	Glu	Asp	Tyr	Ala	Ala	Tyr	Ala	Asp	Val	Val	Tyr	Pro	Lys	Leu	Thr	
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Val	Asp	Val	Leu	Glu	Trp	Lys	Pro	Ile	Asp	Arg	Thr	Glu	Pro	Phe	Gly	
		55				60					65					
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Tyr	Val	Asp	Arg	Ala	Gly	Arg	Tyr	Ser	Ala	Thr	Leu	Ser	Lys	Pro	Arg	
		70			75					80					85	
gtg	att	gag	cgt	tac	ctc	cgc	gaa	caa	ctc	gag	cgt	ctc	acc	agt	aat	403
Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu	Arg	Leu	Thr	Ser	Asn	
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Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
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Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly	
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gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp	
		135				140					145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro	
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ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile	
				170					175					180		
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Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu	
			185				190						195			
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met	
		200					205					210				
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggc	cta	tcc	ttg	cca	787
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro	
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aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa	835
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu	
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acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile	
				250					255					260		
acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro	
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tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa 979
 Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu
 280 285 290

gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc 1027
 Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg
 295 300 305

atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att 1075
 Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc 1168
 Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser
 345 350 355

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<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

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 20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile

165										170					175				
Ala	Cys	Ala	Arg	Ile	Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val				
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Gln	Lys	Tyr	Ile	Leu	Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe				
		195					200					205							
Val	His	Phe	Ala	Met	Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val				
		210				215					220								
Gly	Leu	Ser	Leu	Pro	Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr				
225					230					235					240				
Ser	Leu	Gly	Thr	Glu	Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro				
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Arg	Tyr	Asp	Leu	Ile	Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn				
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Ile	Gly	Val	Gly	Pro	Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala				
		275					280					285							
Val	Leu	Arg	Pro	Glu	Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met				
		290				295					300								
Asp	Ala	Arg	Met	Arg	Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln				
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Arg	Glu	Asp	His	Ile	Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile				
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Pro	Ala	Ile	Pro	Glu	Ile	Gln	Lys	Ala	Leu	Glu	Ala	Ser	Val	Asp	Glu				
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Ile	Tyr	Gly	Ser																
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1279)

<223> RXA00147

<400> 973

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Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser	Val	Pro	Ala	Tyr	Leu	
			10						15					20		

gtt	ctt	gca	gac	gga	cgt	acc	ttc	acc	gga	ttt	ggc	ttt	gga	gct	atc	211
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Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala		
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Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu		
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gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451	
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			120				125					130					
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggg	tcc	att	gca	gcg	ggc	atc	ttc	547	
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe		
			135			140					145						
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Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val		
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Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser		
			170					175						180			
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691	
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr		
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gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739	
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe		
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Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe		
			215			220					225						
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835	
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly		
			230		235					240					245		
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883	
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu		
			250					255						260			
gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931	
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln		

265	270	275	
att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc			979
Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly			
280	285	290	
cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc			1027
His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile			
295	300	305	
gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc			1075
Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly			
310	315	320	325
cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc			1123
Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys			
330	335	340	
ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca			1171
Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala			
345	350	355	
tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca			1219
Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala			
360	365	370	
agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag			1267
Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln			
375	380	385	
aag aaa ggc gca taaataacat gccaaagcgt tca			1302
Lys Lys Gly Ala			
390			
<210> 974			
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<212> PRT			
<213> Corynebacterium glutamicum			
<400> 974			
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Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe			
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Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr			
35	40	45	
Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg			
50	55	60	
Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn			
65	70	75	80
Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu			
85	90	95	
Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr			
100	105	110	

Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365
 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
 370 375 380
 Asp Ala Asp Ala Gln Lys Lys Gly Ala
 385 390

<210> 975

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA00145

<400> 975

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agtcacgctc acccgagaag actctgaagg ggattcctag atg aag cac ctc cta 115
                                         Met Lys His Leu Leu
                                         1                               5

tcc att agc gat ctt tcc aaa gat gag att gtt gga ttg ctg gat gaa 163
Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
                        10                        15                        20

gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
                        25                        30                        35

ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
                        40                        45                        50

acg cgc acc cgt tcg tcc ttt gaa acc gca gga aag tgg atg agc gcc 307
Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
                        55                        60                        65

gat gtg att aac att tcg gcc tca tca tcc agc gtg aag aag ggc gag 355
Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
                        70                        75                        80                        85

tcg ctg aaa gat acc ggc ttg act ttg tcg gca atc ggc gcg gat gcg 403
Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
                        90                        95                        100

atc atc atg cgc cac cca gcc tca ggc gcc gcg cag cag ctt gcg cag 451
Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala Gln Gln Leu Ala Gln
                        105                        110                        115

ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
                        120                        125                        130

ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
                        135                        140                        145

cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
                        150                        155                        160                        165

gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
                        170                        175                        180

act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro
                        185                        190                        195

att ggt gtg gag aac tgg cca gtc cga ttc tcc tac gac atg gac gca 739

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Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser Tyr Asp Met Asp Ala
 200 205 210

gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa 787
 Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu
 215 220 225

cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg 835
 Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu
 230 235 240 245

tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc 883
 Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile
 250 255 260

atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag 931
 Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln
 265 270 275

gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt 979
 Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly
 280 285 290

gtg cac atg cgc atg gcc att ttg ttc gcc ctg gtc gca ggc tct gac 1027
 Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp
 295 300 305

gcg act atc taatcgcgac catctgatcg cga 1059
 Ala Thr Ile
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<210> 976

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 976

Met Lys His Leu Leu Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val
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Gly Leu Leu Asp Glu Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg
 20 25 30

Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu
 35 40 45

Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly
 50 55 60

Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser
 65 70 75 80

Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala
 85 90 95

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala
 100 105 110

Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val
 115 120 125


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Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu
 130                               135                               140

Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys
145                               150                               155                               160

Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn
                               165                               170                               175

Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro
                               180                               185                               190

Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser
                               195                               200                               205

Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu
210                               215                               220

Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg
225                               230                               235                               240

Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu
                               245                               250                               255

Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met
                               260                               265                               270

Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln
                               275                               280                               285

Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu
                               290                               295                               300

Val Ala Gly Ser Asp Ala Thr Ile
305                               310

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<210> 977
<211> 1464
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<222> (101)..(1441)
<223> RXA00146

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<400> 977
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gatcgcgaaa ttctagaaaa ggtaacgagg gattaaagaa gtg gtt gac agc aac      115
                               Val Val Asp Ser Asn
                               1                               5

acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca      163
Thr Gln Tyr Pro Glu Thr Gly Ala Leu Ala Pro Ala Pro Ala Asp Ser
                               10                               15                               20

ctc cta atc agc aac gtt ttg gtc tac ggc gaa ggc gag cca acg aat      211
Leu Leu Ile Ser Asn Val Leu Val Tyr Gly Glu Gly Glu Pro Thr Asn

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25	30	35	
gtg ttt gtt aaa gat ggt gtg atc gca gct atc ggc ggc act cat gag			259
Val Phe Val Lys Asp Gly Val Ile Ala Ala Ile Gly Gly Thr His Glu			
40	45	50	
gct gac cgc acc atc gac ggc aat ggg gga gtt ctc ctt cca ggt ttc			307
Ala Asp Arg Thr Ile Asp Gly Asn Gly Gly Val Leu Leu Pro Gly Phe			
55	60	65	
gtg gac atg cac gtt cac ctg cgt gag cca ggc cgc gaa gac act gaa			355
Val Asp Met His Val His Leu Arg Glu Pro Gly Arg Glu Asp Thr Glu			
70	75	80	85
acc att gcc act ggt tct gcc gcc gca gcc aag ggc gga ttc acc gca			403
Thr Ile Ala Thr Gly Ser Ala Ala Ala Lys Gly Gly Phe Thr Ala			
90	95	100	
gta ttc acc atg gcg aac acc act cca gtg atg gat cag ccg gtt atc			451
Val Phe Thr Met Ala Asn Thr Thr Pro Val Met Asp Gln Pro Val Ile			
105	110	115	
gcg gaa tcc gta tgg ttc aag ggc caa aac att ggc ctg tgc gac gtg			499
Ala Glu Ser Val Trp Phe Lys Gly Gln Asn Ile Gly Leu Cys Asp Val			
120	125	130	
cat cca gtt gga tcc atc acc aag ggt ctt gag ggc aag gag ctt act			547
His Pro Val Gly Ser Ile Thr Lys Gly Leu Glu Gly Lys Glu Leu Thr			
135	140	145	
gag ttc ggc atg atg gct cgc tct gaa gcc aag gtg cgc atg ttc tct			595
Glu Phe Gly Met Met Ala Arg Ser Glu Ala Lys Val Arg Met Phe Ser			
150	155	160	165
gat gat ggc aag tgc gtc gat gat cct cag gtc atg cgc cgc gcg ctg			643
Asp Asp Gly Lys Cys Val Asp Asp Pro Gln Val Met Arg Arg Ala Leu			
170	175	180	
gaa tac gcc aag ggc atg gac gtt ttg atc gcc cag cac gct gag gat			691
Glu Tyr Ala Lys Gly Met Asp Val Leu Ile Ala Gln His Ala Glu Asp			
185	190	195	
cac cgc ctg act gag ggc gct tca gca cac gag ggt gaa aac gca gct			739
His Arg Leu Thr Glu Gly Ala Ser Ala His Glu Gly Glu Asn Ala Ala			
200	205	210	
cgt ctg ggt ctg cgc ggc tgg cca cgt gtg gct gag gaa tcc atc gtg			787
Arg Leu Gly Leu Arg Gly Trp Pro Arg Val Ala Glu Glu Ser Ile Val			
215	220	225	
gtg cgc gat gcc atc atg gct cgt gac tac ggc aac cgc gtg cac atc			835
Val Arg Asp Ala Ile Met Ala Arg Asp Tyr Gly Asn Arg Val His Ile			
230	235	240	245
tgc cac gcc tcc act gaa ggc acc gtg gag ttg ctt cgt tgg gct aag			883
Cys His Ala Ser Thr Glu Gly Thr Val Glu Leu Leu Arg Trp Ala Lys			
250	255	260	
tcc cag ggc att cca atc acc gcg gaa gtc acc ccg cac cac ctc acc			931
Ser Gln Gly Ile Pro Ile Thr Ala Glu Val Thr Pro His His Leu Thr			
265	270	275	

ttg acc gat gag cgc ctg gaa acc tac gac gcg gtc aac aaa gtc aat 979
 Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala Val Asn Lys Val Asn
 280 285 290

ccg cca ctg cgc gaa agc cgc gat gcc gaa gcg ctc aag aag gcg ctt 1027
 Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala Leu Lys Lys Ala Leu
 295 300 305

ctc gac ggc acc atc gat gtt gtt gca acc gac cac gct cct cac ggt 1075
 Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp His Ala Pro His Gly
 310 315 320 325

tcc gaa gat aag tgc tgt gaa ttc gaa aac gcc aag cca ggc atg ctc 1123
 Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala Lys Pro Gly Met Leu
 330 335 340

gga ttg gaa acc tca ctg tcc atc atc gtg gac acc ttc gtt gcc acc 1171
 Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp Thr Phe Val Ala Thr
 345 350 355

gga ctt gca gac tgg cgc ttt gtt gcg cgc gtg atg agt gaa cgc cca 1219
 Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val Met Ser Glu Arg Pro
 360 365 370

gca gaa atc acc cgt cta cca ggc cag ggt cgc cca atc gca gaa ggt 1267
 Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg Pro Ile Ala Glu Gly
 375 380 385

gag cca gca aac ctc gcg att gtt gat cca gga aaa acc tgg aca gca 1315
 Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly Lys Thr Trp Thr Ala
 390 395 400 405

tcc ggt gca gac ttt gcg tcc aag gct gaa aat acc cca ttt gag ggc 1363
 Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn Thr Pro Phe Glu Gly
 410 415 420

caa gaa ttc agt gcc aag gtc aca cac acc gtg ctt cgt ggc aag gtg 1411
 Gln Glu Phe Ser Ala Lys Val Thr His Thr Val Leu Arg Gly Lys Val
 425 430 435

act tgt gca gac gga gtt gca caa aac gct taacgggtgg gtgcatagta 1461
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 440 445

tgc 1464

<210> 978

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 978

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 20 25 30

Gly Glu Pro Thr Asn Val Phe Val Lys Asp Gly Val Ile Ala Ala Ile

35					40					45									
Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val				
50					55					60									
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly				
65					70					75					80				
Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys				
85					90					95									
Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met				
100					105					110									
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile				
115					120					125									
Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu				
130					135					140									
Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys				
145					150					155					160				
Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val				
165					170					175									
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala				
180					185					190									
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu				
195					200					205									
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala				
210					215					220									
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly				
225					230					235					240				
Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu				
245					250					255									
Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr				
260					265					270									
Pro	His	His	Leu	Thr	Leu	Thr	Asp	Glu	Arg	Leu	Glu	Thr	Tyr	Asp	Ala				
275					280					285									
Val	Asn	Lys	Val	Asn	Pro	Pro	Leu	Arg	Glu	Ser	Arg	Asp	Ala	Glu	Ala				
290					295					300									
Leu	Lys	Lys	Ala	Leu	Leu	Asp	Gly	Thr	Ile	Asp	Val	Val	Ala	Thr	Asp				
305					310					315					320				
His	Ala	Pro	His	Gly	Ser	Glu	Asp	Lys	Cys	Cys	Glu	Phe	Glu	Asn	Ala				
325					330					335									
Lys	Pro	Gly	Met	Leu	Gly	Leu	Glu	Thr	Ser	Leu	Ser	Ile	Ile	Val	Asp				
340					345					350									
Thr	Phe	Val	Ala	Thr	Gly	Leu	Ala	Asp	Trp	Arg	Phe	Val	Ala	Arg	Val				
355					360					365									

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg
370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly
385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn
405 410 415

Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val
420 425 430

Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala
435 440 445

<210> 979

<211> 1025

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1002)

<223> RXA02208

<400> 979

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atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc 96
Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
20 25 30

acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca 144
Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
35 40 45

tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt 192
Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
50 55 60

ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt 240
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
65 70 75 80

ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac 288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
85 90 95

aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc 336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
100 105 110

acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct 384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
115 120 125

gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat 432

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp
 130 135 140
 ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt 480
 Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly
 145 150 155 160
 ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca 528
 Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala
 165 170 175
 gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac 576
 Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp
 180 185 190
 ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc 624
 Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu
 195 200 205
 aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc 672
 Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly
 210 215 220
 ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc 720
 Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile
 225 230 235 240
 tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc 768
 Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu
 245 250 255
 tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc 816
 Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile
 260 265 270
 agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt 864
 Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu
 275 280 285
 ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga 912
 Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg
 290 295 300
 gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc 960
 Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg
 305 310 315 320
 aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac 1002
 Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn
 325 330
 taaacagacc aaacacacgt gcc 1025

 <210> 980
 <211> 334
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 980
 Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys

1	5	10	15
Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val	20	25	30
Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala	35	40	45
Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu	50	55	60
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	65	70	75
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	85	90	95
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	100	105	110
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	115	120	125
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	130	135	140
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	145	150	155
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	165	170	175
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	180	185	190
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	195	200	205
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	210	215	220
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	225	230	235
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	245	250	255
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	260	265	270
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	275	280	285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	290	295	300
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg	305	310	315
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn	325	330	

<210> 981
 <211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> RXA01660

<400> 981
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 taaacctcaa tcatacaatt aggggaagggc tgggaaatcc atg tca tct aat tcc 115
 Met Ser Ser Asn Ser
 1 5
 att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163
 Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu
 10 15 20
 gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211
 Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp
 25 30 35
 tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259
 Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg
 40 45 50
 ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307
 Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp
 55 60 65
 gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355
 Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile
 70 75 80 85
 atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403
 Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu
 90 95 100
 gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr
 105 110 115
 ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser
 120 125 130
 cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val
 135 140 145
 ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile
 150 155 160 165
 gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu

170

175

180

gga ctc aac taacaccccc ggccccacgg agt
Gly Leu Asn

675

<210> 982

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 982

Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu
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Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser
20 25 30

Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
35 40 45

Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
50 55 60

Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
65 70 75 80

Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
85 90 95

Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
100 105 110

Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
115 120 125

Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
130 135 140

Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
145 150 155 160

Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu
165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn
180

<210> 983

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

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cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115
Met Thr Phe Gly Glu
1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163
Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile
10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211
Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val
25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259
Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp
40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307
Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly
55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355
Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu
70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403
Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser
90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451
Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu
105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499
Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu
120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547
Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val
135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595
Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln
150 155 160 165

aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643
Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala
170 175 180

gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691
Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly
185 190 195

gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739
Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu
200 205 210

ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787
Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala
215 220 225

agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro
 230 235 240 245
 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met
 250 255 260
 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg
 265 270 275
 tca tagtcgcgga aacggccctt aat 957
 Ser

<210> 984

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg
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 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly
 20 25 30
 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val
 35 40 45
 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe
 50 55 60
 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile
 65 70 75 80
 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg
 85 90 95
 Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp
 100 105 110
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu
 115 120 125
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly
 130 135 140
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu
 145 150 155 160
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile
 165 170 175
 Val Asp Gln Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys
 180 185 190
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro

195	200	205
Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala		
210	215	220
Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala		
225	230	235 240
His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro		
245	250	255
Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe		
260	265	270
Pro Gly Phe Pro Arg Ser		
275		

<210> 985

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> RXN01892

<400> 985

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                               Val Thr Thr Ser Ser
                               1 5
gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163
Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly
                               10 15 20
gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211
Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp
                               25 30 35
aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att 259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile
                               40 45 50
gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag 307
Ala Val Val Ile Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln
                               55 60 65
cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc 355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly
                               70 75 80 85
aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc 403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly
                               90 95 100
gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa 451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu

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105	110	115	
cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt			499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val			
120	125	130	
gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc			547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr			
135	140	145	
act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg			595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met			
150	155	160	165
gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca			643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro			
170	175	180	
gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag			691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys			
185	190	195	
ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac			739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn			
200	205	210	
aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct			787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala			
215	220	225	
cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc			829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser			
230	235	240	
tgatacattt agtcttataa aca			852
<210> 986			
<211> 243			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 986			
Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met			
1	5	10	15
Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp			
20	25	30	
Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys			
35	40	45	
Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg			
50	55	60	
Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr			
65	70	75	80
Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe			
85	90	95	

Val Glu Ser

1

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298
 Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu
 70 75 80
 ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346
 Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His
 85 90 95 100
 ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394
 Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala
 105 110 115
 gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442
 Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg
 120 125 130
 gtt gtc atc ttc ggt gct ggc atg ggt atg cgc tac ttt tcc acg gac 490
 Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp
 135 140 145
 acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538
 Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu
 150 155 160
 atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586
 Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn
 165 170 175 180
 cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634
 Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu
 185 190 195
 aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682
 Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp
 200 205 210
 aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730
 Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile
 215 220 225
 gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775
 Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
 230 235 240
 tgatacattt agtcttataa aca 798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met
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Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys

cct tat gaa gac ctt ctt cgg aag att gct gaa gaa ggg tcc cac aag 163
Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu Glu Gly Ser His Lys

	10	15	20	
gac gac cgc acc ggc acc ggc act act tct tta ttc gga caa caa atc				211
Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu Phe Gly Gln Gln Ile				
	25	30	35	
cgc ttt gat ctc aat gaa ggt ttt ccc ctt ctg acc acc aag aag gtc				259
Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu Thr Thr Lys Lys Val				
	40	45	50	
cat ttc cac tct gtt gtg ggt gag ctt ttg tgg ttc ctt cag ggg gat				307
His Phe His Ser Val Val Gly Glu Leu Leu Trp Phe Leu Gln Gly Asp				
	55	60	65	
tcc aac gtc aaa tgg ctg cag gat aac aac atc cgc att tgg aat gaa				355
Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile Arg Ile Trp Asn Glu				
	70	75	80	85
tgg gca gat gag gac ggc gag ctg ggc cct gtt tat ggt gtc cag tgg				403
Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val Tyr Gly Val Gln Trp				
	90	95	100	
cgt tct tgg cca acc cct gat ggt cgt cac att gac cag atc tca ggt				451
Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile Ser Gly				
	105	110	115	
gct tta gaa act ctg cga aac aac cct gat tca cgt cgc aat att gtc				499
Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser Arg Arg Asn Ile Val				
	120	125	130	
tcg gcg tgg aat gtt tcc gag ctt gaa aac atg gct ctt ccc cct tgt				547
Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met Ala Leu Pro Pro Cys				
	135	140	145	
cac ttg ctt ttc cag ctc tat gtc gcc gat ggc aaa ctg tct tgc cag				595
His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly Lys Leu Ser Cys Gln				
	150	155	160	165
ctc tac cag cgt tct gcg gac atg ttc ctg ggt gtg cct ttc aac atc				643
Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly Val Pro Phe Asn Ile				
	170	175	180	
gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg				691
Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu				
	185	190	195	
gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac				739
Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp				
	200	205	210	
aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc				785
Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg				
	215	220	225	
cctacccac ctt				798

<210> 990

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 990

Met Thr Val Pro Thr Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu
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Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu
 20 25 30

Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu
 35 40 45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp
 50 55 60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile
 65 70 75 80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val
 85 90 95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile
 100 105 110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser
 115 120 125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met
 130 135 140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly
 145 150 155 160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly
 165 170 175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala
 180 185 190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp
 195 200 205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser
 210 215 220

Arg
 225

<210> 991

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(709)

<223> RXA00131

<400> 991

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acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115
Met Ile Val Ser Ile
1 5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
10 15 20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
25 30 35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
40 45 50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
55 60 65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
70 75 80 85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
90 95 100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
105 110 115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
135 140 145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu
150 155 160 165

cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg 643
His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val
170 175 180

gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa 691
Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu
185 190 195

ttc ctg ggt act ata aac taatcccaat tagcaggaag gat 732
Phe Leu Gly Thr Ile Asn
200

<210> 992

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 992

Met Ile Val Ser Ile Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu
 1 5 10 15

Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro
 20 25 30

Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His
 35 40 45

Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu
 50 55 60

Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly
 65 70 75 80

Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala
 85 90 95

Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu
 100 105 110

Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp
 115 120 125

Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu
 130 135 140

Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln
 145 150 155 160

Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu
 165 170 175

Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala
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Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn
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<210> 993

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA00266

<400> 993

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agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
 Met Thr Glu Arg Thr
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu

	10	15	20	
atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat				211
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp	25	30	35	
ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac				259
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His	40	45	50	
gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca				307
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala	55	60	65	
cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg				355
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp	70	75	80	85
cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc				403
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly	90	95	100	
acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac				451
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His	105	110	115	
ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc				499
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe	120	125	130	
cct aac ctg taattttttac ggtagaaaa aaa				531
Pro Asn Leu	135			

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<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 994

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Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys			
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Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys			
35	40	45	

His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu			
50	55	60	

Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg			
65	70	75	80

Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala			
85	90	95	

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly			
100	105	110	

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
 115 120 125

Ile Ser Ile Trp Phe Pro Asn Leu
 130 135

<210> 995

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(808)

<223> RXA00718

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 Val Thr Glu Ile Ser
 1 5

aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
 Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
 10 15 20

acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
 Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
 25 30 35

aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
 Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
 40 45 50

ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
 Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
 55 60 65

acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355
 Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Pro Ala Ser Thr Glu
 70 75 80 85

gtg ttg ctc gcg ggc gtc gat gtg caa aag gac atc cgc gga cca gaa 403
 Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp Ile Arg Gly Pro Glu
 90 95 100

gtc acc caa aat gtc tcc gca gtg tcc gcg atc cct gag gtt cgt gaa 451
 Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile Pro Glu Val Arg Glu
 105 110 115

aac ttg gtg gcg ttg cag cgc gca ctc gcc gcc aaa gca cat cgc tgc 499
 Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys
 120 125 130

gtc gtc gaa ggc aga gac atc gga acg gca gtg ctt gtc gac gcg ccc 547
 Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val Leu Val Asp Ala Pro
 135 140 145

atc aag gcg ttt ctc acc gcc tca gcg gaa gtc cgc gcc cag cga cgc 595
 Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg
 150 155 160 165

ttt gac caa gac acc gca gca ggt cgc gac gta gat ttc gac gct gtg 643
 Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val
 170 175 180

ctg gca gat gtt gtt cgc cgc gat gaa cta gat tcc acc cgt gcc gcc 691
 Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp Ser Thr Arg Ala Ala
 185 190 195

tca ccg ctg aaa cca gca gat gat gca cac atc gtg gac acc tct gat 739
 Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp
 200 205 210

atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787
 Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala
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 Ser Ala Glu Arg Ser Asn Gln
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<210> 996

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 996

Val Thr Glu Ile Ser Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile
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 20 25 30

Thr Arg Leu Ser Ala Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val
 35 40 45

Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala
 50 55 60

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp
 65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp
 85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile
 100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala
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Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val
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Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val
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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA01599
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Met Thr Ser Ser Arg															
1 5															
aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc															163
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser															
10 15 20															
tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att															211
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile															
25 30 35															
gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat															259
Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu Asp Pro Tyr Leu Asn															
40 45 50															
gtt gat ccg ggc acc atg aat cct ttt gaa cac ggt gaa gtc ttt gtc															307
Val Asp Pro Gly Thr Met Asn Pro Phe Glu His Gly Glu Val Phe Val															
55 60 65															
acc gaa gac ggg gca gaa aca gac ctg gat ttg ggc cac tac gag cgt															355
Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg															
70 75 80 85															
ttc ctc gat cgc aac ctg ggg ctc aac gcc aat gtc acc acc ggc aag															403
Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn Val Thr Thr Gly Lys															
90 95 100															
gtg tat tcc act gtg atc gcc aag gag cgc agg gga gag tac ctg ggt															451
Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg Gly Glu Tyr Leu Gly															
105 110 115															

aaa act gtg cag gtc atc cca cac atc act gat gag atc aaa gct cgt	499
Lys Thr Val Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Ala Arg	
120 125 130	
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Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly Asn Ala Pro Asp Val	
135 140 145	
gtg atc tct gag gtc ggt ggc acc gtc ggt gac att gaa tcc cag cca	595
Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp Ile Glu Ser Gln Pro	
150 155 160 165	
ttc ctt gaa gca gct cgc cag gta cgc cat gaa att ggt cgt gaa aac	643
Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu Ile Gly Arg Glu Asn	
170 175 180	
tgc ttc ttc atc cac tgt tct ttg gtg cca tac ttg gct acc tca ggt	691
Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr Leu Ala Thr Ser Gly	
185 190 195	
gag ctg aag acc aaa ccc acc cag cat tct gtc gca gag ctg cgc ggc	739
Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val Ala Glu Leu Arg Gly	
200 205 210	
atc ggt att ttg ccg gat gct ctc gtg ctt cgt tgc gat cgg gag gtc	787
Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg Cys Asp Arg Glu Val	
215 220 225	
cct caa ggt ctg aaa gat aag atc gcg atg atg tgc gat gtt gat tat	835
Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met Cys Asp Val Asp Tyr	
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gaa ggc gtt gta tct tgc cct gat tcc agt tct att tac aac att cca	883
Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ile Tyr Asn Ile Pro	
250 255 260	
gat gtc ctc tac cgc gag cac ctg gac acc ttc att att cgt cgc ctg	931
Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe Ile Ile Arg Arg Leu	
265 270 275	
ggc ctt ccg ttc cgt gat gtt gac tgg agc acc tgg cac gat ctg ctg	979
Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr Trp His Asp Leu Leu	
280 285 290	
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Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly	
295 300 305	
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt	1075
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val	
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Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile	
330 335 340	
acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc	1171
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser	
345 350 355	
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Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile
 360 365 370
 gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg 1267
 Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro
 375 380 385
 ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca 1315
 Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala
 390 395 400 405
 cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct 1363
 Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala
 410 415 420
 gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg 1411
 Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val
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 tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct 1459
 Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro
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 gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg 1507
 Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr
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 Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr
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 cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca 1603
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 490 495 500
 cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat 1651
 Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His
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 cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca 1699
 Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro
 520 525 530
 acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag 1747
 Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu
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 Leu Arg Val His Pro
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<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 998

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 35 40 45
 Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His
 50 55 60
 Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu
 65 70 75 80
 Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn
 85 90 95
 Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg
 100 105 110
 Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp
 115 120 125
 Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly
 130 135 140
 Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp
 145 150 155 160
 Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu
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 Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr
 180 185 190
 Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val
 195 200 205
 Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg
 210 215 220
 Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met
 225 230 235 240
 Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser
 245 250 255
 Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe
 260 265 270
 Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr
 275 280 285
 Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr
 290 295 300
 Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser
 305 310 315 320
 Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr
 325 330 335
 Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala

340	345	350
Met Lys Ala Leu Ser Gly Leu	Asp Ala Ile Val Val	Pro Gly Gly Phe
355	360	365
Gly Ile Arg Gly Ile Glu Gly	Lys Ile Gly Ala Ile	Thr Phe Ala Arg
370	375	380
Glu His Lys Ile Pro Leu Leu	Gly Leu Cys Leu Gly	Leu Gln Cys Thr
385	390	395
Val Ile Glu Ala Ala Arg Gln	Ala Gly Leu Glu Gln	Ala Ser Ser Thr
405	410	415
Glu Phe Asp Pro Ala Ala Thr	Gln Pro Val Ile Ala Thr	Met Glu Glu
420	425	430
Gln Lys Ala Ala Val Ser Gly	Glu Ala Asp Leu Gly Gly	Thr Met Arg
435	440	445
Leu Gly Ala Tyr Pro Ala Thr	Leu Glu Glu Gly Ser	Leu Val Ala Glu
450	455	460
Leu Tyr Gly Thr Thr Glu Val	Ser Glu Arg His Arg	His Arg Tyr Glu
465	470	475
Val Asn Asn Ala Tyr Arg Ala	Gln Ile Ala Glu Gly Ser	Asp Leu Val
485	490	495
Phe Ser Gly Thr Ser Pro Asp	Gly His Leu Val Glu Phe	Val Glu Tyr
500	505	510
Pro Lys Glu Val His Pro Tyr	Leu Val Ala Thr Gln	Ala His Pro Glu
515	520	525
Tyr Lys Ser Arg Pro Thr His	Ala His Pro Leu Phe Tyr	Gly Leu Val
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<211> 3462

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<220>

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<223> RXN02234

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	Met Pro Lys Arg Ser	
	1 5	

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Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu				
	25	30	35	
aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg				259
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr				
	40	45	50	
atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc				307
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile				
	55	60	65	
gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc				355
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly				
	70	75	80	85
cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt				403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu				
	90	95	100	
aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc				451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly				
	105	110	115	
gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat				499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp				
	120	125	130	
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg				547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala				
	135	140	145	
cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca				595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala				
	150	155	160	165
gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc				643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly				
	170	175	180	
ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct				691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala				
	185	190	195	
ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa				739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu				
	200	205	210	
tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc				787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr				
	215	220	225	
gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg				835
Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu				
	230	235	240	245
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg				883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu				
	250	255	260	

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc	931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
265 270 275	
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc	979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile	
280 285 290	
aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg	1027
Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val	
295 300 305	
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Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
310 315 320 325	
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Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
330 335 340	
aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac	1171
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
345 350 355	
tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc	1219
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg	1267
Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
375 380 385	
tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc	1315
Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser	
390 395 400 405	
ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc	1363
Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe	
410 415 420	
gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag	1411
Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys	
425 430 435	
cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt	1459
Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu	
440 445 450	
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Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp	
455 460 465	
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Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val	
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 Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile
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 His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser
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 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
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Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp	
850 855 860	
gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt	2640
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg	
865 870 875 880	
cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag	2688
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys	
885 890 895	
tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat	2736

Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc 2784
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca 2832
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc 2880
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc 2928
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat 2976
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt 3024
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg 3072
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
 1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct 3120
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg 3168
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc 3218
 Leu Gln Glu Leu Asp His Ala Val Lys Ala
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gag 3221

<210> 1002

<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His
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Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
 20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
 35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
 50 55 60
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
 65 70 75 80
 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
 85 90 95
 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
 100 105 110
 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
 115 120 125
 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
 130 135 140
 Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
 145 150 155 160
 Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
 165 170 175
 Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
 180 185 190
 Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
 195 200 205
 Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp
 210 215 220
 Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys
 225 230 235 240
 Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile
 245 250 255
 Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala
 260 265 270
 Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
 275 280 285
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala

370	375	380
Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val		
385	390	395 400
Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala		
	405	410 415
Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln		
	420	425 430
Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu		
	435	440 445
Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu		
	450	455 460
Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser		
	465	470 475 480
Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu		
	485	490 495
Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro		
	500	505 510
Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu		
	515	520 525
Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp		
	530	535 540
Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu		
	545	550 555 560
Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp		
	565	570 575
Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met		
	580	585 590
Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile		
	595	600 605
Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys		
	610	615 620
Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met		
	625	630 635 640
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu		
	645	650 655
Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr		
	660	665 670
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val		
	675	680 685
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu		
	690	695 700

Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu
 705 710 715 720
 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu
 725 730 735
 Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
 740 745 750
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
 1010 1015 1020

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

<210> 1003

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN00450

<400> 1003

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
Val Gly Val Leu Pro
1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
90 95 100

ggt gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
105

<210> 1004

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
 100 105

<210> 1005

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1005

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gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403

Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga
 Gly Ala Arg Ile Gly
 105

418

<210> 1006
 <211> 106
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1006
 Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
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 Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30
 Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45
 Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60
 Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80
 Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95
 Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
 100 105

<210> 1007
 <211> 1368
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1345)
 <223> RXN02272

<400> 1007
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 agtttgaaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115
 Val Arg Ile Thr Asn
 1 5
 gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
 10 15 20
 gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag	259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln	
40 45 50	
ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc	307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile	
55 60 65	
cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979


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Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly
    280                      285                      290

gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt 1027
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe
    295                      300                      305

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat 1075
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp
    310                      315                      320                      325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca 1123
Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr
    330                      335                      340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc 1171
Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala
    345                      350                      355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg 1219
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala
    360                      365                      370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga 1267
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg
    375                      380                      385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc 1315
Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser
    390                      395                      400                      405

agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc 1365
Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
    410                      415

ctt 1368

<210> 1008
<211> 415
<212> PRT
<213> Corynebacterium glutamicum

<400> 1008
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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile
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Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
    35                      40                      45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
    50                      55                      60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
    65                      70                      75                      80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
    85                      90                      95

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Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
 370 375 380
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
 405 410 415

<210> 1009
 <211> 1368
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1345)
 <223> FRXA02272

<400> 1009

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 Val Arg Ile Thr Asn
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
 55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
 Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
 70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
 Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
 90 95 100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451
 Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
 105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
 Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
 120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
 Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
 135 140 145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595
 Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
 150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
 Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
 170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691
 Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
 185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
 Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His
 200 205 210

act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc 787
 Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala
 215 220 225

gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat 835
 Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His
 230 235 240 245

tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta 883
 Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu
 250 255 260

ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa 931
 Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu
 265 270 275

aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt 979
 Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly
 280 285 290

gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt 1027
 Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe
 295 300 305

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat 1075
 Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp
 310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca 1123
 Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr
 330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc 1171
 Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala
 345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg 1219
 Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala
 360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga 1267
 Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg
 375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc 1315
 Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser
 390 395 400 405

agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc 1365
 Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
 410 415

ctt

1368

<210> 1010

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

Val Arg Ile Thr Asn Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp
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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile
 20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
 35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
 50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
 65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
 85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly

275					280					285						
Pro	Val	Pro	Arg	Gly	Val	Ala	Pro	Val	Lys	Gln	Leu	Thr	Glu	Trp	Gly	
290					295					300						
Ile	Pro	Val	Ser	Phe	Cys	Gln	Asp	Ser	Leu	Asn	Asp	Pro	Phe	Tyr	Pro	
305					310					315					320	
Met	Gly	Asp	Gly	Asp	Leu	Leu	Arg	Ile	Leu	Asp	Ser	Gly	Leu	His	Val	
325					330					335						
Ser	His	Met	Leu	Thr	Ala	Ser	His	Leu	Lys	Asn	Ala	Leu	Ser	Phe	Ile	
340					345					350						
Thr	Thr	Asn	Pro	Ala	Gly	Asn	Leu	Gly	Leu	Asp	Asn	Tyr	Asp	Ile	Ala	
355					360					365						
Glu	Asn	Ser	Pro	Ala	Asn	Leu	Leu	Val	Leu	Asp	Ala	Ser	Ser	Glu	Lys	
370					375					380						
Glu	Ala	Val	Gln	Arg	Lys	Ala	Ser	Val	Leu	Leu	Ser	Ile	His	Arg	Gly	
385					390					395					400	
Lys	Lys	Val	Leu	Ser	Arg	Glu	Pro	Glu	Gln	Val	Asp	Trp	Asn	Ile		
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<211> 580

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> RXN03004

<400> 1011

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cgtggcccaa	ccctgaacgc	tgaacgctac	actgggtgac	gtg	ctt	ctt	tca	gat	115
				Val	Leu	Leu	Ser	Asp	
				1				5	

cgt	gac	att	cgt	aaa	tca	att	gac	gca	ggc	gac	ttg	gga	att	gaa	cct	163
Arg	Asp	Ile	Arg	Lys	Ser	Ile	Asp	Ala	Gly	Asp	Leu	Gly	Ile	Glu	Pro	
			10					15						20		

ttc	gac	gct	gag	ctg	att	cag	ccg	tcg	agt	gtc	gat	gtc	cgc	atg	gac	211
Phe	Asp	Ala	Glu	Leu	Ile	Gln	Pro	Ser	Ser	Val	Asp	Val	Arg	Met	Asp	
		25					30						35			

cgc	tac	ttc	cgg	gtt	ttc	aat	aac	tct	aag	tac	acc	cac	att	gac	cct	259
Arg	Tyr	Phe	Arg	Val	Phe	Asn	Asn	Ser	Lys	Tyr	Thr	His	Ile	Asp	Pro	
		40				45						50				

aag	ttg	aat	cag	gat	gag	ctg	acc	agc	ctt	gtt	gag	gtt	gag	gac	ggc	307
Lys	Leu	Asn	Gln	Asp	Glu	Leu	Thr	Ser	Leu	Val	Glu	Val	Glu	Asp	Gly	
	55					60					65					

gag	ggc	ttt	gtg	ctg	cat	ccg	ggt	gag	ttt	gtg	ctg	gcg	tcc	acg	ctg	355
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Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu
 70 75 80 85
 gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403
 Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys
 90 95 100
 tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451
 Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe
 105 110 115
 att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499
 Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val
 120 125 130
 gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547
 Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu
 135 140 145
 gct ttg ttc cag atg agt tcc cct gcg gag act 580
 Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
 150 155 160

<210> 1012

<211> 160

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1012

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 Leu Gly Ile Glu Pro Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val
 20 25 30
 Asp Val Arg Met Asp Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr
 35 40 45
 Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val
 50 55 60
 Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val
 65 70 75 80
 Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly
 85 90 95
 Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His
 100 105 110
 Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu
 115 120 125
 Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met
 130 135 140
 Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
 145 150 155 160

<210> 1013
 <211> 225
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(202)
 <223> RXN03137

<400> 1013
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 Leu Glu Leu Asn Lys
 1 5
 gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly
 10 15 20
 tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcggtgc 212
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val
 25 30
 gatttgggca caa 225

<210> 1014
 <211> 34
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1014
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 Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val
 20 25 30
 Ala Val

<210> 1015
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(613)
 <223> RXN03171

<400> 1015
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Met Asp Ile Thr Ile
1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
150 155 160 165

gac gca ttg gcg gaa tct 613
Asp Ala Leu Ala Glu Ser
170

<210> 1016

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1016

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu

35 40 45
 Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60
 Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80
 Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95
 Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110
 Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125
 Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140
 Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160
 Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
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<210> 1017

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> FRXA02857

<400> 1017

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 Met Asp Ile Thr Ile
 1 5
 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355

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Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70              75              80              85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
              90              95              100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
              105              110              115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
              120              125              130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt gcc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
              135              140              145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
              150              155              160              165

gac gca ttg gcg gaa tct
Asp Ala Leu Ala Glu Ser
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<210> 1018

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

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Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
              20              25              30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
              35              40              45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
              50              55              60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
              65              70              75              80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
              85              90              95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
              100              105              110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
              115              120              125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
              130              135              140

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Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
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Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
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<210> 1019

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA02771

<400> 1019

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atggaacatg gaccgttggt ccagaagtga ggaataagta gtg agc gaa caa gct 115
 Val Ser Glu Gln Ala
 1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg
 10 15 20

tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
 25 30 35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
 40 45 50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
 55 60 65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
 70 75 80 85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
 90 95 100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
 105 110 115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
 120 125 130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
 135 140 145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595

Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
 150 155 160 165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val
 170 175 180

aga gat cct cag tagaaggatc gaaagaaagg cgg 678
 Arg Asp Pro Gln
 185

<210> 1020

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 1020

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Asp Lys Lys Thr Arg Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu
 20 25 30

Phe Glu Asp Leu Thr Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala
 35 40 45

Val Val Asp Ala Met Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile
 50 55 60

Ile Gly Gly Leu Asp Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala
 65 70 75 80

Tyr Lys Leu Gly Leu Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu
 85 90 95

Pro Pro Pro Val Val Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala
 100 105 110

Ala Leu Glu Leu Pro Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile
 115 120 125

Val Leu Ile Asp Asp Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala
 130 135 140

Arg Lys Leu Ile Glu Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu
 145 150 155 160

Ala Ile Glu Val Pro Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg
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Pro Val Ile Val Val Arg Asp Pro Gln
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<210> 1021

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01512

<400> 1021

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                                         Met Ser Asn Asn Val
                                         1 5

gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163
Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly
                        10 15 20

acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211
Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg
                        25 30 35

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259
Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu
                        40 45 50

gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307
Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu
                        55 60 65

gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355
Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met
                        70 75 80 85

gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403
Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg
                        90 95 100

atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451
Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile
                        105 110 115

gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499
Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg
                        120 125 130

aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547
Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu
                        135 140 145

cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595
Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly
                        150 155 160 165

ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643
Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala
                        170 175 180

gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691
Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr Leu Glu Pro His Val
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200

<210> 1022

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1022

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20 25 30

Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu
35 40 45

Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly
50 55 60

Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr
65 70 75 80

Gln Ser Glu Phe Met Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser
85 90 95

Ser Gly Val Val Arg Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly
100 105 110

Arg Asp Val Leu Ile Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu
115 120 125

Ser Trp Leu Met Arg Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn
130 135 140

Val Ile Thr Leu Leu Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp
145 150 155 160

Met Phe Asp Ile Gly Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr
165 170 175

Gly Leu Asp Phe Ala Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr
180 185 190

Leu Glu Pro His Val Tyr Ser Asp
195 200

<210> 1023

<211> 597

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(574)

<223> RXA02031

<400> 1023

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               Met Thr Glu Glu Arg
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gag att ctg acc tat gag atg ttc gga aca gca atg cgg gag ctg gcc 163
Glu Ile Leu Thr Tyr Glu Met Phe Gly Thr Ala Met Arg Glu Leu Ala
               10 15 20

caa gaa att att gat gac tac cag cca gat tgc gtg ctg tcc att gcg 211
Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys Val Leu Ser Ile Ala
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Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly Tyr Ala Leu Gly Ile
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Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr Thr Asp Ile Gly Glu
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His Leu Glu Glu Pro Met Met Leu Pro Pro Thr Pro Lys Ala Val Asp
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ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403
Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp Val Ala Asp Thr Gly
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Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu
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gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499
Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro
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gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547
Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser
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<213> Corynebacterium glutamicum

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Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly

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 Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr
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 Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp
 85 90 95
 Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly
 100 105 110
 Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn
 115 120 125
 Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile
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<223> RXA00981

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 Met Ser Glu Asn Leu
 1 5
 cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag 163
 Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
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 aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc 211
 Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
 25 30 35
 att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc 259
 Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
 40 45 50
 cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag 307
 Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
 55 60 65
 aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc 355
 Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
 70 75 80 85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga 403
 Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
 90 95 100

atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg 451
 Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
 105 110 115

acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct 499
 Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
 120 125 130

aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg 547
 Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
 135 140 145

cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag 595
 Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
 150 155 160 165

atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc 643
 Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
 170 175 180

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
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Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
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Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
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Val Thr
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 Met Ser Leu Glu Arg
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aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
 Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
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gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 211
 Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
 Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
 40 45 50

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
 Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
 55 60 65

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
 Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
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acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 403

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Leu	Leu	His	Asp	Thr	Val	Glu	Asp	Thr	Asp	Tyr	Ser	Leu	Asp	Asp	Leu		
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Thr	Arg	Asp	Phe	Gly	Glu	Glu	Val	Ala	Arg	Leu	Val	Asp	Gly	Val	Thr		
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Lys	Leu	Asp	Lys	Val	Ala	Leu	Gly	Ala	Ala	Ala	Glu	Ala	Glu	Thr	Ile		
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cgc	aaa	atg	atc	gtc	gcc	atg	agc	cag	gac	ccc	cgc	gtg	ctg	gtg	att	595	
Arg	Lys	Met	Ile	Val	Ala	Met	Ser	Gln	Asp	Pro	Arg	Val	Leu	Val	Ile		
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Lys	Val	Ala	Asp	Arg	Leu	His	Asn	Met	Arg	Thr	Met	Arg	Phe	Leu	Pro		
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Pro	Glu	Lys	Gln	Ala	Lys	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Val	Ile	Ala		
			185					190					195				
cct	ttg	gca	cac	cgc	ctg	ggc	atg	gcc	agc	gtg	aaa	tgg	gaa	ttg	gaa	739	
Pro	Leu	Ala	His	Arg	Leu	Gly	Met	Ala	Ser	Val	Lys	Trp	Glu	Leu	Glu		
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gat	cta	tcc	ttt	gcc	att	ttg	tac	ccc	aag	aag	tac	gaa	gag	atc	gtg	787	
Asp	Leu	Ser	Phe	Ala	Ile	Leu	Tyr	Pro	Lys	Lys	Tyr	Glu	Glu	Ile	Val		
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cgt	ctt	gtt	gcc	gac	cgc	gcg	ccc	tct	aga	gac	cgg	tac	ctc	aaa	gaa	835	
Arg	Leu	Val	Ala	Asp	Arg	Ala	Pro	Ser	Arg	Asp	Arg	Tyr	Leu	Lys	Glu		
230					235					240					245		
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Ile	Ile	Asp	Gln	Val	Thr	Gly	Gly	Leu	Arg	Glu	Asn	Asn	Ile	Ala	Ala		
			250						255					260			
gaa	gtg	ctt	ggg	cga	cca	aag	cac	tac	tgg	tct	atc	tat	caa	aag	atg	931	
Glu	Val	Leu	Gly	Arg	Pro	Lys	His	Tyr	Trp	Ser	Ile	Tyr	Gln	Lys	Met		
			265					270					275				
atc	gtt	cgc	ggg	cgt	gat	ttt	gac	gat	att	ttt	gat	ctt	gtt	ggc	atc	979	
Ile	Val	Arg	Gly	Arg	Asp	Phe	Asp	Asp	Ile	Phe	Asp	Leu	Val	Gly	Ile		
		280					285					290					
cgc	atc	ctg	gta	gac	aac	gtg	aac	aac	tgt	gta	cgc	cgc	cat	cgg	tgt	1027	
Arg	Ile	Leu	Val	Asp	Asn	Val	Asn	Asn	Cys	Val	Arg	Arg	His	Arg	Cys		
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cgt	gca	ctc	cct	gtt	caa	tgc	tct	gcc	tgg	ccg	att	caa	aga	cta	tat	1075	
Arg	Ala	Leu	Pro	Val	Gln	Cys	Ser	Ala	Trp	Pro	Ile	Gln	Arg	Leu	Tyr		
310					315					320				325			
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Phe	Ser	Pro	Ala	Leu	Arg	Cys	Leu	Pro	Ile	Pro	Ala	His	His	Arg	Asp		

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 Gly Thr Trp Arg
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 35 40 45
 Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
 50 55 60
 Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 65 70 75 80
 Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
 85 90 95
 Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 100 105 110
 Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 115 120 125
 Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 130 135 140
 Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 145 150 155 160
 Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 165 170 175
 Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 180 185 190
 Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 195 200 205
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 210 215 220
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 225 230 235 240
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
 245 250 255

Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser
 260 265 270

Ile Tyr Gln Lys Met Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe
 275 280 285

Asp Leu Val Gly Ile Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val
 290 295 300

Arg Arg His Arg Cys Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro
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Ala His His Arg Asp Gly Thr Trp Arg
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<223> FRXA02772

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 Met Ser Ala Arg Leu
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gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 163
 Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 211
 Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
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gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 259
 Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
 40 45 50

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 307
 Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
 55 60 65

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 355
 Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
 70 75 80 85

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 403
 Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
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acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 451

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Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
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Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
      120                      125                      130

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 547
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
      135                      140                      145

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 595
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
      150                      155                      160                      165

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 643
Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
      170                      175                      180

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691
Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
      185                      190                      195

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 739
Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
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cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787
Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
      215                      220                      225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835
Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
      230                      235                      240                      245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880
Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu Ser Phe Lys Arg
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<213> Corynebacterium glutamicum

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Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro
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Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
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Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
      50                      55                      60

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr

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gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211

Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro
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gtn caa tgc tct gnc tgg ncg ntt caa aga cta tat ttc agc ccc gcg 259
 Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu Tyr Phe Ser Pro Ala
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ctt 262
 Leu

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<400> 1032
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Cys Arg Ala Leu Pro Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu
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Tyr Phe Ser Pro Ala Leu
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 <223> RXA01835

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 Met Asn Thr Ala Ala
 1 5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
 10 15 20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
 25 30 35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
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ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307

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Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
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Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
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aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
                               90                               95                               100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
                               105                               110                               115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499
Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
                               120                               125                               130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547
Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
                               135                               140                               145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
                               150                               155                               160                               165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
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<212> PRT

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<400> 1034

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Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
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Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
                               50                               55                               60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
   65                               70                               75                               80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
                               85                               90                               95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
                               100                               105                               110

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Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
 145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser
 165 170 175

Ala

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 Met Tyr Pro Tyr Ser
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gac gca gac gct ttt cga cgc cag cct gag cgc gcc aag tcc agc caa 163
 Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
 10 15 20

ctg cgt acc agc gcc gta gac acc cgc agc gcg ttc gcc cgc gac cgg 211
 Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
 25 30 35

gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
 Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
 40 45 50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
 Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
 55 60 65

cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
 His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
 70 75 80 85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
 Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
 90 95 100

ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
 Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
 105 110 115

gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
 Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
 120 125 130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
 Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
 135 140 145

ggg ctg aac ttg tcg cgg gct gct ctt gat gct gca tgt aag tat ccg 595
 Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
 150 155 160 165

tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
 Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
 170 175 180

tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
 Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
 185 190 195

gat ctt cgc cca ccg atc gaa gcg cag gtc atg gac ttt tct gat gac 739
 Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp
 200 205 210

att gcc tac tcg gtg cac gat gtg gaa gac ggt att gta tcc ggg cgt 787
 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883
 Asp Lys Gly Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Asp
 265 270 275

ttt gat ttc tca ctg cgt tcc tac gct gcg ctg aag gcg atg act tca 979
 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser
 280 285 290

gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa 1027
 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att 1075
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt 1123
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa 1171
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln
 345 350 355

cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg 1219

Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro
 360 365 370

gga tcg ttg gat ccg atg tat cgc cag tgg ttt att gaa gcg gat tca 1267
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg 1315
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga 1363
 Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly
 410 415 420

ttt ttg gga taattggtta gagcagcagt aag 1395
 Phe Leu Gly

<210> 1036

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 1036

Met Tyr Pro Tyr Ser Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg
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Ala Lys Ser Ser Gln Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala
 20 25 30

Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro
 50 55 60

Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn
 100 105 110

Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn
 165 170 175

Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met
195 200 205

Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly
210 215 220

Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu
225 230 235 240

Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro
245 250 255

Ala Glu Leu Ile Glu Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val
260 265 270

Ala Ala Ala Ala Asp Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu
275 280 285

Lys Ala Met Thr Ser Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile
290 295 300

Glu Ser Thr Lys Lys Thr His Ala Gly Ile Asp Val Gly Arg Met His
305 310 315 320

Gly Asp Leu Ile Ile Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu
325 330 335

Lys Thr Leu Ala Val Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala
340 345 350

Arg Gln Asn Arg Gln Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu
355 360 365

Val Leu Gly Ala Pro Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe
370 375 380

Ile Glu Ala Asp Ser Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln
385 390 395 400

Ile Ala Ser Met Thr Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala
405 410 415

Ala Asp Ile Ser Gly Phe Leu Gly
420

<210> 1037

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1108)

<223> RXN01027

<400> 1037

aatagatgga agtagttttt cattcactta tgtgcgcgtt tttaatctgg tttctaccaa 60

gaactgtgtg caccacaacg cggaagggtga atcgcaccca atg gca aat aag aac 115

															Met	Ala	Asn	Lys	Asn	
															1				5	
aat	aag	cct	cat	gag	gtg	gac	aaa	gac	caa	gat	tca	gcc	atg	ctg	atc	163				
Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp	Ser	Ala	Met	Leu	Ile					
				10					15					20						
aac	ggg	cgc	ctg	caa	cag	atc	ccg	gcg	cgt	ccc	act	gag	gaa	ttc	acc	211				
Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro	Thr	Glu	Glu	Phe	Thr					
				25					30					35						
cgc	cca	act	ctt	gca	gca	ggg	gca	gta	ctg	tgg	cgc	ggc	gac	atc	acc	259				
Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp	Arg	Gly	Asp	Ile	Thr					
				40					45					50						
aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cgc	ccg	cac	tat	gat	307				
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp					
				55					60					65						
gac	tgg	tcc	ctg	gcc	aag	ggc	aaa	gtc	gat	ccc	ggc	gag	tct	att	ccg	355				
Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro					
				70					75					80						
aca	acc	gcg	gcc	cgt	gaa	atc	ctt	gaa	gaa	act	ggc	tac	gac	atc	cgt	403				
Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg					
				90					95					100						
ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451				
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr					
				105					110					115						
aaa	gtg	gtc	tac	tac	tgg	act	gcc	cag	gtt	ctt	ggg	gga	gag	ttt	gtc	499				
Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val					
				120					125					130						
ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547				
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala					
				135					140					145						
tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595				
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala					
				150					155					160						
gca	aag	cgt	ttc	cgc	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cgc	643				
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg					
				170					175					180						
cat	gct	cat	gca	cat	ggg	cgc	caa	acc	tgg	ggg	ggc	gac	gac	aat	aag	691				
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys					
				185					190					195						
cgc	cca	ttg	gac	aaa	aag	ggg	cgt	cga	caa	gca	gaa	atg	ctc	gta	ccc	739				
Arg	Pro	Leu	Asp	Lys	Lys	Gly	Arg	Arg	Gln	Ala	Glu	Met	Leu	Val	Pro					
				200					205					210						
atg	ttg	ttg	ccc	ttc	aaa	ccc	acc	gca	att	tac	tcg	gcg	gtg	ccc	gat	787				
Met	Leu	Leu	Pro	Phe	Lys	Pro	Thr	Ala	Ile	Tyr	Ser	Ala	Val	Pro	Asp					
				215					220					225						
cgc	tgc	caa	gcc	acc	gcg	ctc	ccc	ctt	gcc	gat	gag	ctc	ggc	ctc	gac	835				
Arg	Cys	Gln	Ala	Thr	Ala	Leu	Pro	Leu	Ala	Asp	Glu	Leu	Gly	Leu	Asp					

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230                235                240                245
gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
                250                255                260

gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg 931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
                265                270                275

ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979
Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
                280                285                290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa 1027
Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
                295                300                305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc 1075
Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
                310                315                320                325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct 1128
Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
                330                335

cca 1131

<210> 1038
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 1038
Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp
  1          5          10          15

Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro
          20          25          30

Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
          35          40          45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
          50          55          60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
          65          70          75          80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
          85          90          95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
          100          105          110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
          115          120          125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
          130          135          140

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Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
145                      150                      155                      160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
                      165                      170                      175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
                      180                      185                      190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
                      195                      200                      205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
210                      215                      220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
225                      230                      235                      240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
                      245                      250                      255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
                      260                      265                      270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
275                      280                      285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
290                      295                      300

Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
305                      310                      315                      320

Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
                      325                      330                      335

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<210> 1039

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> FRXA01024

<400> 1039

aatagatgga agtagttttt cattcactta tgtgcgcggtt tttaatctgg tttctaccaa 60

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gaactgtgtg caccacaacg cggaagggtga atcgcaccca atg gca aat aag aac    115
                                   Met Ala Asn Lys Asn
                                   1                      5

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aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc    163
Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
                      10                      15                      20

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aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
      25                      30                      35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr
      40                      45                      50

aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat 307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp
      55                      60                      65

gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg 355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro
      70                      75                      80                      85

aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt 403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg
      90                      95                      100

ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc 451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr
      105                      110                      115

aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc 499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val
      120                      125                      130

ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca 547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala
      135                      140                      145

tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca 595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala
      150                      155                      160                      165

gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc 643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg
      170                      175                      180

cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag 691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys
      185                      190                      195

cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc 739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro
      200                      205                      210

atg ttg ttg ccc ttc aaa 757
Met Leu Leu Pro Phe Lys
      215

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<210> 1040

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1040

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp

1	5	10	15
Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro	20	25	30
Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp	35	40	45
Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His	50	55	60
Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro	65	70	75
Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr	85	90	95
Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro	100	105	110
Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu	115	120	125
Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu	130	135	140
Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu	145	150	155
Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg	165	170	175
Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly	180	185	190
Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala	195	200	205
Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys	210	215	

<210> 1041

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(234)

<223> FRXA01027

<400> 1041

acc gat ccc gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa	48
Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln	
1 5 10 15	

ggt ggc gtg ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg	96
Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met	
20 25 30	

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atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144
Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
      35              40              45

aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192
Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
      50              55              60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234
Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
      65              70              75

taggagcgcg tttaaggcct cca 257

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<210> 1042

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

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Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln
  1              5              10              15

Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
      20              25              30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
      35              40              45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
      50              55              60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
      65              70              75

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<210> 1043

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01528

<400> 1043

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115
                               Val Asn Gln Ala Trp
                               1              5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
      10              15              20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
      25              30              35

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ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
      40                      45                      50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp
      55                      60                      65

aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
      70                      75                      80                      85

ggg gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
      90                      95                      100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
      105                      110                      115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
      120                      125                      130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
      135                      140                      145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
      150                      155                      160                      165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
      170                      175

aac 651

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<210> 1044

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1044

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Val Asn Gln Ala Trp Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr
  1                      5                      10                      15

Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
      20                      25                      30

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
      35                      40                      45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
      50                      55                      60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
      65                      70                      75                      80

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<210> 1045
<211> 541
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101)..(541)  
<223> RXA00072
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				Met	Ser	Phe	Gln	Leu									
				1												5	
gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca																	163
Val	Asn	Ala	Leu	Lys	Asn	Thr	Gly	Ser	Val	Lys	Asp	Pro	Glu	Ile	Ser		
				10					15					20			
ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa																	211
Pro	Glu	Gly	Pro	Arg	Thr	Thr	Thr	Pro	Leu	Ser	Pro	Glu	Val	Ala	Lys		
				25					30					35			
cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc																	259
His	Asn	Glu	Glu	Leu	Val	Glu	Lys	His	Ala	Ala	Ala	Leu	Tyr	Asp	Ala		
				40					45					50			
agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct																	307
Ser	Ala	Gln	Glu	Ile	Leu	Glu	Trp	Thr	Ala	Glu	His	Ala	Pro	Gly	Ala		
				55					60					65			
att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct																	355
Ile	Ala	Val	Thr	Leu	Ser	Met	Glu	Asn	Thr	Val	Leu	Ala	Glu	Leu	Ala		
				70					75					80			
gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac																	403
Ala	Arg	His	Leu	Pro	Glu	Ala	Asp	Phe	Leu	Phe	Leu	Asp	Thr	Gly	Tyr		

90	95	100	
cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat			451
His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr			
105	110	115	
tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag			499
Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln			
120	125	130	
gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg			541
Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala			
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<210> 1046

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

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Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser			
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Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala			
35	40	45	
Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu			
50	55	60	
His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val			
65	70	75	80
Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe			
85	90	95	
Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln			
100	105	110	
Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu			
115	120	125	
Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser			
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Asn Pro Ala			
145			

<210> 1047

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(979)

<223> RXA01878

<400> 1047

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                                         Met Glu Glu Pro Ser
                                         1                               5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag 163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys
                        10                        15                        20

ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat 211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp
                        25                        30                        35

ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac 259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn
                        40                        45                        50

gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc 307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala
                        55                        60                        65

ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt 355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg
                        70                        75                        80                        85

ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt 403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu
                        90                        95                        100

gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa 451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln
                        105                        110                        115

tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac 499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr
                        120                        125                        130

aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc 547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr
                        135                        140                        145

atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg 595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu
                        150                        155                        160                        165

gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg 643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala
                        170                        175                        180

tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc 691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val
                        185                        190                        195

ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg
                        200                        205                        210

gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787

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Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp
 215 220 225
 ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct 835
 Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala
 230 235 240 245
 gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
 250 255 260
 cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275
 act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys
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 tgaaaattac cgctaaggcg tgg 1002

<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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 20 25 30
 Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala
 35 40 45
 Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60
 Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80
 Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95
 Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110
 Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val
 115 120 125
 Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140
 Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160
 Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
 275 280 285

Gln Lys Asp Glu Lys
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<210> 1049

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02281

<400> 1049

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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat	403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	
90 95 100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg	451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	
105 110 115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt	499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att	1075
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile	
310 315 320 325	

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac 1171
 Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
 345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac 1219
 Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
 360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc 1267
 Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
 375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga 1315
 Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
 390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg 1363
 Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
 410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac 1411
 Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
 425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa 1459
 Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
 440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg 1507
 Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
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 Thr Leu Gly Glu Val Pro Phe Arg
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<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

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 20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu	Ser	Lys	Pro	Arg	Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu		
				85						90						95	
Arg	Leu	Thr	Ser	Asn	Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp		
			100						105							110	
Ile	Arg	Ile	Pro	Pro	Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu		
		115						120								125	
Ala	Arg	Arg	Ala	Gly	Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu		
		130						135								140	
Asp	Glu	Val	His	Asp	Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn		
		145						150								155	
Gly	Pro	Glu	Leu	Pro	Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile		
			165						170							175	
Ala	Cys	Ala	Arg	Ile	Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val		
			180						185							190	
Gln	Lys	Tyr	Ile	Leu	Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe		
		195						200								205	
Val	His	Phe	Ala	Met	Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val		
		210						215								220	
Gly	Leu	Ser	Leu	Pro	Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr		
		225						230								235	
Ser	Leu	Gly	Thr	Glu	Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro		
			245						250							255	
Arg	Tyr	Asp	Leu	Ile	Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn		
		260						265								270	
Ile	Gly	Val	Gly	Pro	Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala		
		275						280								285	
Val	Leu	Arg	Pro	Glu	Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met		
		290						295								300	
Asp	Ala	Arg	Met	Arg	Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln		
		305						310								315	
Arg	Glu	Asp	His	Ile	Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile		
			325						330							335	
Pro	Ala	Ile	Pro	Glu	Ile	Gln	Lys	Ala	Leu	Glu	Ala	Ser	Val	Asp	Glu		
		340						345								350	
Ile	Tyr	Gly	Ser	Asp	Asn	Ser	Leu	Met	Arg	Thr	Gly	Thr	Val	Leu	Ser		
		355						360								365	
Thr	Asp	Asp	Arg	Asn	Trp	Glu	Trp	His	Thr	Pro	Glu	Asn	Leu	Trp	Asn		
		370						375								380	
Trp	Leu	Lys	Gly	Ser	Thr	Ala	Ala	Ala	Val	Asp	Met	Glu	Ser	Ser	Thr		
		385						390								395	
															400		

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Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
			105					110					115			

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Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	
120 125 130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac	547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	
135 140 145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg	595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	
150 155 160 165	
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc	643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	
170 175 180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg	691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	
185 190 195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg	739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	
200 205 210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca	787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	
215 220 225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa	835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	
230 235 240 245	
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc	883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	
250 255 260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca	931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	
265 270 275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa	979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	
280 285 290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc	1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	
295 300 305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att	1075
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile	
310 315 320 325	
ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa	1123
Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu	
330 335 340	
atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc	1168
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<210> 1052

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 1052

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300

Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320

Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350

Ile Tyr Gly Ser
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<210> 1053

<211> 1146

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1123)

<223> RXN01240

<400> 1053

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ctgcacagga aagtttagcgg cgctactatg aacgatcgat atg tct gac aac act 115
 Met Ser Asp Asn Thr
 1 5

ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163
 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro
 10 15 20

atg gcc gac gtc gaa ttc ctc cta gca att gaa gaa tta ctt acg gac 211
 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp
 25 30 35

ggg ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser
 40 45 50

agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc 355
 Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile
 70 75 80 85

acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa 403
 Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln
 90 95 100

gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc 451
 Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg
 105 110 115

atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc 499
 Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val
 120 125 130

gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa 547
 Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu
 135 140 145

gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac 595
 Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His
 150 155 160 165

gat atc cgc tat aaa cgc gcc gat gtg tcc aac cca gaa gac ttc agc 643
 Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser
 170 175 180

gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta 691
 Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu
 185 190 195

gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga 739
 Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg
 200 205 210

gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt 787
 Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val
 215 220 225

ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac 835
 Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn
 230 235 240 245

tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg 883
 Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val
 250 255 260

gtg cag ctg cgc gag ctg ctc aac ccc acc gac att gaa gtg ctg ttg 931
 Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu
 265 270 275

aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac 979
 Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp
 280 285 290

gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc 1027
 Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val
 295 300 305

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa 1075
 Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys
 310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac 1123
 Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu Val Glu Pro Pro Asn
 330 335 340

taaagttccc ccaaagtttag ccc 1146

<210> 1054

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

Met Ser Asp Asn Thr Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe
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Arg Arg Ala His Pro Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu
20 25 30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu
210 215 220

Thr Leu Pro Gly Val Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg
225 230 235 240

Pro Arg Ser Thr Asn Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn
245 250 255

Ser Ile Thr Ser Val Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp
260 265 270

Ile Glu Val Leu Leu Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln
275 280 285

Ile Arg Ile Ile Asp Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His
290 295 300

Ile Asp Ala Thr Val Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg
305 310 315 320

His Arg Gln Leu Lys Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu
325 330 335

Val Glu Pro Pro Asn
340

<210> 1055

<211> 1234

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1234)

<223> RXN02008

<400> 1055

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cttgttggca tccgcatacct ggtagacaac gtgaacaact gtg tac gcc gcc atc 115
Val Tyr Ala Ala Ile
1 5

ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163
Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp
10 15 20

tat att tca gcc ccg cgc ttc ggt gtc tac caa tcc ctg cac acc acc 211
Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr
25 30 35

gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259
Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His
40 45 50

gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307
Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala His Trp Arg Tyr
55 60 65

aaa gaa acc aaa ggc agc cac agt ggc gag caa gcc gaa gtg gat caa 355
Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln Ala Glu Val Asp Gln
70 75 80 85

atg gcg tgg atg cgc caa ctt ctg gac tgg caa aaa gaa gca gcc gac 403
Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln Lys Glu Ala Ala Asp
90 95 100

ccc aac gag ttc ctg gac agc ctg cgc tac gat ctg act tcc aag cag 451
Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp Leu Thr Ser Lys Gln
105 110 115

atc ttc gtg ttc aca ccc aaa ggt gat gtg gtc aac ctg ccg gtg aac 499
Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val Asn Leu Pro Val Asn
120 125 130

tcc acc ccg gtg gac ttc gcc tac gcg gtg cac acc gaa gtg ggg cac 547

BGI-121CP-1402-1055-1234-DNA-CDS-RXN02008-Corynebacterium glutamicum

Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His	Thr	Glu	Val	Gly	His	
135						140					145					
cgc	tgc	atc	ggc	gcc	aaa	atc	aac	ggc	aaa	ctg	gtc	gct	ttg	gaa	acg	595
Arg	Cys	Ile	Gly	Ala	Lys	Ile	Asn	Gly	Lys	Leu	Val	Ala	Leu	Glu	Thr	
150					155					160					165	
aaa	ctc	aaa	tcc	ggc	gat	cgt	gtt	gaa	gtc	ttt	acc	tcc	aag	gac	caa	643
Lys	Leu	Lys	Ser	Gly	Asp	Arg	Val	Glu	Val	Phe	Thr	Ser	Lys	Asp	Gln	
				170					175					180		
aac	gct	ggc	cca	agt	agg	gga	tgg	caa	gaa	ttt	gtt	gtc	tca	cct	cgt	691
Asn	Ala	Gly	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe	Val	Val	Ser	Pro	Arg	
			185					190					195			
gca	aag	gcc	aag	att	cgc	cag	tgg	ttt	gcc	aag	gaa	cga	cgc	gaa	gaa	739
Ala	Lys	Ala	Lys	Ile	Arg	Gln	Trp	Phe	Ala	Lys	Glu	Arg	Arg	Glu	Glu	
		200					205					210				
tac	cta	gaa	gcc	gga	cgc	gat	gcg	ctg	gca	gca	gtt	att	cag	cgt	ggc	787
Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala	Val	Ile	Gln	Arg	Gly	
	215					220					225					
ggc	ctg	cca	atg	cac	cgc	ttg	ttc	acc	gcg	tcc	tcc	atg	aag	acg	gtg	835
Gly	Leu	Pro	Met	His	Arg	Leu	Phe	Thr	Ala	Ser	Ser	Met	Lys	Thr	Val	
230					235					240					245	
gca	aca	gag	ctg	cac	tac	cca	gat	gta	gat	gcg	ctc	tac	aca	gcc	atc	883
Ala	Thr	Glu	Leu	His	Tyr	Pro	Asp	Val	Asp	Ala	Leu	Tyr	Thr	Ala	Ile	
				250					255					260		
ggc	tcc	ggg	tct	gta	tct	gcg	caa	cac	gta	gtc	aac	cgt	ctc	atg	gct	931
Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val	Asn	Arg	Leu	Met	Ala	
			265				270						275			
atc	ttt	ggg	gac	gaa	gaa	gat	gcc	gaa	gac	gca	ttg	gtt	gca	cgc	acc	979
Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr	
		280					285					290				
cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc	1027
Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr	Glu	Ser	Ser	Thr	
	295					300					305					
ggc	atc	ctg	gtc	gaa	ggc	agc	cca	gat	gtc	atg	gct	aag	ctc	gct	aaa	1075
Gly	Ile	Leu	Val	Glu	Gly	Ser	Pro	Asp	Val	Met	Ala	Lys	Leu	Ala	Lys	
310					315					320					325	
tgc	tgt	atg	cca	gtg	cca	gga	gat	gaa	atc	ttt	gga	ttc	gtc	acc	cgt	1123
Cys	Cys	Met	Pro	Val	Pro	Gly	Asp	Glu	Ile	Phe	Gly	Phe	Val	Thr	Arg	
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ggg	ggc	ggg	gt													

375

<210> 1056

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

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Val Tyr Ala Ala Ile Gly Val Val His Ser Leu Phe Asn Ala Leu Pro
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Gly Arg Phe Lys Asp Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln
      20             25             30

Ser Leu His Thr Thr Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val
      35             40             45

Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala
      50             55             60

Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln
      65             70             75             80

Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln
      85             90             95

Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp
      100            105            110

Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val
      115            120            125

Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His
      130            135            140

Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu
      145            150            155            160

Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe
      165            170            175

Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe
      180            185            190

Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys
      195            200            205

Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala
      210            215            220

Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser
      225            230            235            240

Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala
      245            250            255

Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val
      260            265            270

Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala

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275	280	285
Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr		
290	295	300
Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met		
305	310	315
Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe		
325	330	335
Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys		
340	345	350
Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val		
355	360	365
Ser Trp Ala Ser Glu Gly Gln Gly Ser Val		
370	375	

<210> 1057
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXN01940

<400> 1057
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 Met Thr Thr Lys Ile
 1 5
 atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc 163
 Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu
 10 15 20
 gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc 211
 Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly
 25 30 35
 ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc 259
 Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala
 40 45 50
 acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca 307
 Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro
 55 60 65
 ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc 355
 Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly
 70 75 80 85
 atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa 403
 Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu
 90 95 100

gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag 451
 Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu
 105 110 115

ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg 499
 Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala
 120 125 130

ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt 547
 Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val
 135 140 145

gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct 595
 Val Leu Met Gly Gly Glu Tyr His Val Gly Asn Trp Thr Ala Val Ala
 150 155 160 165

gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac 643
 Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn
 170 175 180

gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg 691
 Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala
 185 190 195

ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac 739
 Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp
 200 205 210

gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac 787
 Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr
 215 220 225

cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct 835
 Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala
 230 235 240 245

gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca 883
 Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro
 250 255 260

ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag 1027
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys
 295 300 305

cgc atc gga tagacctgtt cacaaggttg tta 1059
 Arg Ile Gly
 310

<210> 1058

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 1058

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Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn
      35             40             45

Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg
      50             55             60

Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile
      65             70             75             80

His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro
      85             90             95

Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr
      100             105             110

Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro
      115             120             125

Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu
      130             135             140

Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn
      145             150             155             160

Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala
      165             170             175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp
      180             185             190

Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn
      195             200             205

Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala
      210             215             220

Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val
      225             230             235             240

His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr
      245             250             255

Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr
      260             265             270

Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr
      275             280             285

Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val
      290             295             300

Ile Asp Ala Val Lys Arg Ile Gly

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305

310

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<211> 602

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(579)

<223> FRXA01940

<400> 1059

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gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc	96
Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu	
20 25 30	
atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc	144
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe	
35 40 45	
aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag	192
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys	
50 55 60	
tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca	240
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala	
65 70 75 80	
aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc	288
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala	
85 90 95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac	336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp	
100 105 110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca	384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala	
115 120 125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat	432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp	
130 135 140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc	480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe	
145 150 155 160	
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg	528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu	
165 170 175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc	576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile	
180 185 190	

gga tagacctgtt cacaaggttg tta
Gly

<210> 1060

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 1060

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20 25 30

Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe
35 40 45

Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys
50 55 60

Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala
65 70 75 80

Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala
85 90 95

Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp
100 105 110

Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala
115 120 125

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp
130 135 140

Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe
145 150 155 160

Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu
165 170 175

Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile
180 185 190

Gly

<210> 1061

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA02559

<400> 1061

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 Met Ile Pro Val Leu
 1 5

atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu
 10 15 20

gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr
 25 30 35

acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp
 40 45 50

gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln
 55 60 65

cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly
 70 75 80 85

gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu
 90 95 100

ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
 Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
 120 125 130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
 Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
 135 140 145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
 Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
 150 155 160 165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
 Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
 170 175 180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
 Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
 185 190 195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
 Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
 200 205 210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787

Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
 215 220 225
 gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
 Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
 230 235 240 245
 cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
 Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
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 ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931
 Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
 265 270 275
 cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
 Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
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 Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala
 35 40 45
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro
 50 55 60
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr
 65 70 75 80
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His
 85 90 95
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu
 100 105 110
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu
 115 120 125
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr
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 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile

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																							Val	Arg	Leu	Gly	Val	5					
																							1										
tta																		gat	gtg	ggc	agc	aat	act	gtc	cac	cta	gtt	gca	gta	gac	gcg	cgt	163
Leu																		Asp	Val	Gly	Ser	Asn	Thr	Val	His	Leu	Val	Ala	Val	Asp	Ala	Arg	
																					10					15					20		
ccc																		ggt	gga	cac	ccc	acc	ccg	atg	agc	aat	tgg	cgt	acc	cca	ctg	cgc	211
Pro																		Gly	Gly	His	Pro	Thr	Pro	Met	Ser	Asn	Trp	Arg	Thr	Pro	Leu	Arg	
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ctt																		gtt	gag	ctt	ctt	gat	gac	tcc	ggg	gcg	atc	tcc	gaa	aag	ggc	atc	259
Leu																		Val	Glu	Leu	Leu	Asp	Asp	Ser	Gly	Ala	Ile	Ser	Glu	Lys	Gly	Ile	
																			40					45					50				
aac																		aaa	ctc	acc	tca	gca	gtc	ggg	gaa	gca	gca	gac	cta	gcg	aaa	acg	307
Asn																		Lys	Leu	Thr	Ser	Ala	Val	Gly	Glu	Ala	Ala	Asp	Leu	Ala	Lys	Thr	
																		55					60					65					
ctc																		ggc	tgc	gct	gaa	ctg	atg	cca	ttt	gct	aca	tcg	gca	gtc	cgc	tcc	355

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<213> Corynebacterium glutamicum

<400> 1064

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Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
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Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
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Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
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Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
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Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
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Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
      115              120              125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
      130              135              140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
      145              150              155              160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
      165              170              175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
      180              185              190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
      195              200              205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
      210              215              220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
      225              230              235              240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
      245              250              255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
      260              265              270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
      275              280              285

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Asp Lys Gly Leu Glu
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<222> (101)..(2203)

<223> RXN01079

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 Met Asp Phe His Ala
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ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259
 Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu
 40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307
 Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe
 55 60 65

cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355
 Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg
 70 75 80 85

ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403
 Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu
 90 95 100

aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451
 Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val
 105 110 115

tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499
 Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu
 120 125 130

aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547
 Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro
 135 140 145

acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595

Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys		
150					155					160					165		
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643	
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile		
				170					175					180			
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggg	ggc	gta	gcg	ttg	ctg	691	
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu		
			185					190					195				
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggg	gca	ccg	att	aag	aag	att	gaa	aac	739	
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn		
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cag	tct	tcc	ggg	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787	
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe		
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tcc	tac	gct	aac	cag	ctg	ggg	gct	cgt	cag	ggg	gca	ggg	gct	gtg	tac	835	
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr		
		230			235				240						245		
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883	
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg		
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gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggg	gtt	931	
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val		
			265				270						275				
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979	
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met		
		280					285					290					
tac	ctg	ttc	tcc	cca	tac	gat	gtg	gag	cgc	att	tac	ggc	aag	cct	ttc	1027	
Tyr	Leu	Phe	Ser	Pro	Tyr	Asp	Val	Glu	Arg	Ile	Tyr	Gly	Lys	Pro	Phe		
		295				300					305						
gca	gac	gtc	tca	atc	acc	gag	cac	tac	gac	gag	atg	gtg	gat	gat	gac	1075	
Ala	Asp	Val	Ser	Ile	Thr	Glu	His	Tyr	Asp	Glu	Met	Val	Asp	Asp	Asp		
		310			315					320					325		
cgc	atc	cgc	aag	acc	aag	atc	aac	gcg	cgt	cag	ttc	ttc	cag	acc	ctg	1123	
Arg	Ile	Arg	Lys	Thr	Lys	Ile	Asn	Ala	Arg	Gln	Phe	Phe	Gln	Thr	Leu		
				330					335					340			
gca	gaa	atc	cag	ttc	gag	tcc	ggg	tac	cca	tac	atc	atg	tat	gaa	gac	1171	
Ala	Glu	Ile	Gln	Phe	Glu	Ser	Gly	Tyr	Pro	Tyr	Ile	Met	Tyr	Glu	Asp		
			345					350					355				
acc	gtg	aat	gca	tcc	aac	cca	atc	gaa	ggg	cgc	atc	acc	cac	tca	aac	1219	
Thr	Val	Asn	Ala	Ser	Asn	Pro	Ile	Glu	Gly	Arg	Ile	Thr	His	Ser	Asn		
			360				365					370					
ctg	tgc	tct	gag	atc	ctt	cag	gtg	tcc	acc	cca	tct	gaa	ttc	aac	gat	1267	
Leu	Cys	Ser	Glu	Ile	Leu	Gln	Val	Ser	Thr	Pro	Ser	Glu	Phe	Asn	Asp		
		375				380					385						
gac	ctg	act	tac	gca	gag	gtc	ggc	gaa	gac	att	tct	tgt	aac	ttg	ggg	1315	
Asp	Leu	Thr	Tyr	Ala	Glu	Val	Gly	Glu	Asp	Ile	Ser	Cys	Asn	Leu	Gly		

390	395	400	405	
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc				1363
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr				
410		415	420	
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc				1411
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser				
425		430	435	
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc				1459
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala				
440		445	450	
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac				1507
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His				
455		460	465	
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt				1555
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe				
470		475	480	485
gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act				1603
Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr				
490		495	500	
gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc				1651
Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr				
505		510	515	
ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc				1699
Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser				
520		525	530	
gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc				1747
Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr				
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Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu				
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Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr				
570		575	580	
atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag				1891
Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu				
585		590	595	
atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac				1939
Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His				
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atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc				1987
Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly				
615		620	625	
tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac				2035
Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp				
630		635	640	645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt 2083
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gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc 2131
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 665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt 2179
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Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
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Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
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Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
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Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
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Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile

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Tyr	Gly	Lys	Pro	Phe	Ala	Asp	Val	Ser	Ile	Thr	Glu	His	Tyr	Asp	Glu
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Asn	Phe	Glu	Lys	Thr	Ile	Glu	Thr	Glu	Ile	Arg	Gly	Leu	Thr	Ala	Val
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Pro	Glu	Gln	Thr	Ser	Ile	Asp	Ser	Val	Pro	Ser	Ile	Arg	Lys	Gly	Asn
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Glu	Ala	Ala	His	Ala	Ile	Gly	Leu	Gly	Gln	Met	Asn	Leu	His	Gly	Tyr
	450					455					460				
Phe	Gly	Arg	Glu	His	Met	His	Tyr	Gly	Ser	Glu	Glu	Ala	Leu	Asp	Phe
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Thr	Asn	Ala	Tyr	Phe	Ala	Ala	Val	Leu	Tyr	Gln	Cys	Leu	Arg	Ala	Ser
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Asn	Gln	Ile	Ala	Thr	Glu	Arg	Gly	Glu	Arg	Phe	Lys	Asn	Phe	Glu	Asn
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Ser	Lys	Tyr	Ala	Thr	Gly	Glu	Tyr	Phe	Asp	Asp	Phe	Asp	Ala	Asn	Asp
		515					520					525			

Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn
530 535 540

Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val
545 550 555 560

Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr
565 570 575

Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile
580 585 590

Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr
595 600 605

Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp
610 615 620

Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala
625 630 635 640

Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp
645 650 655

Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg
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Met Asp Phe His Ala
1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
		40					45					50				
gtt	gaa	aac	aag	tac	tat	gac	cca	atc	gtt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60					65					
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
	70				75					80					85	
ttc	cag	tcc	ttc	ctc	ggc	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90					95					100		
aag	acc	ttc	gac	ggc	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
		105						110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
	150				155					160					165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggc	gta	gca	ttg	ctg		691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190				195				
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggc	gca	ccg	att	aag	aag	att	gaa	atc	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Ile	
		200					205					210				
cag	tct	tcc	ggc	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220					225					
tcc																790
Ser																
230																

<210> 1068

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 1068

Met	Asp	Phe	His	Ala	Leu	Asn	Ala	Leu	Leu	Asn	Leu	Tyr	Asp	Asp	Asn	
1				5					10						15	

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
 20 25 30
 Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
 35 40 45
 Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
 50 55 60
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220
 Leu Glu Asp Ala Phe Ser
 225 230

<210> 1069

<211> 1364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1341)

<223> FRXA01084

<400> 1069

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 Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
 1 5 10 15

aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg 96
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag 144
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45

cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac 192
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60

gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg 240
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80

cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac 288
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95

cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa 336
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110

ggt cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc 384
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125

acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa 432
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140

gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat 480
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160

gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act 528
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175

gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag 576
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190

ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac 624
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205

ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg 672
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220

gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt 720
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240

gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc 768
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255

gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca 816
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala
 260 265 270

aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag 864
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285

tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc 912
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac 1008
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc 1056
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc 1104
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct 1152
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc 1200
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca 1248
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt 1296
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg 1341
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
 435 440 445

taaaagcact taaaaatata ccc 1364

<210> 1070

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
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Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45

Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala
 260 265 270
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
370 375 380

Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
385 390 395 400

Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
405 410 415

Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
420 425 430

Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
435 440 445

<210> 1071

<211> 1125

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1102)

<223> RXN01920

<400> 1071

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cgaaaagcaa aaaaatttgt agaagggaag agcgcaccta atg gct gct gat tct 115
Met Ala Ala Asp Ser
1 5

gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163
Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val
10 15 20

aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211
Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val
25 30 35

tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259
Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val
40 45 50

tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307
Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala
55 60 65

gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355
Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln
70 75 80 85

ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403
Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His
90 95 100

gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451
Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala
105 110 115

aag agt tac tcc aac atc ttc atg act ctg gcc tcc acc gcg gaa atc 499
Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala Ser Thr Ala Glu Ile
120 125 130

aac gat gcg ttc cgt tgg tct gag gaa aat gaa aac ctg cag cgc aag 547
Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu Asn Leu Gln Arg Lys
135 140 145

gca aag atc atc ctg tct tac tat gag ggc gat gat cca cta aag cgc 595
Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp Asp Pro Leu Lys Arg
150 155 160 165

aag atc gcc tcc gtg atc ctg gag tcc ttc ctg ttc tac tcc gcc ttc 643
Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu Phe Tyr Ser Gly Phe
170 175 180

tac ctc cca atg tat tgg tcc agc cac tcc aag ctg gcc aac acc gcc 691
Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys Leu Ala Asn Thr Ala
185 190 195

gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac gcc tac tac 739
Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr Tyr
200 205 210

att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag cgt 787
Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu Arg
215 220 225

cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt tac 835
Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu Tyr
230 235 240 245

gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga tgg 883
Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly Trp
250 255 260

acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc ctc 931
Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala Leu
265 270 275

aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag gtg 979
Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys Val
280 285 290

tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac cac 1027
Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn His
295 300 305

gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca gaa 1075
Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala Glu
310 315 320 325

aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 1122
Asn Thr Glu Asp Asp Asp Trp Asp Phe
330

cgc 1125

<210> 1072

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1072

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Met Ala Ala Asp Ser Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu
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His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser
      20           25           30

Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro
      35           40           45

Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn
      50           55           60

Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu
      65           70           75           80

Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp
      85           90           95

Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met
      100          105          110

Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala
      115          120          125

Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu
      130          135          140

Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp
      145          150          155          160

Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu
      165          170          175

Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys
      180          185          190

Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala
      195          200          205

Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys
      210          215          220

Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu
      225          230          235          240

Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr
      245          250          255

Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn
      260          265          270

Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala
      275          280          285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn
      290          295          300

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Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val
305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01920

<400> 1073

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Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
1 5 10 15

tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96
Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
20 25 30

cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144
Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
35 40 45

tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192
Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
50 55 60

tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240
Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
65 70 75 80

ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288
Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
85 90 95

gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336
Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
100 105 110

cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384
His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
115 120 125

gaa aac acc gag gat gat gac tgg gac ttc taactttttaaa aaagctgaag 434
Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
130 135

cgc 437

<210> 1074

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 1074

Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
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 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
 20 25 30
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
 35 40 45
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
 50 55 60
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
 65 70 75 80
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
 85 90 95
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
 100 105 110
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
 115 120 125
 Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 130 135

<210> 1075

<211> 567

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(544)

<223> RXA01080

<400> 1075

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 Met Leu Ile Val Tyr
 1 5
 ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp
 10 15 20
 tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys
 25 30 35
 atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
 40 45 50
 tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg

55	60	65	
ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca			355
Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala			
70	75	80	85
ggg gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc			403
Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile			
	90	95	100
att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg			451
Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met			
	105	110	115
ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac			499
Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn			
	120	125	130
gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga			544
Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg			
	135	140	145
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<210> 1076			
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<400> 1076			
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Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val			
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Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr			
	35	40	45
Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro			
	50	55	60
Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile			
	65	70	75
Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly			
	85	90	95
Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr			
	100	105	110
Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly			
	115	120	125
Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro			
	130	135	140
Val Thr Ser Arg			
145			

<210> 1077

<211> 650

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

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Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	
gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct	576
Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala	
180 185 190	
gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag	624

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

gac taattagttc tggctagatc ggg
 Asp

650

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr
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Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
 20 25 30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

Asp

<210> 1079

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(630)

<223> RXA01416

<400> 1079

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gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca	96
Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro	
20 25 30	
ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt	144
Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val	
35 40 45	
gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag	192
Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu	
50 55 60	
gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg	240
Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu	
65 70 75 80	
ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac	288
Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr	
85 90 95	
atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac	336
Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr	
100 105 110	
agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct	384
Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala	
115 120 125	
gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc	432
Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg	
130 135 140	
atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt	480
Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val	
145 150 155 160	
gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag	528
Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu	
165 170 175	
acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag	576
Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln	
180 185 190	
caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac	624
Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His	
195 200 205	
tac aac	630
Tyr Asn	

210

<210> 1080

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

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Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

Tyr Asn
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<210> 1081

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA01486

<400> 1081

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atcgccgagc agaactaaac atgaggagac ctactcgcac atg agc gat gta aag 115
Met Ser Asp Val Lys
1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
185 190 195

gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739
Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys
200 205 210

acc ttc tcc gac gtc gca 757

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Thr Phe Ser Asp Val Ala
215

<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

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20 25 30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr
35 40 45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn
50 55 60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu
65 70 75 80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg
85 90 95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp
100 105 110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln
115 120 125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val
130 135 140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro
145 150 155 160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu
165 170 175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His
180 185 190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg
195 200 205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala
210 215

<210> 1083

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01678

<400> 1083

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cggtatatatc tctgcaactg cagctcaccc cgggtgcagca atg ctg aaa tgt gca 115
 Met Leu Lys Cys Ala 5
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gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
 Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly 20
 10 15

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
 Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu 35
 25 30

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
 Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val 50
 40 45

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
 Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val 65
 55 60

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
 Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu 85
 70 75 80

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
 Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys 100
 90 95

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
 Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn 115
 105 110

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
 Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr 130
 120 125

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
 Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val 145
 135 140

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
 Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu 165
 150 155 160

aat atc gac gtt gtt ttc gca ggt cac acc cac taagtctgtg atctaggaac 648
 Asn Ile Asp Val Val Phe Ala Gly His Thr His 175
 170

cga 651

<210> 1084

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1084

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Met Leu Lys Cys Ala Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala
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Phe Val Ser Ser Gly Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser
      20          25          30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
      35          40          45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
      50          55          60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
      65          70          75          80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
      85          90          95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
      100          105          110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
      115          120          125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
      130          135          140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
      145          150          155          160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
      165          170          175

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<210> 1085

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA01679

<400> 1085

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ctaagttcgt gatctaggaa cgcacaacgg tccactaatc atg cag tct gga aac      115
                                     Met Gln Ser Gly Asn
                                     1          5

tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc      163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr
      10          15          20

ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc      211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile

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Asn	Ala	Cys	Glu	Asn	Pro	Asp	Asp	Thr	Ile	Ala	Asp	Ile	Val	Ala	Gln																								
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Ala	Glu	Leu	Asp	Ala	Gly	Glu	Ala	Gly	Lys	Glu	Val	Val	Ala	Thr	Ile																								
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Asp	Gly	Asp	Phe	Leu	Arg	Ala	Ser	Asp	Glu	Gly	Ala	Glu	Ser	Gly	Ser																								
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Asn	Tyr	Gly	Ala	Glu	Ser	Gln	Leu	Val	Asn	Met	Ile	Ala	Ser	Ala	Val																								
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cgt	tgg	tcc	atg	tcc	acc	aat	acc	gcc	acc	acc	gca	gac	att	ggg	ctt	451																							
Arg	Trp	Ser	Met	Ser	Thr	Asn	Thr	Ala	Thr	Thr	Ala	Asp	Ile	Gly	Leu																								
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Met	Asn	Ala	Gly	Gly	Leu	His	Thr	Asp	Leu	Phe	Ser	Gly	Asp	Val	Thr																								
120										125										130																			
tac	gcc	gaa	gct	ttt	gaa	atc	cag	cct	ttc	tcc	ggg	gaa	gat	tca	ttt	547																							
Tyr	Ala	Glu	Ala	Phe	Glu	Ile	Gln	Pro	Phe	Ser	Gly	Glu	Asp	Ser	Phe																								
135										140										145																			
gtc	acc	ctc	aag	gga	tca	gtc	ttc	aaa	gat	gcc	ctt	gac	cag	cag	tgg	595																							
Val	Thr	Leu	Lys	Gly	Ser	Val	Phe	Lys	Asp	Ala	Leu	Asp	Gln	Gln	Trp																								
150										155										160										165									
gaa	gaa	ggg	tct	gca	cga	cca	gtg	gca	gca	ctt	ggc	gta	tcc	gac	aac	643																							
Glu	Glu	Gly	Ser	Ala	Arg	Pro	Val	Ala	Ala	Leu	Gly	Val	Ser	Asp	Asn																								
170										175										180																			
gtt	tcc	tac	acc	tac	gac	atc	aac	cgt	cca	atc	ggg	gac	cgc	gtc	act	691																							
Val	Ser	Tyr	Thr	Tyr	Asp	Ile	Asn	Arg	Pro	Ile	Gly	Asp	Arg	Val	Thr																								
185										190										195																			
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Ser	Val	Thr	Ile	Asp	Asp	Thr	Pro	Leu	Asp	Pro	Glu	Arg	Asp	Tyr	Val																								
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gtt	gca	gct	tcc	ctg	tac	ctc	cag	tcc	ggc	aac	gaa	ggg	atg	acc	gca	787																							
Val	Ala	Ala	Ser	Leu	Tyr	Leu	Gln	Ser	Gly	Asn	Glu	Gly	Met	Thr	Ala																								
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230										235										240										245									
tcc	acc	atc	gga	tac	ttg	tcc	aac	aac	aat	gtc	acc	cca	cgt	act	ggg	883																							
Ser	Thr	Ile	Gly	Tyr	Leu	Ser	Asn	Asn	Asn	Val	Thr	Pro	Arg	Thr	Gly																								
250										255										260																			
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Gln	Ala	Gln	Ile	Ser	Ile	Thr	Pro	Ser	Gly	Glu	Phe	Asn	Ala	Gly	Glu																								
265										270										275																			

acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr
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gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca 1027
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro
 295 300 305

att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg 1075
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala
 310 315 320 325

aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc 1123
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu
 330 335 340

gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att 1171
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile
 345 350 355

gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta 1219
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu
 360 365 370

gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta 1267
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu
 375 380 385

gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag 1315
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln
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atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat 1359
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 410

<210> 1086

<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

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Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu
 20 25 30

Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala
 35 40 45

Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu
 50 55 60

Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly
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Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met
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Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr
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 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe
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 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser
 130 135 140
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala
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 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu
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 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile
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 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro
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 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn
 210 215 220
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly
 225 230 235 240
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val
 245 250 255
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu
 260 265 270
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr
 275 280 285
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu
 290 295 300
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly
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 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser
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 Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala
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 Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile
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Met Ser Lys Lys Ala																	
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Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr																	
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His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu																	
120 125 130																	
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Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val																	
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 Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln
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 Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr
 200 205 210

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 Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala
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 Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro
 230 235 240 245

 ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883
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 Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala
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 Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile
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<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 1088

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 Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn
 35 40 45

 Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr
 50 55 60

 Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu
 65 70 75 80

 Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu
 85 90 95

aaacattgtc ctccccattt cttgagtaag ggaaaatacc gtg gcc cgt gta gtt 115
Val Ala Arg Val Val
1 5

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gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163
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gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc 211
Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
      25                      30                      35

cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259
Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
      40                      45                      50

gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307
Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
      55                      60                      65

gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353
Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
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<211> 81

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<213> Corynebacterium glutamicum

<400> 1090

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Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
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Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
      35                      40                      45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
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Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
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Lys

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<211> 498

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(475)

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$\langle 211 \rangle$ 125

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50 55 60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
65 70 75 80

Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
85 90 95

Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
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Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
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<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXC01088

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 Met Gly Leu Trp Ile
 1 5

gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20

gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
 25 30 35

atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
 40 45 50

caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
 55 60 65

cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70 75 80 85

cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403
 Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
 90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451
 Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
 105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499
 His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
 120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547
 Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
 135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595

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<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

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 35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
 50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
 65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
 85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
 100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
 115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
 130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
 145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
 165 170 175

Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
 180 185 190

Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
 195 200 205

Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
 210 215 220

Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
 225 230 235 240

Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
 245 250 255

Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
 260 265 270

Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro

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Thr Thr Phe Gly Ile Arg	Ser Trp Glu Val Glu Arg	Glu Gly Leu Asp
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Arg Arg Phe Glu Gln Val	Glu Val Asp Gly His Thr	Ile Asn Ile Lys
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Ile Gly Ser Arg Asp Asp	Gln Val Ile Ser Ala Gln	Ser Glu Phe Glu
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<212> DNA

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<222> (101)..(1396)

<223> RXC02624

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 Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met
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 Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu
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 Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile
 40 45 50

tca gta ctg ccc acg ctt ccc ggc ttt ata ttc ctc tgg gcc atc gcc 307
 Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala
 55 60 65

gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta 355
 Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu
 70 75 80 85

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Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr	
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 Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu
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 His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly
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 Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
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 Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80
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 Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
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 Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp

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Glu	Val	Glu	Glu	Gly	Val	Glu	Glu	Val	Glu	Glu	Asp	Asp	Ala	Glu	Asp
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Pro	Glu	Glu	Asn	Pro	Glu	Glu	Glu	Glu	Ser	Asp	Glu	Glu	Ile	Glu	Thr
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(580)
 <223> RXC02665

<400> 1097

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Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly
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aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211
Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys
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gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259
Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala
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Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
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ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
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gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
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Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
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gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
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<400> 1098

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Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
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Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
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Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
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Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
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Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
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Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
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Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
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<223> RXC02770

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tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
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caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr

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Arg	Val	Asp	Cys	Val	Ser	Gly	Ser	Lys	Val	Ala	Thr	Val	Val	Phe	Lys															
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Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala	
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Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val	
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Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp	
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Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val	
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His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn	
360 365 370	
gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga	1267
Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly	
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Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys	
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Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser	
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ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag	1411
Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln	
425 430 435	
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Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His	
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Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr	
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agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta	1555
Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu	
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Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val	
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Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp	
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1689

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<212> PRT

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<400> 1100

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 35 40 45

Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
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Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65 70 75 80

Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
 85 90 95

Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
 100 105 110

Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
 115 120 125

Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
 130 135 140

Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
 145 150 155 160

Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
 165 170 175

Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
 180 185 190

Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
 195 200 205

Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
 210 215 220

Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
 225 230 235 240

Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
 245 250 255

Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
 260 265 270

Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
 275 280 285
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
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 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
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 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
 325 330 335
 Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
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 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
 355 360 365
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415
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 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
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 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
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<212> DNA

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Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
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Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
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gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
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tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
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act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
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cac 408

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Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35           40           45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50           55           60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu	
20 25 30	
gag gca cgc atc ctc gac cag cag ctt aaa acc ctg tcc ggc ggc cag	144
Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln	
35 40 45	
cgc cgc cgc gtc gag ttg gcg cag atc ctc ttc gcc gcc acc aac ggc	192
Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly	
50 55 60	
tcc ggc aaa tca aaa acc aca ttg ctt ctc gac gag ccc acc aac cac	240
Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His	
65 70 75 80	
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Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His	
85 90 95	
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Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala	
100 105 110	
gta tgt aac aag att tgg tac ctc gac gca gta cgc agc gaa gcc gat	384
Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp	
115 120 125	
gtc tac aac atg ggc ttt agc aaa tac gtc gat gca cgt gca ctc gat	432
Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp	
130 135 140	
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Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly	
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Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala	
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Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn	
180 185 190	
ctc gac gaa atc cgc gta gct gac cgc gcc gcc aac atc gtt ttc cca	624
Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro	
195 200 205	
gaa cca gca ccc tgt gga aaa acc cca ctc aac gcc aag ggc ctg acc	672

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Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys		
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Gly	Gly	Ile	Val	Thr	Gly	Tyr	Leu	Lys	Ile	Gly	Tyr	Phe	Ala	Gln			
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gaa	cac	gac	acc	atc	gac	ccc	gac	aaa	tcc	gtc	tgg	caa	aac	acc	atc	912	
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gaa	gcc	tgc	gcc	gac	gcc	gac	caa	caa	agc	ctc	cgc	agc	ctc	ctc	gga	960	
Glu	Ala	Cys	Ala	Asp	Ala	Asp	Gln	Gln	Ser	Leu	Arg	Ser	Leu	Leu	Gly		
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Ser	Gly	Gly	Glu	Lys	Thr	Arg	Leu	Ala	Leu	Ala	Thr	Leu	Val	Ser	Ser		
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Arg	Ala	Asn	Val	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	Asn	Leu	Asp	Pro		
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Ile	Ser	Arg	Glu	Gln	Val	Leu	Asp	Ala	Leu	Arg	Thr	Tyr	Thr	Gly	Ala		
	370					375					380						
gtc	gtc	ctg	gtt	acc	cac	gac	ccg	ggg	gca	gtc	aag	gcc	ctt	gag	cca	1200	
Val	Val	Leu	Val	Thr	His	Asp	Pro	Gly	Ala	Val	Lys	Ala	Leu	Glu	Pro		
385					390					395					400		
gaa	cgc	gtc	atc	gtg	ctt	cct	gat	ggc	acc	gag	gat	ctt	tgg	aat	gat	1248	
Glu	Arg	Val	Ile	Val	Leu	Pro	Asp	Gly	Thr	Glu	Asp	Leu	Trp	Asn	Asp		
				405					410				415				
cag	tac	atg	gaa	atc	gtg	gaa	ttg	gcg	taggtttctaa	ggctgtttat						1295	
Gln	Tyr	Met	Glu	Ile	Val	Glu	Leu	Ala									
			420					425									
gct																	1298

<210> 1104

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 1104

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Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
 1           5           10           15

Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
      20           25           30

Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
      35           40           45

Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
      50           55           60

Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
      65           70           75           80

Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
      85           90           95

Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
      100           105           110

Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
      115           120           125

Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
      130           135           140

Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
      145           150           155           160

Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
      165           170           175

Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
      180           185           190

Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
      195           200           205

Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
      210           215           220

Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
      225           230           235           240

Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
      245           250           255

Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
      260           265           270

Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
      275           280           285

Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
      290           295           300

Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly

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<211> 613
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(613)
<223> RXN03171
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cggctcttctt ctggggcggca atgattttaac atgtgaagct atg gac atc acc atc																115
Met Asp Ile Thr Ile																
1 5																
gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag																163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu																
10 15 20																
cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc																211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala																
25 30 35																
atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac																259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp																
40 45 50																
acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca																307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro																
55 60 65																
ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca																355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro																
70 75 80 85																

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1106

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1107

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> FRXA02857

<400> 1107

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cgggtcttctt ctgggcgga atgatttaac atgtgaagct atg gac atc acc atc 115
              Met Asp Ile Thr Ile
              1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
              10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
              25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
              40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
              55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
              70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
              90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
              105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
              120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
              135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
              150 155 160 165

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gac gca ttg gcg gaa tct
 Asp Ala Leu Ala Glu Ser
 170

<210> 1108
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1108
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 Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30
 Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45
 Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60
 Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80
 Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95
 Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110
 Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125
 Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140
 Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160
 Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1109
 <211> 424
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(424)
 <223> RXN00450

<400> 1109
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 gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

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gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
      10              15              20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
      25              30              35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
      40              45              50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
      55              60              65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
      70              75              80              85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
      90              95              100

ggt gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
      105

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<210> 1110

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1110

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Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1              5              10              15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20              25              30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35              40              45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50              55              60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
      65              70              75              80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
      85              90              95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
      100              105

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<210> 1111

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1111

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                                         Val Gly Val Leu Pro
                                         1                               5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
                        10                15                20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
                        25                30                35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
                        40                45                50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
                        55                60                65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
                        70                75                80                85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
                        90                95                100

ggg gct cga atc gga 418
Gly Ala Arg Ile Gly
                        105

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<210> 1112

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1112

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Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1                               5                10                15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20                25                30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35                40                45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50                55                60

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Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80
 Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95
 Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
 100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

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 caagcgctac cagcggttgat gcgagggttg agcgcctaac atg act gaa gat gac 115
 Met Thr Glu Asp Asp
 1 5
 tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
 10 15 20
 cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Val Asp Pro Phe Gly Ala
 25 30 35
 gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
 40 45 50
 cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
 55 60 65
 tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
 70 75 80 85
 atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
 90 95 100
 gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
 105 110 115
 gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
 120 125 130
 ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu

135 140 145

ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
 150 155 160

tagcgctggg catgtgactt taa 615

<210> 1114

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1114

Met Thr Glu Asp Asp Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala
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Thr Gln Ala Leu Lys Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val
 20 25 30

Asp Pro Phe Gly Ala Val Val Phe Glu Asp His Asn Arg Asp Ala Asp
 35 40 45

Gly Asp Leu Thr Lys His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile
 50 55 60

Glu Asn Tyr Ser Ala Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser
 65 70 75 80

Thr Glu His Cys Ala Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu
 85 90 95

Gly Lys Ile Tyr Cys Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr
 100 105 110

Ala Lys Trp Gly Ala Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp
 115 120 125

Lys Ile Ser Pro Asn Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu
 130 135 140

Glu Val Leu Tyr Glu Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro
 145 150 155 160

Asn Lys Ala Leu

<210> 1115

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXA00717

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Val	Thr	Pro	Pro	Ala												
1				5												
cgc	cga	gat	ggc	aca	ccg	gac	aag	aag	cag	agc	aat	cgc	tct	ggc	gga	163
Arg	Arg	Asp	Gly	Thr	Pro	Asp	Lys	Lys	Gln	Ser	Asn	Arg	Ser	Gly	Gly	
			10						15					20		
tac	cgg	tct	tca	gtt	cg	ggc	tac	aag	cca	gga	tca	tcc	cg	cca	aac	211
Tyr	Arg	Ser	Ser	Val	Arg	Gly	Tyr	Lys	Pro	Gly	Ser	Ser	Arg	Pro	Asn	
			25					30					35			
aca	cg	cag	cag	cct	cag	aag	aag	gat	gag	att	ctt	ctc	tcc	aac	gct	259
Thr	Arg	Gln	Gln	Pro	Gln	Lys	Lys	Asp	Glu	Ile	Leu	Leu	Ser	Asn	Ala	
		40					45					50				
aag	cct	gcc	aag	aag	caa	aac	gta	aaa	tcc	gac	gac	gat	tgg	tcg	atg	307
Lys	Pro	Ala	Lys	Lys	Gln	Asn	Val	Lys	Ser	Asp	Asp	Asp	Trp	Ser	Met	
	55					60					65					
ggt	ttc	tta	aac	cg	aat	gac	tct	gac	gga	gtt	cg	ctg	cag	aag	gtg	355
Gly	Phe	Leu	Asn	Arg	Asn	Asp	Ser	Asp	Gly	Val	Arg	Leu	Gln	Lys	Val	
	70				75				80						85	
ctt	gcc	caa	gca	ggt	gtg	gca	tca	cg	cga	cac	gca	gaa	atc	ctg	att	403
Leu	Ala	Gln	Ala	Gly	Val	Ala	Ser	Arg	Arg	His	Ala	Glu	Ile	Leu	Ile	
			90						95					100		
gat	cag	ggc	cg	gtg	gag	gtc	aac	gat	cg	atc	gtg	acc	acc	cag	ggc	451
Asp	Gln	Gly	Arg	Val	Glu	Val	Asn	Asp	Arg	Ile	Val	Thr	Thr	Gln	Gly	
			105					110					115			
gtg	cg	gtg	gat	cca	aac	aac	gat	gtc	atc	cg	gtt	gac	ggc	gtc	cg	499
Val	Arg	Val	Asp	Pro	Asn	Asn	Asp	Val	Ile	Arg	Val	Asp	Gly	Val	Arg	
		120					125					130				
atc	cac	atc	aac	gag	gac	ctc	gag	tac	ttc	gtg	ctc	aac	aag	cct	cg	547
Ile	His	Ile	Asn	Glu	Asp	Leu	Glu	Tyr	Phe	Val	Leu	Asn	Lys	Pro	Arg	
	135					140					145					
ggc	atg	cac	tcc	acc	atg	agc	gat	gaa	ctt	ggt	cg	cca	tgc	gtg	ggt	595
Gly	Met	His	Ser	Thr	Met	Ser	Asp	Glu	Leu	Gly	Arg	Pro	Cys	Val	Gly	
	150				155					160					165	
gat	ctg	gtc	agt	gag	aag	act	gca	tct	gga	cag	cg	ctg	ttc	cac	gtc	643
Asp	Leu	Val	Ser	Glu	Lys	Thr	Ala	Ser	Gly	Gln	Arg	Leu	Phe	His	Val	
			170						175					180		
ggt	cg	ctc	gac	gcg	gac	acc	gaa	ggt	ttg	ctg	ctg	ctc	acc	aac	gat	691
Gly	Arg	Leu	Asp	Ala	Asp	Thr	Glu	Gly	Leu	Leu	Leu	Leu	Thr	Asn	Asp	
			185					190					195			
ggt	gag	ttg	gct	aac	cg	ctc	atg	cac	cct	aag	tac	gaa	gtg	tcc	aag	739
Gly	Glu	Leu	Ala	Asn	Arg	Leu	Met	His	Pro	Lys	Tyr	Glu	Val	Ser	Lys	

gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac 835
 Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp
 230 235 240 245

ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc 883
 Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile
 250 255 260

gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu
 265 270 275

ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val
 280 285 290

cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct 1027
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser
 295 300 305

gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg 1080
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
 310 315 320

cct 1083

<210> 1116
 <211> 320
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1116
 Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser
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 Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly
 20 25 30
 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile
 35 40 45
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp
 50 55 60
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val
 65 70 75 80
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His
 85 90 95
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile
 100 105 110
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg
 115 120 125
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val
 130 135 140
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly

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145              150              155              160
Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln
              165              170              175
Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu
              180              185              190
Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys
              195              200              205
Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr
              210              215              220
Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly
              225              230              235              240
Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys
              245              250              255
Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg
              260              265              270
Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr
              275              280              285
Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg
              290              295              300
Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
              305              310              315              320

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<210> 1117

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01894

<400> 1117

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                                     Met Pro Lys Pro Lys
                                     1           5

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aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163
Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
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ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211
Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
              25              30              35

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tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt	259
Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly	
40 45 50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc	307
Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile	
55 60 65	
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg	355
Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met	
70 75 80 85	
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc	403
Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe	
90 95 100	
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg	451
Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg	
105 110 115	
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga	499
Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly	
120 125 130	
agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt	547
Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly	
135 140 145	
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg	595
Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val	
150 155 160 165	
ggc ggg tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg	643
Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro	
170 175 180	
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc	691
Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val	
185 190 195	
tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac	739
Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His	
200 205 210	
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc	787
His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala	
215 220 225	
acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc	835
Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile	
230 235 240 245	
aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt	883
Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg	
250 255 260	
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt	931
Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser	
265 270 275	
gtg atc agc agc tcg tat ccg tcg taaagcttgg gccagcttta agt	978

Val Ile Ser Ser Ser Tyr Pro Ser
280 285

<210> 1118

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 1118

Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile
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20 25 30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
260 265 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
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<210> 1119

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXA02536

<400> 1119

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 Met Asp Asn Phe Ala
 1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
 10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
 25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
 40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
 55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
 70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
 90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
 105 110 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
 120 125 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
 135 140 145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
 150 155 160 165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala
 170 175 180

ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro
 185 190 195

gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser
 200 205 210

atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu
 215 220 225

cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile
 230 235 240 245

cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879
 Arg Glu Ala Leu Pro Val Leu
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<210> 1120

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 1120

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Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe
 20 25 30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe
 35 40 45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
 50 55 60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr
 65 70 75 80

Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His
 85 90 95

Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu
 100 105 110

Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp
 115 120 125

Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
 130 135 140

Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
 145 150 155 160

Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
 165 170 175

Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
 225 230 235 240

Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 1121

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> RXN01209

<400> 1121

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ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451

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Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln	Cys	Ala	Glu	Thr	Gly		
		120					125					130					
gtg	gca	ttg	ccc	gat	gtg	att	ggc	att	ggg	ccg	gtg	gcc	tct	act	gcg	547	
Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro	Val	Ala	Ser	Thr	Ala		
		135					140					145					
acc	aaa	cca	gat	gcg	gca	ccc	gca	ttg	ggg	gtg	gag	ggc	atc	gct	gag	595	
Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val	Glu	Gly	Ile	Ala	Glu		
		150				155				160					165		
atc	gcc	gct	gta	gct	caa	gac	cac	ggc	atc	gca	tca	gta	gct	att	gga	643	
Ile	Ala	Ala	Val		Gln	Asp	His	Gly	Ile	Ala	Ser	Val	Ala	Ile	Gly		
			170						175					180			
ggc	gtt	ggg	cta	cgc	aac	gcg	gcc	gaa	ctc	gct	gct	acg	ccc	atc	gac	691	
Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala	Ala	Thr	Pro	Ile	Asp		
			185					190					195				
ggg	ctg	tgc	gtg	gtc	tct	gaa	atc	atg	acc	gcc	gcc	aat	cca	gca	gct	739	
Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala	Ala	Asn	Pro	Ala	Ala		
		200					205					210					
gcg	gca	act	cgc	ctg	cgg	act	gct	ttt	caa	cct	act	ttc	tgc	cct	gaa	787	
Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro	Thr	Phe	Ser	Pro	Glu		
		215				220					225						
act	caa	act	gaa	ctc	tct	caa	aca	gaa	ctc	caa	gga	gcc	ttc	gtg	aat	835	
Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln	Gly	Ala	Phe	Val	Asn		
		230				235				240					245		
tgc	cct	tct	gcc	cca	cgt	gtg	ttg	tct	att	gca	ggc	act	gat	ccc	aca	883	
Ser	Pro	Ser	Ala	Pro	Arg	Val	Leu	Ser	Ile	Ala	Gly	Thr	Asp	Pro	Thr		
				250					255					260			
ggg	ggg	gca	ggg	att	cag	gct	gat	ctg	aag	tcc	att	gca	gca	ggg	ggc	931	
Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ser	Ile	Ala	Ala	Gly	Gly		
			265					270					275				
ggc	tac	ggc	atg	tgc	gtt	gtg	acc	tgc	ctg	gtc	gcg	caa	aac	acc	cac	979	
Gly	Tyr	Gly	Met	Cys	Val	Val	Thr	Ser	Leu	Val	Ala	Gln	Asn	Thr	His		
		280					285					290					
ggc	gtc	aac	acg	atc	cac	acc	cca	ccc	ttg	acc	ttt	ttg	gaa	gaa	cag	1027	
Gly	Val	Asn	Thr	Ile	His	Thr	Pro	Pro	Leu	Thr	Phe	Leu	Glu	Glu	Gln		
		295				300					305						
ctg	gaa	gcg	gtc	ttt	tcc	gat	gtc	acc	gtc	gat	gcc	atc	aag	ctc	ggc	1075	
Leu	Glu	Ala	Val	Phe	Ser	Asp	Val	Thr	Val	Asp	Ala	Ile	Lys	Leu	Gly		
		310				315				320					325		
atg	ttg	ggc	tct	gcc	gac	acc	gtc	gat	ctg	gtg	gct	tca	tgg	ctt	ggg	1123	
Met	Leu	Gly	Ser	Ala	Asp	Thr	Val	Asp	Leu	Val	Ala	Ser	Trp	Leu	Gly		
				330					335					340			
tcc	cac	gag	cac	ggg	ccc	gtg	gtg	ctt	gat	ccc	gtc	atg	atc	gcc	acc	1171	
Ser	His	Glu	His	Gly	Pro	Val	Val	Leu	Asp	Pro	Val	Met	Ile	Ala	Thr		

345	350	355	
agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc			1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg			
360	365	370	
ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc			1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala			
375	380	385	
gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct			1315
Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala			
390	395	400	405
cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag			1363
Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys			
410	415	420	
ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc			1411
Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro			
425	430	435	
gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac			1459
Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn			
440	445	450	
tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc			1507
Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile			
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gcc gcc ggc gaa agc gtg gaa			1528
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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp			
35	40	45	
Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys			
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Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu			
65	70	75	80
Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp			
85	90	95	
Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu			
100	105	110	

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
465 470 475

<210> 1123

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> PRXA01209

<400> 1123

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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115
Met Cys Glu Arg Pro
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly
120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala

135	140	145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag			595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu			
150	155	160	165
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga			643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly			
	170	175	180
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac			691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp			
	185	190	195
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct			739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala			
	200	205	210
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa			787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu			
	215	220	225
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat			835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn			
	230	235	240
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca			883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr			
	250	255	260
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc			931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly			
	265	270	275
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac			979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His			
	280	285	290
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag			1027
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln			
	295	300	305
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc			1075
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly			
	310	315	320
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt			1123
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly			
	330	335	340
tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc			1171
Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr			
	345	350	355
agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc			1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg			
	360	365	370
ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc			1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala			
	375	380	385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa 1528
 Ala Ala Gly Glu Ser Val Glu
 470 475

<210> 1124

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
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Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

<210> 1125
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> RXN01617

<400> 1125
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tggttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115
 Leu Ile Leu Lys Thr
 1 5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
 10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
 25 30 35

ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu
 40 45 50

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307
 Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys
 55 60 65

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc 355
 Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg
 70 75 80 85

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu
 90 95 100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu
 105 110 115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val
 120 125 130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu
 135 140 145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp
 150 155 160 165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala
 170 175 180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys
 185 190 195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro
 200 205 210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt aaacaagctc 792
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 215 220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
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Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
 20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr
 85 90 95

Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110

Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125

Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140

Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160

Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175

Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190

Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys
 185 190 195
 cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro
 200 205 210
 ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt aaacaagctc 792
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 215 220
 cct 795
 <210> 1126
 <211> 224
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1126
 Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
 1 5 10 15
 Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
 20 25 30
 Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr
 85 90 95
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205

Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 1127

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA01617

<400> 1127

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Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val	
1 5 10 15	
aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc	96
Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr	
20 25 30	
gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg	144
Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu	
35 40 45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc	192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala	
50 55 60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac	240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn	
65 70 75 80	
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac	288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp	
85 90 95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac	336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr	
100 105 110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac	384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp	
115 120 125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc	432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile	
130 135 140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc	480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile	
145 150 155 160	
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc	528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr	
165 170 175	

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

aaacaagctc cct 638

<210> 1128

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 1128

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg	cgtgtccacc	cttagatcta	caatgtgac	atg	gtt	tcg	aag	atg		115
				Met	Val	Ser	Lys	Met		
				1				5		

cac	att	ccc	ggt	acc	cat	gag	ttc	acg	gtg	aca	gat	act	gaa	ctg	ttg	163
His	Ile	Pro	Gly	Thr	His	Glu	Phe	Thr	Val	Thr	Asp	Thr	Glu	Leu	Leu	
			10						15					20		

tta	gag	tcc	cca	att	ttg	ggc	gtt	cgt	cga	gat	tca	ttg	atc	atg	ccg	211
Leu	Glu	Ser	Pro	Ile	Leu	Gly	Val	Arg	Arg	Asp	Ser	Leu	Ile	Met	Pro	
			25					30					35			

ggt	ggt	tcc	act	gcc	cgc	cgt	gaa	gtg	gtt	gaa	cac	ttt	ggg	gcg	gtc	259
Gly	Gly	Ser	Thr	Ala	Arg	Arg	Glu	Val	Val	Glu	His	Phe	Gly	Ala	Val	
			40				45					50				

gca	gtg	gtt	gcc	ttt	gat	ggt	gaa	aac	att	gcg	atg	gtc	aag	cag	tac	307
Ala	Val	Val	Ala	Phe	Asp	Gly	Glu	Asn	Ile	Ala	Met	Val	Lys	Gln	Tyr	
	55					60					65					

cgt	cgc	agc	gtg	ggg	gat	tcc	ttg	tgg	gag	ctg	cct	gca	ggt	ttg	ttg	355
Arg	Arg	Ser	Val	Gly	Asp	Ser	Leu	Trp	Glu	Leu	Pro	Ala	Gly	Leu	Leu	
	70				75				80					85		

gat	att	gct	gat	gag	gat	gaa	ctc	acg	ggc	gcg	cag	cgc	gag	ctc	atg	403
Asp	Ile	Ala	Asp	Glu	Asp	Glu	Leu	Thr	Gly	Ala	Gln	Arg	Glu	Leu	Met	
			90						95					100		

gag	gag	gct	ggt	ttg	gag	gcc	agt	gag	tgg	tcc	gtg	ctc	act	gat	ttg	451
Glu	Glu	Ala	Gly	Leu	Glu	Ala	Ser	Glu	Trp	Ser	Val	Leu	Thr	Asp	Leu	
			105					110					115			

att	acc	tcg	cct	ggt	ttc	tgc	gat	gaa	gcg	gtg	cgt	gtc	ttt	cta	gcc	499
Ile	Thr	Ser	Pro	Gly	Phe	Cys	Asp	Glu	Ala	Val	Arg	Val	Phe	Leu	Ala	
		120					125					130				

cga	ggc	ctc	aca	aag	gtt	gag	cgc	ccg	aag	gtt	atg	ggc	gat	gaa	gaa	547
Arg	Gly	Leu	Thr	Lys	Val	Glu	Arg	Pro	Lys	Val	Met	Gly	Asp	Glu	Glu	
	135					140					145					

gcg	gac	atg	att	aac	cag	tgg	gtt	ccg	cta	cat	gag	gca	gtg	gga	atg	595
Ala	Asp	Met	Ile	Asn	Gln	Trp	Val	Pro	Leu	His	Glu	Ala	Val	Gly	Met	
	150				155					160					165	

gtg	ttt	agt	ggc	cag	ttg	gtt	aac	tcc	att	gcc	att	gcg	ggt	gtc	atg	643
Val	Phe	Ser	Gly	Gln	Leu	Val	Asn	Ser	Ile	Ala	Ile	Ala	Gly	Val	Met	
			170					175						180		

gct	gct	gat	gct	gtg	att	gcg	ggt	cgt	gcg	tct	gcg	cgt	gcc	gtc	acc	691
Ala	Ala	Asp	Ala	Val	Ile	Ala	Gly	Arg	Ala	Ser	Ala	Arg	Ala	Val	Thr	
			185					190					195			

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
 200 205 210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220

aaa 792

<210> 1130

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr
 1 5 10 15

Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp
 20 25 30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
 35 40 45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
 50 55 60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65 70 75 80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
 85 90 95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
 100 105 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
 210 215 220

<210> 1131
 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> RXC01622

<400> 1131
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gccatgcgag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
 Met Ser Asp Phe Tyr
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403
 Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
 90 95 100

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
 105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
 135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
 150 155 160 165

tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
 170 175 180

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
 185 190 195

cct tca gat aat tagatgagtt ccgaaaattt aaa 726
 Pro Ser Asp Asn
 200

<210> 1132

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
 1 5 10 15

Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
 20 25 30

Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
 35 40 45

Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
 50 55 60

Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
 65 70 75 80

Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
 85 90 95

Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
 100 105 110

Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
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Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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cgttgatcgc	tccagagaca	ccgtgggaag	gggagcagca	gtg	agt	aaa	att	tcg	115
				Val	Ser	Lys	Ile	Ser	
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acg	aaa	ctg	aag	gcc	ctc	acc	gcg	gtg	ctg	tct	gtg	acc	act	ctg	gtg	163
Thr	Lys	Leu	Lys	Ala	Leu	Thr	Ala	Val	Leu	Ser	Val	Thr	Thr	Leu	Val	
				10				15						20		

gct	ggg	tgt	tcc	acg	ctt	ccg	cag	aac	acg	gat	ccg	caa	gtg	ctg	cgc	211
Ala	Gly	Cys	Ser	Thr	Leu	Pro	Gln	Asn	Thr	Asp	Pro	Gln	Val	Leu	Arg	
				25				30					35			

tca	ttt	tcc	ggg	tcc	caa	agc	aca	caa	gag	ata	gca	ggg	ccg	acc	ccg	259
Ser	Phe	Ser	Gly	Ser	Gln	Ser	Thr	Gln	Glu	Ile	Ala	Gly	Pro	Thr	Pro	
			40				45					50				

aat	caa	gat	ccg	gat	ttg	ttg	atc	cgc	ggc	ttc	ttc	agc	gca	ggg	gcg	307
Asn	Gln	Asp	Pro	Asp	Leu	Leu	Ile	Arg	Gly	Phe	Phe	Ser	Ala	Gly	Ala	
			55			60					65					

tat	ccg	act	cag	cag	tat	gaa	gcg	gcg	aag	gcg	tat	ctg	acg	gaa	ggg	355
Tyr	Pro	Thr	Gln	Gln	Tyr	Glu	Ala	Ala	Lys	Ala	Tyr	Leu	Thr	Glu	Gly	
					75					80				85		

acg	cgc	agc	acg	tgg	aat	ccg	gct	gcg	tcg	act	cgt	att	ttg	gat	cgc	403
Thr	Arg	Ser	Thr	Trp	Asn	Pro	Ala	Ala	Ser	Thr	Arg	Ile	Leu	Asp	Arg	
				90					95					100		

att	gat	ctg	aac	act	ctg	cca	ggg	tcg	acg	aat	gcg	gaa	cga	acg	att	451
Ile	Asp	Leu	Asn	Thr	Leu	Pro	Gly	Ser	Thr	Asn	Ala	Glu	Arg	Thr	Ile	
			105					110					115			

gcg	atc	cgt	gga	acg	cag	gtc	gga	acg	ttg	ctc	agc	ggg	ggc	gtg	tat	499
Ala	Ile	Arg	Gly	Thr	Gln	Val	Gly	Thr	Leu	Leu	Ser	Gly	Gly	Val	Tyr	
			120				125					130				

cag	ccg	gag	aat	gcg	gag	ttt	gaa	gct	gag	atc	acg	atg	cgt	cgg	gaa	547
Gln	Pro	Glu	Asn	Ala	Glu	Phe	Glu	Ala	Glu	Ile	Thr	Met	Arg	Arg	Glu	
			135			140					145					

gat	ggg	gag	tgg	cgt	atc	gat	gct	ttg	ccg	gac	ggg	att	tta	tta	gag	595
Asp	Gly	Glu	Trp	Arg	Ile	Asp	Ala	Leu	Pro	Asp	Gly	Ile	Leu	Leu	Glu	
					155				160						165	

aga	aac	gat	ctg	cgg	aac	cat	tac	act	ccg	cac	gat	gtg	tat	ttc	ttt	643
Arg	Asn	Asp	Leu	Arg	Asn	His	Tyr	Thr	Pro	His	Asp	Val	Tyr	Phe	Phe	
			170					175					180			

gat	cct	tct	ggc	cag	gtg	ttg	gtg	ggg	gat	cgg	cgt	tgg	ttg	ttc	aat	691
Asp	Pro	Ser	Gly	Gln	Val	Leu	Val	Gly	Asp	Arg	Arg	Trp	Leu	Phe	Asn	
			185				190						195			

gag	tcg	cag	tcg	atg	tcc	acg	gtg	ctg	atg	gcc	ctt	ctg	gtt	aat	ggg	739
Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala	Leu	Leu	Val	Asn	Gly	

200						205					210					
cct	tcg	ccg	gca	att	tct	cct	ggt	gtg	gtc	aat	cag	ctg	tcc	acg	gat	787
Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	Gln	Leu	Ser	Thr	Asp	
215						220					225					
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggg	ttg	835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu	
230						235					240					245
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg	883
Gly	Asn	Leu	Asp	Asp	Asp	Ala	Arg	Leu	Arg	Phe	Ala	Ala	Gln	Ala	Val	
250						255					260					
tgg	acg	ttg	gcg	cat	gct	gat	gtc	gca	ggc	ccc	tac	act	ttg	gtc	gct	931
Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	Tyr	Thr	Leu	Val	Ala	
265						270					275					
gac	ggc	gcg	ccg	ttg	ctg	tcg	gag	ttc	cca	acg	ctc	acc	acc	gat	gac	979
Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	Leu	Thr	Thr	Asp	Asp	
280						285					290					
ctc	gcc	gaa	tac	aac	cca	gag	gct	tac	acc	aac	acg	gtg	tcc	acg	ttg	1027
Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	Thr	Val	Ser	Thr	Leu	
295						300					305					
ttt	gcg	ttg	cag	gat	gga	tcg	ttg	tcg	agg	gtc	agt	tcc	ggc	aat	gtg	1075
Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	Ser	Ser	Gly	Asn	Val	
310						315					320					325
agt	cca	cta	cag	ggc	att	tgg	agc	ggg	gga	gat	atc	gat	tct	gca	gcg	1123
Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala	
330						335					340					
att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac	1171
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn	
345						350					355					
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg	1219
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala	
360						365					370					
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt	1267
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser	
375						380					385					
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga	1315
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg	
390						395					400					405
tcg	gca	aca	acc	ggg	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg	1363
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu	
410						415					420					
cca	agg	gat	gtg	acg	ggg	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act	1411
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr	
425						430					435					
ggg	gtc	cgg	gcc	gcc	atg	atc	att	gaa	ggc	aag	gtg	tac	gtg	ggc	gtc	1459
Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys	Val	Tyr	Val	Gly	Val	
440						445					450					

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat 1651
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
 520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
 535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
 550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc 1827
 Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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 20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
 35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys

435					440					445					
Val	Tyr	Val	Gly	Val	Val	Thr	Arg	Pro	Gly	Pro	Gly	Glu	Arg	Arg	Val
450					455					460					
Thr	Asn	Ile	Thr	Glu	Val	Ala	Pro	Ser	Leu	Gly	Glu	Ala	Ala	Leu	Ser
465					470					475					480
Ile	Asn	Trp	Arg	Pro	Asp	Gly	Ile	Leu	Leu	Val	Gly	Thr	Ser	Ile	Pro
				485					490					495	
Glu	Thr	Pro	Leu	Trp	Arg	Val	Glu	Gln	Asp	Gly	Ser	Ala	Ile	Ser	Ser
			500					505					510		
Met	Pro	Ser	Gly	Asn	Leu	Ser	Ala	Pro	Val	Val	Ala	Val	Ala	Ser	Ser
			515				520					525			
Ala	Thr	Thr	Val	Tyr	Val	Thr	Asp	Ser	His	Ala	Met	Leu	Gln	Leu	Pro
			530				535					540			
Thr	Ala	Asp	Asn	Asp	Ile	Trp	Arg	Glu	Val	Pro	Gly	Leu	Leu	Gly	Thr
545					550					555					560
Arg	Ala	Ala	Pro	Val	Val	Ala	Tyr								
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<210> 1135

<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXC01709

<400> 1135

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gaaattaggt gtcgatgcag caatacggaa ctttgccaat  gtg ttt gaa caa gct   115
                                   Val Phe Glu Gln Ala
                                   1                               5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg   163
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly
                                   10                               15                               20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc   211
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
                                   25                               30                               35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca   259
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
                                   40                               45                               50

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc   307
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
                                   55                               60                               65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa   355

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Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
 70              75              80              85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
              90              95              100

atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
              105              110              115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
              120              125              130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
              135              140

gat 555

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<210> 1136
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

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<400> 1136
Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly
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Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
              20              25              30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
              35              40              45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
              50              55              60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
              65              70              75              80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
              85              90              95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
              100              105              110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
              115              120              125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
              130              135              140

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<210> 1137
<211> 898

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXC02207

<400> 1137

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																Met	Arg	Arg	Arg	Ser
																1				5

cgt	gtg	tcc	cgt	ttg	ctt	ccc	gcc	aca	gct	ttg	ctg	gcc	tca	act	gca	163
Arg	Val	Ser	Arg	Leu	Leu	Pro	Ala	Thr	Ala	Leu	Leu	Ala	Ser	Thr	Ala	
				10					15					20		

ctt	ctt	tta	agt	gca	tgt	acg	caa	ggg	gta	acg	gac	tcc	ccg	gat	atg	211
Leu	Leu	Leu	Ser	Ala	Cys	Thr	Gln	Gly	Val	Thr	Asp	Ser	Pro	Asp	Met	
			25					30					35			

ggc	aag	gca	act	ccc	gct	gtc	tcc	ccc	gca	gca	agc	aac	ccg	gat	ggc	259
Gly	Lys	Ala	Thr	Pro	Ala	Val	Ser	Pro	Ala	Ala	Ser	Asn	Pro	Asp	Gly	
		40					45					50				

caa	gta	att	gag	ttc	ggc	aac	atc	act	gac	atg	gaa	gtc	act	gat	ggc	307
Gln	Val	Ile	Glu	Phe	Gly	Asn	Ile	Thr	Asp	Met	Glu	Val	Thr	Asp	Gly	
		55				60					65					

gac	atc	ctc	ggc	gta	cgc	acc	gaa	gac	gca	ctc	gct	att	ggc	aca	gtc	355
Asp	Ile	Leu	Gly	Val	Arg	Thr	Glu	Asp	Ala	Leu	Ala	Ile	Gly	Thr	Val	
	70				75				80					85		

tcc	gac	ttc	gaa	gcg	ggc	agc	cag	gtg	gaa	ctg	gac	gtc	gat	aag	caa	403
Ser	Asp	Phe	Glu	Ala	Gly	Ser	Gln	Val	Glu	Leu	Asp	Val	Asp	Lys	Gln	
			90					95						100		

tgc	ggc	gac	ctg	acc	gca	acc	ggc	ggc	act	ttc	gtg	ctc	ccc	tgc	gcc	451
Cys	Gly	Asp	Leu	Thr	Ala	Thr	Gly	Gly	Thr	Phe	Val	Leu	Pro	Cys	Ala	
			105				110						115			

gat	ggc	gtt	tat	ttg	att	gat	gcc	aag	gac	ccg	gat	ctg	gat	gag	ttg	499
Asp	Gly	Val	Tyr	Leu	Ile	Asp	Ala	Lys	Asp	Pro	Asp	Leu	Asp	Glu	Leu	
		120				125						130				

cgt	gca	act	gac	aag	cca	gtc	acg	gtg	gca	gcc	ttg	acc	agc	gat	gat	547
Arg	Ala	Thr	Asp	Lys	Pro	Val	Thr	Val	Ala	Ala	Leu	Thr	Ser	Asp	Asp	
	135					140					145					

cag	ctt	ctg	gtg	ggc	aat	ggc	gaa	gat	gaa	gaa	ctc	acc	atc	tac	cgc	595
Gln	Leu	Leu	Val	Gly	Asn	Gly	Glu	Asp	Glu	Glu	Leu	Thr	Ile	Tyr	Arg	
	150				155				160						165	

gag	ggc	gaa	gag	cca	gaa	acc	ttc	acc	gtc	gcg	ggc	ccc	aat	acc	cag	643
Glu	Gly	Glu	Glu	Pro	Glu	Thr	Phe	Thr	Val	Ala	Gly	Pro	Asn	Thr	Gln	
				170					175					180		

ctc	atc	gcc	gtt	cct	gtc	att	gat	cgc	cac	gac	gcc	gtt	gtg	cgc	acc	691
Leu	Ile	Ala	Val	Pro	Val	Ile	Asp	Arg	His	Asp	Ala	Val	Val	Arg	Thr	

185	190	195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt			739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg			
200	205	210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt			787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly			
215	220	225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att			835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile			
230	235	240	245
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc			883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro			
250	255	260	
cac cga cga gga acc			898
His Arg Arg Gly Thr			
265			

<210> 1138

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 1138

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
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Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
 180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
 195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
 210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
 225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
 245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
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<210> 1139

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<222> (101)..(868)

<223> RXA00347

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 Met Thr Leu Thr Ile
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gag gaa atc gcc aag acc aaa aag ctt ttg gtt gtg tcc gat ttt gat 163
 Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val Val Ser Asp Phe Asp
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gga acc atc gca gga ttt agc aag gac gct tac aac gtt cct atc aac 211
 Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr Asn Val Pro Ile Asn
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cag aaa tcc ctc aag gcg gta aaa gac ctc tcc caa caa gca gac act 259
 Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser Gln Gln Ala Asp Thr
 40 45 50

gat gtt gtc att ttg tcg gga cgt cac ctg gag gga ttg aag acg gtt 307
 Asp Val Val Ile Leu Ser Gly Arg His Leu Glu Gly Leu Lys Thr Val
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ctt gat ctt ggt cag tac gac atc acc atg gtg ggt tca cac ggt tct 355
 Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val Gly Ser His Gly Ser
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 Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro Glu Glu Val Ala Arg
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Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg Val Leu His Phe Ile
      120                125                130

cgt gtt tcc gac aag gac aaa gtc caa gga atc ctc gcc caa gca gca 547
Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile Leu Ala Gln Ala Ala
      135                140                145

cac gta gac tct tcc ggc ctg aag gtt act aac ggc aag agc atc atc 595
His Val Asp Ser Ser Gly Leu Lys Val Thr Asn Gly Lys Ser Ile Ile
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Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr Trp Leu Lys Glu Tyr
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Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr
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acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac 787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp
      215                220                225

gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc 835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg
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Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser
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Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu
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 Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro
 85 90 95
 Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile
 100 105 110
 Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg
 115 120 125
 Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile
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 Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn
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 Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr
 165 170 175
 Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe
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 Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn
 195 200 205
 Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala
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 Met Ala Arg Pro Ile
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Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu	
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Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala	
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Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile	
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Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala	
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Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His	
90 95 100	
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Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu	
105 110 115	
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Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp	
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His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly	
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Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr	
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Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu	
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Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val	
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Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His	
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Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly	
230 235 240 245	
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Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu	
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 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
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 aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355
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 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His
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 Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp
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 His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly
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 Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr
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 Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val
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 aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat 787
 Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His
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 Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly
 230 235 240 245
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 Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu
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 cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa 931

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Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro	Arg	Leu	Ala	Val	Asp		
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Thr	Glu	Asp	Lys	Leu	Ser	Glu	Thr	Ile	Ile	Glu	Leu	Val	Ala	Ala	Met		
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Pro	Val	Tyr	Arg	Ala	Asp	Tyr	Ile	Ser	Leu	Ser	Arg	Thr	Thr	Ala	Thr		
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Phe	Ala	Gln	Val	Cys	Gly	Ala	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr		
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Thr	Phe	Tyr	Arg	Ala	Ser	Arg	Leu	Val	Ala	Leu	Gln	Glu	Val	Gly	Gly		
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Ala	Pro	Gly	Arg	Phe	Gly	Val	Ser	Ala	Ala	Glu	Phe	His	Leu	Leu	Gln		
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Glu	Glu	Arg	Ser	Leu	Leu	Trp	Pro	Arg	Thr	Met	Thr	Thr	Leu	Ser	Thr		
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 65 70 75 80

 Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
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 Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
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 Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
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 Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
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 Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
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 Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
 165 170 175

 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg
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 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg

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225					230					235					240	
Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Asp	His	Pro	Asp	Gly	Leu	Ser	Asp	
245					250					255						
Pro	Phe	Gly	Tyr	Leu	His	Arg	Leu	Arg	Asp	Leu	Ile	Gly	Pro	Asp	Arg	
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Trp	Leu	Ile	Ile	Glu	Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro	
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Glu	Ala	Lys	Ile	Arg	Phe	Ala	Gln	Val	Cys	Gly	Ala	Val	Met	Ala	Lys	
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Gln	Glu	Val	Gly	Gly	Ala	Pro	Gly	Arg	Phe	Gly	Val	Ser	Ala	Ala	Glu	
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Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Gly	Glu	Asp	Thr	Arg	Ala	
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Arg	Ile	Ile	Ser	Leu	Ser	Glu	Val	Pro	Asp	Met	Tyr	Ser	Glu	Leu	Val	
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 545 550 555 560
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
 565 570 575
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe
 580 585 590
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
 595 600 605
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
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 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
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 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
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 Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp
 675 680 685
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
 690 695 700
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
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 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
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 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA01239

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 Met Ala Arg Pro Ile
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tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
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ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu
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aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala
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atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
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 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His
 90 95 100

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 Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu
 105 110 115

aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg 499
 Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp
 120 125 130

cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt 547
 His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly
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gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag 595
 Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu
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gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg 691
 Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu
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cac	aga	ctc	cgc	gac	ctc	att	gga	cct	gac	cgc	tgg	ctg	atc	atc	gaa	931	
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Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro	Arg	Leu	Ala	Val	Asp		
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Ser	Arg	Glu	Ser	Glu	Asp	Lys	Phe	Ser	Met	Leu	Ala	Leu	Thr	His	Ser		
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Ala	Arg	Ala	Met	Arg	Arg	Asp	Asn	Phe	Ser	Thr	Ala	Gly	Thr	Asn	Val		
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Pro	Val	Tyr	Arg	Ala	Asp	Tyr	Ile	Ser	Leu	Ser	Arg	Thr	Thr	Ala	Thr		
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gtc	atc	gcg	gag	atg	tcc	aaa	cgc	ttc	ccc	tcc	cgg	cgt	gac	gca	ctc	1363	
Val	Ile	Ala	Glu	Met	Ser	Lys	Arg	Phe	Pro	Ser	Arg	Arg	Asp	Ala	Leu		
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Asp	Leu	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Asn	Gly	Glu	Ala	Lys	Ile	Arg		
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cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu 505 510 515			1651
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 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
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 gaa ttt cgt gca agc ttt gtt ggt gga gat cat cag gca gta ttt ggc 2275
 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
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 gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac 2323
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp
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 cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc 2371
 Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
 745 750 755
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 Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly
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 Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
 775 780 785
 cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta 2515
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<210> 1144

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1144

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 35 40 45
 Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
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 Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
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 Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
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 Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
 100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
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 Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
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 Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
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 Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
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 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg
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 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp
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 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg
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 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro
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 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu
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 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu
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 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu
 370 375 380
 Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser
 385 390 395 400
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser
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 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly
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625					630					635					640	
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Gln	Ala	Val	Phe	Gly	Glu	Gly	Arg	Ala	Glu	Ser	His	Ile	Met	Gly	Ile	
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Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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<210> 1145

<211> 1953

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1930)

<223> RXA02645

<400> 1145

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Met Leu Lys Asp Leu
1 5

acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca 163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser
10 15 20

cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg 211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met
25 30 35

ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta 259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val
40 45 50

cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc 307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly
55 60 65

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Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly
70 75 80 85

ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc 403
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro
90 95 100

cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc 451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser
105 110 115

gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc 499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu
120 125 130

cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat 547

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Asp	Gly	Asn	Tyr	Asn	Gly	Gln	Phe	Gly	Pro	Tyr	Thr	Ser	Gly	Gly	Ser		
230					235				240						245		
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Thr	Gly	Trp	Gly	Asp	Val	Val	Asn	Ile	Asn	Gly	His	Asp	Ser	Asp	Glu		
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Ser	Gly	Glu	Arg	Asn	Gly	Tyr	Tyr	Ser	Asp	Phe	Gly	Ser	Val	Asp	Thr		
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tta	gcc	aaa	acc	ctg	cgt	gaa	gta	ttt	gaa	cac	acc	gga	aac	tac	tcc	1267	
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Thr	Tyr	Arg	Gly	Arg	Asn	His	Gly	Arg	Pro	Val	His	Pro	Asp	Ile	Thr					
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cct	gcc	tcg	cgc	ttt	gtc	acc	tac	acc	acc	acc	cat	gat	cag	acc	ggc	1363				
Pro	Ala	Ser	Arg	Phe	Val	Thr	Tyr	Thr	Thr	Thr	His	Asp	Gln	Thr	Gly					
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Cys	Ser	His	Thr	Asp	Pro	Glu	Leu	Asn	Arg	Leu	Thr	Ser	Glu	Gly	Arg					
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His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala
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Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys
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Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly
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Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly
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Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro
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Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
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Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His
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Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile
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His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln
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Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His
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Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met

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Leu	Asp	Trp	Glu	Phe	Thr	Ala	Glu	Gln	Arg	Arg	Ile	Asn	Asp	Ala	Tyr
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Lys	Gln	Leu	Leu	His	Leu	Arg	His	Thr	Leu	Gly	Phe	Ser	Gln	Pro	Asn
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	Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn					
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 244
 PRT
 Corynebacterium glutamicum
 1148

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 Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Ala Ser Cys
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 Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile
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 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp
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 120 125 130

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Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe
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Ile	Lys	Pro	Ser	Gln	Ile	Ile	Ala	Ser	Gly	Ile	Val	Val	Leu	Leu	Ala		
230					235					240					245		
ggc	ttg	aca	ctc	gtg	caa	tct	ctg	cag	gac	ggc	atc	acg	ggc	gct	ccg	883	
Gly	Leu	Thr	Leu	Val	Gln	Ser	Leu	Gln	Asp	Gly	Ile	Thr	Gly	Ala	Pro		
				250					255					260			
gtg	aca	gca	agt	gca	cga	ttt	ttc	gaa	aca	ctc	ctg	ttt	acc	ggc	ggc	931	
Val	Thr	Ala	Ser	Ala	Arg	Phe	Phe	Glu	Thr	Leu	Leu	Phe	Thr	Gly	Gly		
			265					270					275				
att	gtt	gct	ggc	gtg	ggc	ttg	ggc	att	cag	ctt	tct	gaa	atc	ttg	cat	979	
Ile	Val	Ala	Gly	Val	Gly	Leu	Ile	Gln	Leu	Ser	Glu	Ile	Leu	His			
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gtc	atg	ttg	cct	gcc	atg	gag	tcc	gct	gca	gca	cct	aat	tat	tcg	tct	1027	
Val	Met	Leu	Pro	Ala	Met	Glu	Ser	Ala	Ala	Ala	Pro	Asn	Tyr	Ser	Ser		
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Val	Gly	Cys	Tyr	Ala	Glu	Trp	Ser	Ser	Val	Ile	Ile	Ala	Gly	Leu	Thr		
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gcg	ctg	atg	ggc	tct	gcg	ttt	tat	tac	ctc	ttc	gtt	gtt	tat	tta	ggc	1171	
Ala	Leu	Met	Gly	Ser	Ala	Phe	Tyr	Tyr	Leu	Phe	Val	Val	Tyr	Leu	Gly		
			345					350					355				
ccc	gtc	tct	gcc	gct	gcg	att	gct	gca	aca	gca	gtt	ggc	ttc	act	ggc	1219	
Pro	Val	Ser	Ala	Ala	Ala	Ile	Ala	Ala	Thr	Ala	Val	Gly	Phe	Thr	Gly		
		360					365					370					
ggc	ttg	ctt	gcc	cgt	cga	ttc	ttg	att	cca	ccg	ttg	att	gtg	gcg	att	1267	
Gly	Leu	Leu	Ala	Arg	Arg	Phe	Leu	Ile	Pro	Pro	Leu	Ile	Val	Ala	Ile		
		375				380					385						
gcc	ggc	atc	aca	cca	atg	ctt	cca	ggc	cta	gca	att	tac	cgc	gga	atg	1315	
Ala	Gly	Ile	Thr	Pro	Met	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Arg	Gly	Met		
390					395					400					405		
tac	gcc	acc	ctg	aat	gat	caa	aca	ctc	atg	ggc	ttc	acc	aac	att	gcg	1363	
Tyr	Ala	Thr	Leu	Asn	Asp	Gln	Thr	Leu	Met	Gly	Phe	Thr	Asn	Ile	Ala		
				410					415					420			
gtt	gct	tta	gcc	act	gct	tca	tca	ctt	gcc	gct	ggc	gtg	gtt	ttg	ggc	1411	
Val	Ala	Leu	Ala	Thr	Ala	Ser	Ser	Leu	Ala	Ala	Gly	Val	Val	Leu	Gly		
			425					430					435				
gag	tgg	att	gcc	cgc	agg	cta	cgt	cgt	cca	cca	cgc	ttc	aac	cca	tac	1459	
Glu	Trp	Ile	Ala	Arg	Arg	Leu	Arg	Arg	Pro	Pro	Arg	Phe	Asn	Pro	Tyr		
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cgt	gca	ttt	acc	aag	gcg	aat	gag	ttc	tcc	ttc	cag	gag	gaa	gct	gag	1507	
Arg	Ala	Phe	Thr	Lys	Ala	Asn	Glu	Phe	Ser	Phe	Gln	Glu	Glu	Ala	Glu		

455 460 465

cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc 1555
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 Gly Asn Lys Arg

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<212> PRT

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<400> 1152

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 20 25 30

Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly
 35 40 45

Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
 50 55 60

Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
 65 70 75 80

Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
 85 90 95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
 100 105 110

Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
 115 120 125

Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
 130 135 140

Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
 145 150 155 160

Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
 165 170 175

Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
 180 185 190

Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
 195 200 205

Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
 210 215 220

Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
 225 230 235 240

Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
 245 250 255
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
 260 265 270
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
 275 280 285
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
 290 295 300
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
 305 310 315 320
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
 325 330 335
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe
 340 345 350
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
 355 360 365
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
 370 375 380
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
 385 390 395 400
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
 405 410 415
 Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
 420 425 430
 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
 435 440 445
 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
 450 455 460
 Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys
 465 470 475 480
 Thr Asn Gln Arg Phe Gly Asn Lys Arg
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<211> 440

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(417)

<223> RXS03183

<400> 1153

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 1 5 10 15
 aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
 20 25 30
 aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
 35 40 45
 atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
 50 55 60
 cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
 65 70 75 80
 cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
 85 90 95
 cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
 100 105 110
 gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
 115 120 125
 gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser
 130 135
 ttc 440

<210> 1154

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 1154

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 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
 20 25 30
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
 35 40 45
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
 50 55 60
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
 65 70 75 80
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg

	85		90		95
Pro Val Ser	Pro Phe Tyr	Pro Ala Ile	Ser Lys Ala	Ile Gln Asp	Asn
	100		105		110
Ala Tyr Ala	Ala Leu Asn	Gly Asn Val	Asp Val Asp	Gln Ala Thr	Thr
	115		120		125
Asp Met Lys	Ala Ala Ile	Glu Asn Ala	Ser Ser		
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<223> RXC00874

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				Met Ser Ile Gly Gln	
				1 5	

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac	163
His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp	
	10 15 20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct	211
Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala	
	25 30 35

gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat	259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp	
	40 45 50

ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc	307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe	
	55 60 65

gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca	355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro	
	70 75 80 85

ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa	403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys	
	90 95 100

gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat	451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp	
	105 110 115

gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc	499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile	
	120 125 130

ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc	547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa	643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
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Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
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Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc	835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga	931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	
265 270 275	
cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc	979
Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser	
280 285 290	
atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac	1027
Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn	
295 300 305	
gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa	1075
Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln	
310 315 320 325	
gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc	1123
Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala	
330 335 340	
tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg	1171
Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala	
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<400> 1156

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Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
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Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
          50           55           60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
          65           70           75           80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
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Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
          100          105          110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
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Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
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Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
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Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
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Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
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Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
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Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
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Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
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His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
          245          250          255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
          260          265          270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
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Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His

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290					295					300						
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Ser	Ile	Glu	Asp	Gln	Glu	Leu	Leu	Asn	Ala	Tyr	Ile	Leu	Asp	Lys	Ala	
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Leu	Tyr	Glu	Val	Ala	Tyr	Glu	Ile	Asn	Asn	Arg	Pro	Asp	Trp	Val	Lys	
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Ile	Pro	Leu	Glu	Ala	Val	Glu	Arg	Leu	Leu	Asp						
		355					360									